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(54) Title: METHODS OF DETECTING SOFT TISSUE SARCOMA, COMPOSITIONS AND METHODS OF SCREENING FOR SOFT TISSUE SARCOMA MODULATORS

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of soft tissue sarcoma cancer phenotypes and soft tissue sarcoma cancer-associated diseases. Also described herein are methods that can be used to identify modulators of soft tissue sarcoma cancer



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METHODS OF DETECTING SOFT TISSUE SARCOMA,
COMPOSITIONS AND METHODS OF SCREENING FOR SOFT
TISSUE SARCOMA MODULATORS

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PRIORITY INFORMATION

This application claims the benefit of U.S. Provisional Application No.
60/429,739, filed November 26, 2002.

FIELD OF THE INVENTION

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The invention relates to the identification of nucleic acid and protein
expression profiles and nucleic acids, products, and antibodies thereto that are
involved in soft tissue sarcomas; and to the use of such expression profiles and
compositions in diagnosis and therapy of such cancers. The invention further relates
to methods for identifying and using agents and/or targets that modulate these
cancers.

15

BACKGROUND OF THE INVENTION

Background on Soft Tissue Sarcomas is available, e.g., from Montgomery and
Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker; ISBN:
0824702905; Brennan, et al. "Soft tissue sarcoma" pp 1738-1788 in DeVita, et al.
(eds. 1997) Cancer: Principles and Practice of Oncology (5th ed.) Lippincott-Raven
Philadelphia, PA; Pisters, et al. (2001) Cancer Management: A Multidisciplinary
Approach (5th ed.) PRR; p 127-137 in American Joint Committee on Cancer (1992)
Manual for Staging of Cancer (4th ed.) Lippincott, . Philadelphia; Schajowicz (1994)
Tumors and Tumor-like Lesions of Bone: Pathology, Radiology and Treatment (2d
ed.) Springer-Verlag, NY; Cotran, et al. (1999) Pathologic Basis of Disease Saunders;
and various websites, e.g., NCI, Memorial Sloan-Kettering Cancer Center;
cancerindex.com; cancersource.com; cancernetwork.com; and sarcoma.net.

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Soft-tissue sarcomas are rare, representing only about 1 percent of all cancer
cases. According to the American Cancer Society, approximately 8,700 new cases of
soft-tissue sarcoma are diagnosed each year in adults and children in the United
States. The age-adjusted incidence is 2 cases per 100,000 persons. There is a slight
male predominance, with a male to female ratio of 11:10. The age distribution in

adult soft-tissue sarcoma studies is: <40 years, 20.7% of patients; 40-60 years, 27.6% of patients; > 60 years, 51.7% of patients.

In the United States, of the 8,700 new cases of soft-tissue sarcoma are identified annually, 4,400 patients die of the disease each year. The five-year survival percentages of soft tissue sarcomas range from 30% to 95% based on subtype and grade. The range for extremity sarcomas is 90%-95%, for trunk sarcomas 50%-75%, and for retroperitoneal lesions 30%-50%. In each of the three locations, higher-grade sarcomas have a poorer survival rate.

In a survey of approximately 5,000 soft-tissue sarcoma patients admitted to Memorial Sloan-Kettering Cancer Center from 1982 to 2001: 32 percent of sarcomas were found in the lower extremities; 18 percent in the viscera (organs located within the chest and abdomen, such as the stomach, kidney, uterus, etc.); 15 percent in the abdominal and retroperitoneal region; 13 percent in the upper extremities; 8 percent in the trunk and 14 percent in other sites.

The histological subtypes of soft tissue sarcomas include malignant fibrous histiocytoma, liposarcoma, fibrosarcoma, synovial sarcoma, rhabdomyosarcoma, and leiomyosarcoma. They occur over 50% of the time in extremities; the remainder occur in the head and neck and retroperitoneum. In addition, many of these tumors dedifferentiate. This results in a variety of overlapping patterns, making uniform classification difficult. The current histopathologic classification is based on the putative cell of origin of each lesion. Such classification based on histogenesis is reproducible for the more differentiated tumors. However, as the degree of histologic differentiation declines, it becomes increasingly difficult to determine cellular origin.

Liposarcomas are malignant tumors that develop from fat tissue. They can develop anywhere in the body, but they most often grow in the retroperitoneum (tissue at the back of the abdominal cavity). Fat tissue may also originate from other locations, usually in the arms, legs, or body cavities.

Rhabdomyosarcomas are malignant tumors that resemble developing skeletal muscle. These tumors most commonly grow in the arms or legs, but can also develop in the head or neck area, as well as the urinary and reproductive organs.

Synovial sarcomas are malignant tumors made up of cells that resemble the cells in joints. ("Synovial cells" line the joints.) However, synovial sarcomas do not necessarily arise in a joint, and the name is probably a misnomer, since the cancer

cells are probably quite different from normal joint cells. Synovial sarcomas can arise in any location in the body, and they often appear in young adults.

Fibrosarcomas are cancer of the fibroblast-type cells in the body. Fibroblasts form scars and do other important connective functions. Fibrosarcomas often occur in tendons and ligaments (fibrous tissue), usually in the arms, legs, or trunk. Fibrosarcomas are rare, accounting for fewer than 7% of primary malignant bone tumors. The five- and ten-year survival rates after radical surgery have been reported at 28% and 21.8%, respectively.

Chondrosarcomas are tumors of cells that form cartilage. Chondrosarcomas account for approximately 14% of malignant bone tumors. The incidence is greatest in individuals between 30 and 60 years of age, and among males. The most frequent sites of chondrosarcomas include the pelvic bone, long bones, scapula, and ribs. Less frequent sites include bones of the hand and foot, the nose, the maxilla, and the base of the skull. At present, chondrosarcomas remain nearly totally refractory to chemotherapeutic efforts inasmuch as chondrosarcomas usually have a poor blood supply. Consequently, drugs given intravenously generally do not reach the tumor in concentrations that are high enough to be therapeutically effective.

Malignant Fibrous Histiocytomas occur most commonly in the extremities (70-75%, with lower extremities accounting for 59% of cases), followed by the retroperitoneum. Tumors typically arise in deep fascia or skeletal muscle.

Leiomyosarcomas are malignant tumors that develop from smooth muscle tissue. They can arise anywhere in the body but the uterus or gastrointestinal tract are two relatively common locations.

In the majority of cases of soft-tissue sarcoma, no specific etiologic agent is identifiable. More commonly, an injury brings a preexisting neoplasm to the attention of the individual. However, a number of predisposing factors have been recognized.

Soft tissue sarcomas occur with greater frequency in patients with von Recklinghausen's disease (neurofibromatosis), Gardner's syndrome, Werner's syndrome, tuberous sclerosis, basal cell nevus syndrome, and among Li-Fraumeni kindreds (p53 mutations). The occurrences of bone tumors are also associated with hyperpara-thyroidism, chronic osteomyelitis, old bone infarct, osteochondromas, and enchondromas. Immunosuppressed patients such as renal transplant recipients and persons with autoimmune deficiency syndrome (AIDS) have a higher risk for soft tissue sarcomas.

Soft-tissue sarcomas have been reported to originate in radiation fields following therapeutic radiation for a variety of solid tumors. Exposure to various chemicals in specific occupations or situations has been linked with the development of soft-tissue sarcoma. These include the phenoxy acetic acids (forestry and
5 agriculture workers), chlorophenols (sawmill workers), Thorotrast (diagnostic x-ray technicians), vinyl chloride (individuals working with this gas, used in making plastics and as a refrigerant), and arsenic (vineyard workers).

Soft-tissue sarcomas have been reported after previous exposure to alkylating chemotherapeutic agents, most commonly after treatment of pediatric acute
10 lymphocytic leukemia.

Related conditions include Reactive pseudosarcomatous proliferans (non-neoplastic lesions that mimic sarcomas), nodular fasciitis (infiltrative or pseudosarcomatous fasciitis), proliferative fasciitis, proliferative myositis, myositis ossificans, malignant giant cell tumor, malignant lymphoma of bone (reticulum cell
15 sarcoma), Ewing's tumor (Ewing's sarcoma) and Osteosarcoma (osteogenic sarcoma).

Signs and symptoms of soft-tissue sarcoma depend, in large part, on the anatomic site of origin. Since 50% of soft-tissue sarcomas arise in an extremity, the majority of patients present with a palpable soft-tissue mass. Pain at presentation is noted in only one-third of cases.

20 Because there are so many varied subtypes, and because their characteristics are so different, the risk and seriousness of soft-tissue sarcomas can vary widely. In some patients, sarcomas are minor, non-threatening tumors that can be cured with simple surgical excision. In others, the tumors can be large and much more aggressive, and require chemotherapy and radiation therapy as well as surgery. In
25 addition, the capacity of sarcomas to metastasize to other sites also varies widely. If metastasis occurs, it can sometimes be cured with surgery, but at other times it can be a life-threatening problem. In general, bone and soft tissue tumors tend to involve contiguous tissue and muscle, and aggressively metastasize early to the lungs via the hematogenous route. Occasionally, soft tissue sarcomas can spread to regional lymph
30 nodes.

The prognosis for patients with adult soft tissue sarcomas depends on several factors, including the patient's age and the size, histologic grade, and stage of the tumor. Factors associated with a poorer prognosis include age older than 60 years of age, tumors larger than 5 centimeters, or high-grade histology. While low-grade

tumors are usually curable by surgery alone, higher-grade sarcomas (as determined by the mitotic index and the presence of hemorrhage and necrosis) are associated with higher local treatment failure rates and increased metastatic potential. Some histological subtypes such as rhabdomyosarcomas, synovial sarcomas, and malignant histiocyto-
5 mas are considered poor prognosticators due to their high grade. If there is distant metastasis to the lymph nodes, lungs, or other bones, the prognosis is also lowered.

Standard treatment options include: Surgical excision, surgical excision with preoperative or postoperative radiation therapy, and if the tumor is unresectable, high-
10 dose preoperative radiation therapy may be used, followed by surgical resection and postoperative radiation therapy. Today, doctors often give chemotherapy (Doxorubicin and ifosfamide) before surgery to patients with large, fast-growing sarcomas.

The development of advanced surgical techniques (e.g., microvascular tissue transfer, bone and joint replacement, and vascular reconstruction) and the application of multimodality approaches have allowed most patients to retain a functional extremity without any compromise in survival. Limb-sparing surgery employing adjuvant radiation to facilitate maximal local control has become the standard approach for large (T2) extremity soft-tissue sarcomas. In most centers, upwards of
15 90% of patients are treated with limb-sparing approaches. Amputation is reserved as a last resort option for local control, and is used with the knowledge that it does not affect survival.

Improved methods of diagnosis and prognosis of soft tissue sarcomas and effective treatment would be desirable. Accordingly, provided herein are methods
25 that can be used in earlier diagnosis and prognosis of such cancers. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, them. Additionally provided herein are molecular targets and compositions for therapeutic intervention in these and other metastatic cancers.

30 SUMMARY OF THE INVENTION

The present invention provides compositions and methods for detecting or modulating soft tissue sarcoma associated sequences.

In one aspect, the invention provides a method of detecting a sarcoma cancer-associated transcript in a cell in a patient, the method comprising contacting a

biological sample from the patient with a polynucleotide that selectively hybridized to a sequence at least 80% identical to a sequence as shown in Tables 1A-11C. In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, such as mRNA.

5 In another embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide. Often, the polynucleotide comprises a sequence as shown in the Tables. The polynucleotide can be labeled, e.g., with a fluorescent label and can be immobilized on a solid surface.

10 In other embodiments the patient is undergoing a therapeutic regimen to treat a disease associated with these sarcomas or the patient is suspected of having a sarcoma-associated disorder.

In another aspect, the invention comprises an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in the Tables. The nucleic acid
15 molecule can be labeled, e.g., with a fluorescent or radioactive label.

In other aspects, the invention provides an expression vector comprising an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in the Tables or a host cell comprising the expression vector.

In another aspect, the invention provides an isolated polypeptide which is
20 encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-11C.

In another embodiment, the invention provides an antibody that specifically binds a polypeptide which is encoded by a nucleotide sequence of the Tables. The antibody can be conjugated or fused to an effector component such as a fluorescent
25 label, a toxin, or a radioisotope. In some embodiments, the antibody is an antibody fragment or a humanized antibody.

In another aspect, the invention provides a method of detecting a cell undergoing such a cancer in a biological sample from a patient, the method comprising contacting the biological sample with an antibody that specifically binds
30 to a polypeptide encoded by a nucleotide sequence of Tables 1A-11C. In some embodiments, the antibody is further conjugated or fused to an effector component, e.g., a fluorescent label.

In another embodiment, the invention provides a method of detecting antibodies specific to a sarcoma in a patient, the method comprising contacting a

biological sample from the patient with a polypeptide which is encoded by a nucleotide sequence of Tables 1A-11C.

The invention also provides a method of identifying a compound that modulates the activity of a sarcoma-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a polypeptide encoded by a nucleotide sequence of Tables 1A-11C; and (ii) detecting an increase or a decrease in the activity of the polypeptide. In one embodiment, the polypeptide is encoded by a nucleotide sequence of Tables 1A-11C. In another embodiment, the polypeptide is expressed in a cell.

The invention also provides a method of identifying a compound that modulates the sarcoma, the method comprising steps of: (i) contacting the compound with a cell undergoing such cancer; and (ii) detecting an increase or a decrease in the expression of a polypeptide encoded by a nucleotide sequence of the Tables. In one embodiment, the detecting step comprises hybridizing a nucleic acid sample from the cell with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in the Tables. In another embodiment, the method further comprises detecting an increase or decrease in the expression of a second sequence encoded by a nucleotide sequence of the Tables.

In another embodiment, the invention provides a method of inhibiting neoplastic properties in a cell that expresses a polypeptide at least 80% identical to a sequence encoded by a nucleotide sequence of Tables 1A-11C, the method comprising the step of contacting the cell with a therapeutically effective amount of an inhibitor of the polypeptide. In one embodiment, the polypeptide is encoded by a nucleotide sequence of Tables 1A-11C. In another embodiment, the inhibitor is an antibody.

Other aspects of the invention will become apparent by the following description of the invention.

Tables 1A-11C provide nucleotide sequence of genes that exhibit changes in expression levels as a function of time in tissue involved in cancer compared to normal or unaffected tissue.

DETAILED DESCRIPTION OF THE TABLES

Table 1A lists about 523 genes upregulated in chondrosarcoma relative to normal body tissues. These genes were selected from 59680 probesets on the

Eos/Affymetrix Hu03 GENECHIP[®] (DNA microchip) array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 2A lists about 763 genes upregulated in dermatofibrosarcoma protuberans relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GENECHIP[®] array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 3A lists about 625 genes upregulated in fibrosarcoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GENECHIP[®] array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 4A lists about 906 genes upregulated in liposarcoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GENECHIP[®] array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 5A lists about 595 genes upregulated in synovial sarcoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GENECHIP[®] array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 6A lists about 977 genes upregulated in rhabdomyosarcoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GENECHIP[®] array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 7A lists about 973 genes upregulated in soft tissue sarcomas relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GENECHIP[®] array. Gene expression data for each probeset

obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 8A lists about 712 genes upregulated in soft tissue sarcomas relative to normal soft tissues (muscle, skin, bone, adipose tissue). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GENECHIP[®] array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 9A lists about 1078 genes upregulated in malignant fibrous histiocytoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GENECHIP[®] array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 10A lists about 501 genes upregulated in soft tissue sarcoma relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 GENECHIP[®] array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Tables 1B-11B list the accession numbers for those Pkey's lacking UnigeneID's for tables 1A – 11A, respectively. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 1C-11C list the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in tables 1A-11A, respectively. For each predicted exon,

genomic sequence source used for prediction is also listed and cross-referenced.
Nucleotide locations of each predicted exon are also listed.

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

5 In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for soft tissue sarcomas cancer (sometimes referred to herein as sarcoma disorders or STSD), as well as methods for screening for compositions which modulate those cancers or similar disorders. Also provided are methods for treating these cancers and related conditions.

10 In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively recognize those markers. For example, therapeutic methods may take the

15 form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of soft tissue sarcoma cancer or related diseases, which subsets may

20 actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to

25 determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Related conditions to these soft tissue sarcomas include, e.g., soft tissue

30 tumors (e.g., fibrosarcoma, liposarcoma, leiomyosarcoma, histiocytoma, fibrohistiocytic sarcoma), smooth muscle tumors (e.g., rhabdomyoma, rhabdomyosarcoma) tumors of the blood and lymph vessels (e.g., angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma), perivascular tumors (e.g., glomus tumors, hemangiopericytoma), synovial tumors (e.g., mesothelioma), neural tumors (e.g.,

neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, extraskeletal Ewing's sarcoma, schwannoma, neuroma, ganglioneuroma), paraganglioma, extraskeletal cartilaginous and osseous tumors (e.g., chondrosarcoma, osteosarcoma),
5 pluripotential mesenchymal tumors, epithelioid sarcomas, rhabdoid tumors, desmoplastic small cell tumors, and alveolar sarcomas. These markers may be similarly useful for addressing these related conditions, e.g., diagnosis, therapy, prognosis, etc.

Tables 1A-11C provide unigene cluster identification numbers for the
10 nucleotide sequence of genes that exhibit increased or decreased expression in soft tissue sarcoma cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

15 The term "soft tissue sarcoma cancer protein" or "soft tissue sarcoma cancer polynucleotide" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 92%, 94%, 96%, 97%, 98%, or 99% or greater nucleotide sequence
20 identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-11C; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence of Tables 1A-11C, and conservatively modified variants thereof; (3) specifically hybridize under
25 stringent hybridization conditions to an anti-sense strand corresponding to a nucleic acid sequence of Tables 1A-11C and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of
30 at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-11C. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "soft tissue sarcoma cancer

polypeptide" and a "soft tissue sarcoma cancer polynucleotide," include both naturally occurring or recombinant forms.

5 A "full length" soft tissue sarcoma cancer protein or nucleic acid refers to a soft tissue sarcoma cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type soft tissue sarcoma cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

10 "Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, and frozen sections taken for histologic purposes. A biological sample is typically obtained from a eukaryotic organism, most preferably a
15 mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a
20 sample of cells from a mammal, such as a human or animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

25 The terms "identical" or "percent identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region,
30 when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site or the like). Such sequences are then said to be "substantially identical." This definition also refers to,

or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or
5 nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are
10 designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

15 A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting of from about 20-600, usually about 50-200, more usually about 100-150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for
20 comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l Acad. Sci. USA 85:2444-2448, by
25 computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

30 Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402; and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the

nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, $M=5$, $N=-4$ and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5787. One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells, e.g., CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of

a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode a given protein. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at a position where an alanine is specified by a codon, the codon can be altered to one of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only

codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

5 As to amino acid sequences, it will be recognized that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" particularly where the alteration results in the substitution of an amino acid with a chemically similar amino
10 acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4)
15 Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M). See, e.g., Creighton (1984) *Proteins: Structure and Molecular Properties* Freeman).

 Macromolecular structures such as polypeptide structures can be described in
20 terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (eds. 2001) *Molecular Biology of the Cell* (4th ed.) Garland; and Cantor and Schimmel (1980) *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three
25 dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure
30 of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) *Oligonucleotides and Analogues: A Practical Approach* Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in US Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) *Carbohydrate Modifications in Antisense Research* ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) *Tetrahedron* 49:1925-1963 and references therein; Letsinger (1970) *J. Org. Chem.* 35:3800-3803; Sprinzl, et al. (1977) *Eur. J. Biochem.* 81:579-589; Letsinger, et al. (1986) *Nuc. Acids Res.* 14:3487-499; Sawai, et al. (1984) *Chem. Lett.* 805; Letsinger, et al. (1988) *J. Am. Chem. Soc.* 110:4470-4471; and Pauwels, et al. (1986) *Chemica Scripta* 26:141-149), phosphorothioate (Mag, et al. (1991) *Nuc. Acids Res.* 19:1437-441; and US Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) *J. Am. Chem. Soc.* 111:2321-322), O-methylphosphoroamidite linkages (see Eckstein (1992) *Oligonucleotides and Analogues: A Practical Approach*, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) *J. Am. Chem. Soc.* 114:1895-1897; Meier, et al. (1992) *Chem. Int. Ed. Engl.* 31:1008-1010; Nielsen (1993) *Nature* 365:566-568; and Carlsson, et al. (1996) *Nature* 380:207). Other analog nucleic acids

include those with positive backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101); non-ionic backbones (US Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597-xxx; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; and Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in US Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. See Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176. Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly useful are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to about 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine,

xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. Useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the soft tissue sarcoma cancer nucleic acids, proteins, and antibodies. Many methods known for conjugating the antibody to the label may be employed. See, e.g., Hunter, et al. (1962) *Nature* 144:945; David, et al. (1974) *Biochemistry* 13:1014-1021; Pain, et al. (1981) *J. Immunol. Meth.* 40:219-230; and Nygren (1982) *J. Histochem. and Cytochem.* 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; chemoattractant or immunomodulating entities; lipases; antibiotics; or radioisotopes, e.g., emitting "hard" beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g.,
5 A, C, G, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences
10 lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select
15 sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the
20 alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by
25 the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operable linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is
30 understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture

of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications, Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a soft tissue sarcoma cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the cancer protein, e.g., a physiological, functional, physical, or chemical effect, such as the ability to increase or decrease soft tissue sarcoma cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a soft tissue sarcoma cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and

protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of soft tissue sarcoma cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of soft tissue sarcoma cancer proteins, e.g., antagonists. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate soft tissue sarcoma cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of soft tissue sarcoma cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of soft tissue sarcoma cancer can also be identified by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more soft tissue sarcoma cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more cancer proteins, such as soft tissue sarcoma cancer proteins comprising the sequences set out in the Tables.

Samples or assays comprising soft tissue sarcoma cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a soft tissue sarcoma cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably

150%, more preferably about 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth or proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney
5 (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2001) Culture of
15 Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology
25 (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100-110 or more

amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-
5 characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab'
10 monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) *Fundamental Immunology* (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, it will be appreciated that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also
15 includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (e.g., McCafferty, et al. (1990) *Nature* 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal
20 antibodies, many techniques can be used. See, e.g., Kohler and Milstein (1975) *Nature* 256:495-497; Kozbor, et al. (1983) *Immunology Today* 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) *Monoclonal Antibodies and Cancer Therapy* Liss; Coligan (1991) *Current Protocols in Immunology* Lippincott; Harlow and Lane (1988) *Antibodies: A Laboratory Manual* CSH Press; and Goding (1986)
25 *Monoclonal Antibodies: Principles and Practice* (2d ed.) Academic Press. Techniques for the production of single chain antibodies (US Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and
30 heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) *Nature* 348:552-554; Marks, et al. (1992) *Biotechnology* 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification, Expression of soft tissue sarcoma cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from sarcoma disorder tissue. By comparing expression profiles of tissue in known different soft tissue sarcoma cancer states, e.g., stages or disease course outcomes, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of cancer processes.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate soft tissue sarcoma cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Cancer tissue can be compared to non-cancerous conditions, or be analyzed to determine the stage of soft tissue sarcoma cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This

may be done by making biochips comprising sets of the important soft tissue sarcoma cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in soft tissue sarcoma cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "soft tissue sarcoma cancer sequences". As outlined below, soft tissue sarcoma cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in disorders associated with soft tissue sarcoma cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In one embodiment, the soft tissue sarcoma cancer sequences are from humans; however, as will be appreciated, soft tissue sarcoma cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other soft tissue sarcoma cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc) and pets (e.g., dogs, cats, etc.). Soft tissue sarcoma cancer sequences from other organisms may be obtained using the techniques outlined below.

Soft tissue sarcoma cancer sequences can include both nucleic acid and amino acid sequences. In one embodiment, the soft tissue sarcoma cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the soft tissue sarcoma cancer sequences.

A soft tissue sarcoma cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying soft tissue sarcoma cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancer tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In another embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In one embodiment, soft tissue sarcoma cancer sequences are those that are up-regulated in soft tissue sarcoma cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is desired.

Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan

(DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and
5 sequencing of isolated nucleic acids.

In another embodiment, soft tissue sarcoma cancer sequences are those that are down-regulated in cancer; that is, the expression of these genes is lower compared to non-cancer tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-
10 fold or higher being useful.

By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid e.g., using polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by
15 ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced
20 recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at
25 least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least
30 about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a soft tissue sarcoma cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made

at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In one embodiment, the soft tissue sarcoma cancer sequences are nucleic acids. Soft tissue sarcoma cancer sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes to the cancer sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) *Oligonucleotides and Analogues: A Practical Approach*, Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in US Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) *Carbohydrate Modifications in Antisense Research ACS Symposium Series 580*. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

Nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly useful are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting

temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of a complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A soft tissue sarcoma cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the soft tissue sarcoma cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying soft tissue sarcoma cancer-associated sequences, the cancer screen typically includes comparing genes identified in cancer cells with genes identified in controls. Samples of normal tissue and tissue associated with soft tissue sarcoma cancer are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate,

small intestine, large intestine, spleen, bone, and placenta. In another embodiment, those genes identified during the cancer screen that are expressed in significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that
5 the target be disease specific, to minimize possible side effects.

In one embodiment, soft tissue sarcoma cancer sequences are those that are up-regulated in soft tissue sarcoma cancer disorders; that is, the expression of these genes is higher in the disease tissue as compared to normal tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three
10 fold change, with at least about five-fold or higher being preferred. Accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. See, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan
15 (DDBJ). In addition, most genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine, and spleen.

In another embodiment, soft tissue sarcoma cancer sequences are those that are down-regulated in the soft tissue sarcoma cancer disorder; that is, the expression
20 of these genes is lower in cancer tissue as compared to normal tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

25 The ability to identify genes that undergo changes in expression with time during soft tissue sarcoma cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with
30 soft tissue sarcoma cancer-associated disease. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation. See Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA. Subcellular toxicological information can also be utilized in a

biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see, US Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

5 Thus, in another embodiment, the present invention provides a database that includes at least one set of data assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on an
10 electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

 The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay
15 data acquired using an assay of the invention.

 The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample exhibiting soft tissue sarcoma cancer, e.g., the identification of soft tissue sarcoma cancer-associated sequences described herein, provide an
20 abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, prior data processing using high-speed computers may be
25 utilized.

 An array of methods for indexing and retrieving biomolecular information is available. For example, US Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein
30 function hierarchies. US Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. US Patent 5,706,498 discloses a gene database

retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. US Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer

5 databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. US Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension.

10 US Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Mount (2001) *Bioinformatics: Sequence and Genome Analysis* CSH Press, NY; Durbin, et

15 al. (eds. 1999) *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* Cambridge Univ. Press; Baxevanis and Ouellette (eds. 1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (2d ed.) Wiley-Liss; Rashidi and Buehler (1999) *Bioinformatics: Basic Applications in Biological Science and Medicine* CRC Press; Setubal, et al. (eds. 1997) *Introduction to Computational Molecular Biology* Brooks/Cole; Misener and Krawetz (eds. 2000) *Bioinformatics: Methods and Protocols* Humana Press; Higgins and Taylor (eds. 2000) *Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach* Oxford Univ. Press; Brown (2001) *Bioinformatics: A Biologist's Guide to Biocomputing and the Internet* Eaton Pub.; Han and Kamber (2000) *Data Mining: Concepts and Techniques* Kaufmann Pub.; and Waterman (1995) *Introduction to Computational Biology: Maps, Sequences, and Genomes* Chap and Hall.

25

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from

30 which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for soft tissue sarcoma

cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3)
5 absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices,
10 including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides
15 such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising
20 performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a
25 peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also may provide a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette
30 or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone

line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from
5 an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data
10 from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In one embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on
15 the degree of identity and gap weight to the target data. A central processor is initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an
20 assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and
25 the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or
30 magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Soft tissue sarcoma cancer-associated sequences

Soft tissue sarcoma cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the soft tissue sarcoma cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus or associated with the intracellular side of the plasma membrane. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes. See, e.g., Alberts, et al. (eds. 1994) *Molecular Biology of the Cell* (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may

provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) *Nuc. Acids Res.* 28:263-266; Sonnhammer, et al. (1997) *Proteins* 28:405-420; Bateman, et al. (1999) *Nuc. Acids Res.* 27:260-262; and Sonnhammer, et al. (1998) *Nuc. Acids Res.* 26:320-322.

10 In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular
15 domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

20 Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell
25 surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed or flanked by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular
30 protein, the localization and number of transmembrane domains within the protein may be predicted. Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor

receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains.

- 5 Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

- Soft tissue sarcoma cancer proteins that are transmembrane are useful in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful markers of neoplastic disease.

- A transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted

proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. Secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Soft tissue sarcoma cancer proteins that are secreted proteins are included in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Soft tissue sarcoma cancer-associated nucleic acids

A soft tissue sarcoma cancer sequence is typically initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. One method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a nucleic acid of Tables 1A-11C, or its complement, or is also found on naturally

occurring mRNAs is considered a soft tissue sarcoma cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g., moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The soft tissue sarcoma cancer nucleic acid sequences of the invention, e.g.,
5 the sequences in Tables 1A-11C, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of the cancer genes can be obtained, using techniques well known for cloning either longer
10 sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences, e.g., systems such as UniGene.

Once the soft tissue sarcoma cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire cancer nucleic
15 acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can be further-used as a probe to identify and isolate other soft tissue sarcoma cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make
20 modified or variant cancer nucleic acids and proteins.

The soft tissue sarcoma cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense
25 applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In another embodiment, nucleic acid probes to soft tissue sarcoma cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the
30 complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be

perfect; there may be a number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In one embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four, or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific

reactive group on either the solid support or the probe or both molecules.

Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways.

- 5 As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or
10 association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and includes, but is not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other
15 materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 00/55627.

- 20 Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

- 25 In one embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes
30 can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using available linkers; e.g., homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages

155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In one embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; US Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GENECHIP[®] (DNA microchip array) technology.

Often, amplification-based assays are performed to measure the expression level of soft tissue sarcoma cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a soft tissue sarcoma cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of soft tissue sarcoma cancer-associated RNA. Methods of quantitative amplification are well known. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TAQMAN[®] (reagents for nucleic acid amplification) based assay is used to measure expression. TAQMAN[®] based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AMPLITAQ[®]

(enzyme for diagnostic applications), results in the cleavage of the TAQMAN[®] probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer).

- 5 Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) *Genomics* 4:560-569, Landegren, et al. (1988) *Science* 241:1077-1080, and Barringer, et al. (1990) *Gene* 89:117-122), transcription amplification (Kwoh, et al. (1989) *Proc. Nat'l Acad. Sci. USA* 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) *Proc. Nat'l Acad. Sci. USA* 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of soft tissue sarcoma cancer-associated proteins from nucleic acids

- In one embodiment, soft tissue sarcoma cancer nucleic acids, e.g., encoding soft tissue sarcoma cancer proteins are used to make a variety of expression vectors to
15 express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) *Gene Expression Systems* Academic Press) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate
20 into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the soft tissue sarcoma cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g.,
25 include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

- Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a
30 presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding

sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the soft tissue sarcoma cancer protein; e.g., transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the soft tissue sarcoma cancer protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In another embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) *Proc. Nat'l Acad. Sci. USA* 92:9146-9150.

In addition, in another embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are available and will vary with the host cell used.

The soft tissue sarcoma cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for soft tissue sarcoma cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In one embodiment, the soft tissue sarcoma cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated

transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In one embodiment, soft tissue sarcoma cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, 5 synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression 10 vector may also include a signal peptide sequence that provides for secretion of the soft tissue sarcoma cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection 15 of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. 20 Expression vectors for bacteria include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

25 In one embodiment, soft tissue sarcoma cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In another embodiment, a soft tissue sarcoma cancer protein is produced in yeast cells. Yeast expression systems include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*. 30

The soft tissue sarcoma cancer protein may also be made as a fusion protein, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the soft

tissue sarcoma cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the soft tissue sarcoma cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the soft tissue sarcoma cancer protein is a peptide, the nucleic acid encoding the peptide may be linked to another nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In one embodiment, the soft tissue sarcoma cancer protein is purified or isolated after expression. Soft tissue sarcoma cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) *Proteins: Biochemistry and Biotechnology* Wiley; Hardin, et al. (eds. 2001) *Cloning, Gene Expression and Protein Purification* Oxford Univ. Press; Wilson, et al. (eds. 2000) *Encyclopedia of Separation Science* Academic Press; and Scopes (1993) *Protein Purification* Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the soft tissue sarcoma cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

In one embodiment, the soft tissue sarcoma cancer nucleic acids, proteins, and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope, or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C ,

32P, 35S, or 125I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al.
5 (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

Accordingly, the present invention also provides soft tissue sarcoma cancer protein sequences. A cancer protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides.
10 Nucleic acid sequences of the invention can be used to generate protein sequences, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the soft tissue sarcoma cancer protein has an identifiable motif or homology to some protein in the database being used. Generally, the nucleic acid sequences are
15 input into a program that will search all three frames for homology. This is done in an embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise.
20 The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Variants of soft tissue sarcoma cancer-associated proteins

25 Also included within one embodiment of soft tissue sarcoma cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments
30 the homology will be as high as about 93-95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Soft tissue sarcoma cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in one embodiment, included within the definition of soft tissue sarcoma cancer proteins are portions or fragments of the wild type sequences herein. In addition, as outlined above, the soft tissue
5 sarcoma cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In another embodiment, the soft tissue sarcoma cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, the derivative cancer peptide will often contain at least one amino acid substitution,
10 deletion, or insertion, with amino acid substitutions being particularly useful at an appropriate position.

Also included within one embodiment of soft tissue sarcoma cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants.
15 These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other appropriate techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in
20 vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected
25 which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for
30 the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1-20 residues, although in some cases deletions may be much larger.

5 Substitutions, deletions, insertions or a combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino
10 acid substitution chart described.

The variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of
15 the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those provided in the definition of "conservative substitution". For example, substitutions may be made which more
20 significantly affect: the structure of the polypeptide backbone in the area of the alteration, e.g., the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic sidechain, e.g., serine or threonine, is
25 substituted for (or by) a hydrophobic sidechain, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative side chain, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine,
30 is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

The variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants

also are selected to modify the characteristics of the soft tissue sarcoma cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

5 Covalent modifications of these cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, e.g., for
10 crosslinking cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-cancer polypeptide antibodies or screening assays. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters
15 such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimideate.

Other modifications include deamidation of glutamine and asparagine residues to the corresponding glutamic and aspartic acid residues, respectively, hydroxylation
20 of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine, or tyrosine residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) *Proteins: Structure and Molecular Properties* Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

25 Another type of covalent modification of a cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present
30 in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types may be used to express cancer-associated sequences to exhibit different glycosylation patterns.

Addition of glycosylation sites to soft tissue sarcoma cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites).

- 5 The soft tissue sarcoma cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

- 10 Another means of increasing the number of carbohydrate moieties on the soft tissue sarcoma cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

- Removal of carbohydrate moieties present on the soft tissue sarcoma cancer polypeptide may be accomplished chemically or enzymatically or by mutational
15 substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases.
20 See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

- Another type of covalent modification of soft tissue sarcoma cancer protein comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in US Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417;
25 4,791,192; or 4,179,337.

- Soft tissue sarcoma cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag
30 polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the soft tissue sarcoma cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the soft tissue sarcoma cancer polypeptide

to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6, and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Mol. Cell. Biol. 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included with an embodiment of soft tissue sarcoma cancer protein are other soft tissue sarcoma cancer proteins of the functional family, and counterpart cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer sequences include unique areas of the soft tissue sarcoma cancer nucleic acid sequence. PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known. See, e.g., Innis, PCR Protocols, supra.

In addition, as is outlined herein, soft tissue sarcoma cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Soft tissue sarcoma cancer proteins may also be identified as being encoded by soft tissue sarcoma cancer nucleic acids. Thus, soft tissue sarcoma cancer proteins are

encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

Antibodies to soft tissue sarcoma cancer-associated proteins

5 In one embodiment, when the soft tissue sarcoma cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the soft tissue sarcoma cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context
10 of MHC. Thus, in most instances, antibodies made to a smaller, e.g., fragment of, cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In one embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In another embodiment, the epitope is selected from a protein sequence set out in Tables 1A-11C.

15 Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may
20 include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of
25 adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by
30 Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide

encoded by a nucleic acid of Tables 1A-11C, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an

5 immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) *Monoclonal Antibodies: Principles and Practice* Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The

10 hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT

15 medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the

20 binding specificities is for a protein encoded by a nucleic acid Tables 1A-11C or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

Alternatively, tetramer-type technology may create multivalent reagents.

In one embodiment, the antibodies to soft tissue sarcoma cancer protein are

25 capable of reducing or eliminating a biological function of a soft tissue sarcoma cancer protein, as is described below. That is, the addition of anti-soft tissue sarcoma cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue may reduce or eliminate the neoplastic or malignant cancer activity. Generally, at least about 25% decrease in activity, growth, size or the like may be used, with at

30 least about 50% being particularly useful and about 95-100% decrease being especially useful.

In another embodiment the antibodies to the soft tissue sarcoma cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.). Humanized forms of non-human (e.g.,

murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (US Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely

inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in US Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) *Bio/Technology* 10:779-783; Lonberg, et al. (1994) *Nature* 368:856-859; Morrison (1994) *Nature* 368:812-13; Fishwild, et al. (1996) *Nature Biotechnology* 14:845-851, commented on in Neuberger (1996) *Nature Biotechnology* 14:826; and Lonberg and Huszar (1995) *Intern. Rev. Immunol.* 13:65-93.

10 By immunotherapy is meant treatment of soft tissue sarcoma cancer or related disease with an antibody raised against, e.g., proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

20 In one embodiment the soft tissue sarcoma cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

25 In another embodiment, the soft tissue sarcoma cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment often bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-competitive, or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may be an antagonist of the cancer protein. Further, the antibody prevents activation of the transmembrane cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the

antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody
5 belongs to a sub-type that activates serum complement, or a similar effector function, when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, soft tissue sarcoma cancer is treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or
10 otherwise provide means to locally ablate cells.

In another embodiment, the antibody is conjugated or fused to an effector moiety. The effector moiety can be a labeling moiety, e.g., a radioactive or fluorescent label, or a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the soft tissue sarcoma cancer protein.
15 In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the soft tissue sarcoma cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase activity associated with the cancer, or be an attractant of other cells, such as NK cells. See, e.g., Groh, et al. (2002) Nature 419:734-738.

20 In one embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to soft tissue sarcoma cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins.
25 Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against soft tissue sarcoma cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the
30 antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another embodiment, the soft tissue sarcoma cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated or fused to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid
5 encoding the antibody is administered to the individual or cell. Moreover, wherein the soft tissue sarcoma cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The soft tissue sarcoma cancer antibodies of the invention specifically bind to
10 soft tissue sarcoma cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_D of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important

15
Detection of soft tissue sarcoma cancer-associated sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the soft tissue sarcoma cancer phenotype. Expression levels of genes
20 in normal tissue (e.g., not exhibiting soft tissue sarcoma cancer) and in soft tissue sarcoma cancer tissue (and in some cases, for varying severities of soft tissue sarcoma cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have a particular gene
25 similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine
30 whether a tissue sample has the gene expression profile of normal or cancer tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression

patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A

5 qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated,

10 resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques, e.g., as by use of Affymetrix GENECHIP[®] expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As

15 outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially useful.

Evaluation may be at the gene transcript, or the protein level. The amount of

20 gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the soft tissue sarcoma cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel

25 electrophoresis assays, etc. Proteins corresponding to soft tissue sarcoma cancer genes, e.g., those identified as being important in a soft tissue sarcoma cancer phenotype, can be evaluated in a soft tissue sarcoma cancer diagnostic test. In one embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well. Similarly,

30 these assays may be performed on an individual basis as well.

In this embodiment, the soft tissue sarcoma cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of soft

tissue sarcoma cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In one embodiment nucleic acids encoding the soft tissue sarcoma cancer protein are detected. Although DNA or RNA encoding the soft tissue sarcoma cancer protein may be detected, of particular interest are methods wherein an mRNA
5 encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is
10 detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient
15 time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example, a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.
20

In one embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The soft tissue sarcoma cancer proteins, antibodies, nucleic acids, modified proteins and cells containing cancer sequences are used in diagnostic assays.
25 This can be performed on an individual gene or corresponding polypeptide level. In another embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, soft tissue sarcoma cancer proteins, including
30 intracellular, transmembrane, or secreted proteins, find use as markers of soft tissue sarcoma cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative soft tissue sarcoma cancer tissue allows for detection, prognosis, or diagnosis of cancer, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect soft tissue sarcoma cancer proteins. One method

separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

5 In another method, antibodies to the soft tissue sarcoma cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) *Methods in Cell Biology: Antibodies in Cell Biology* (vol. 37) Academic Press. In this method cells are contacted with from one to many antibodies to the soft tissue sarcoma cancer protein(s). Following washing to remove non-specific antibody
10 binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the soft tissue sarcoma cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another embodiment each one of multiple primary antibodies contains a
15 distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of soft tissue sarcoma cancer proteins. Many other histological imaging techniques are also provided by the invention.

 In one embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a
20 fluorescence activated cell sorter (FACS) can be used in the method.

 In another embodiment, antibodies find use in diagnosing soft tissue sarcoma cancer from biological samples, such as blood, urine, sputum, semen, or other bodily fluids. As previously described, certain cancer proteins are secreted/circulating molecules. Blood or semen samples, therefore, are useful as samples to be probed or
25 tested for the presence of secreted cancer proteins. Antibodies can be used to detect a soft tissue sarcoma cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous soft tissue sarcoma cancer
30 protein.

 In one embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a

standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory
5 conditions or may be predictive of outcomes.

Assays for Prognosis of Soft Tissue Sarcoma Disorders

In one embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing cancer sequences are used in prognosis assays. As
10 above, gene expression profiles can be generated that correlate to soft tissue sarcoma cancer severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes included. For example, P-glycoprotein and Ki-67 antigen are promising markers for 5-year overall and disease-free survival for soft tissue sarcoma patients. Levine E.A. et al., Evaluation of new prognostic
15 markers for adult soft tissue sarcomas, J. Clin. Oncol. 15:3249-57 (1997). Other markers may be similarly

identified that correlate to soft tissue sarcoma cancer severity, or survival rates of soft tissue sarcoma patients.

As above, cancer probes may be attached to biochips for the detection and
20 quantification of cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Genes useful in prognostic assays are genes that are differentially expressed according to the stage of illness of the patient. In one embodiment, the genes may be
25 uniquely expressed according to the stage of the patient. In another embodiment, the genes may be expressed at differential levels according to the stage of the patient.

INSERT EXAMPLE OF PROGNOSTIC ASSAY The correlation of genes expressed in the different stages, either uniquely expressed or have differential expression levels according to the stage, may be used to determine the viability of inducing remission in
30 a patient. In addition, genes that are expressed indicating onset of long-term complications may also be useful as a prognostic tool.

Assays for therapeutic compounds

The soft tissue sarcoma cancer proteins, antibodies, nucleic acids, modified proteins and cells containing soft tissue sarcoma cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In one embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-994.

In one embodiment, the soft tissue sarcoma cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified soft tissue sarcoma cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the soft tissue sarcoma cancer phenotype or an identified physiological function of a soft tissue sarcoma cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In one embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In one embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in soft tissue sarcoma cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The amount of modulation will depend on the original change of the gene expression in normal versus tissue exhibiting soft tissue sarcoma cancer, with changes of at least about 10%, preferably about 50%, more preferably about 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product

itself can be monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

5 In one embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the soft tissue sarcoma cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g.,
10 of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of soft tissue sarcoma cancer

Expression monitoring can be performed to identify compounds that modify
15 the expression of one or more soft tissue sarcoma cancer-associated sequences, e.g., a polynucleotide sequence set out in the Tables. Generally, in one embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate soft tissue sarcoma cancer, modulate soft tissue sarcoma cancer proteins, bind to a soft tissue sarcoma cancer protein, or interfere with
20 the binding of a soft tissue sarcoma cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to
25 directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In several embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a soft tissue sarcoma cancer phenotype, e.g., to a normal tissue fingerprint. In another embodiment, a
30 modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Small molecules may be less than 2000, or less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly useful are peptides.

In one aspect, a modulator will neutralize the effect of a soft tissue sarcoma cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and thereby has substantially no effect on a cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a soft tissue sarcoma cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., US Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (US Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., US Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14:309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and US Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&E News); isoprenoids (US Patent No. 5,569,588); thiazolidinones and metathiazanones (US Patent No. 5,549,974); pyrrolidines (US Patent Nos. 5,525,735 and 5,519,134); morpholino compounds (US Patent No. 5,506,337); benzodiazepines (US Patent No. 5,288,514); and the like.

Devices for the preparation of combinatorial libraries are commercially available. See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY;

Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available. See, e.g., ComGenex, Princeton, NJ; Asinex, Moscow, Ru; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD; etc.

The assays to identify modulators are amenable to high throughput screening. Assays thus detect enhancement or inhibition of cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known, as are binding assays and reporter gene assays. Thus, e.g., US Patent No. 5,559,410 discloses high throughput screening methods for proteins, US Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while US Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available. See, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc., Fullerton, CA; Precision Systems, Inc., Natick, MA, etc. These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing

screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts
5 containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly useful in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, including human proteins. Particularly useful test compound will be directed to the class of proteins to which the
10 target belongs, e.g., substrates for enzymes or ligands and receptors.

In one embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or
15 grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate nucleotide or amino acid variations. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of
20 the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants. In one embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited
25 number of possibilities. For example, in one embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for
30 phosphorylation sites, etc., or to purines, etc.

Modulators of soft tissue sarcoma cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random

nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In one embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

5 After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as
10 appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In one embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting
15 the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or
20 compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich
25 assays", which include the use of multiple probes. See, e.g., US Patent Nos. 5,681,702; 5,597,909; 5,545,730; 5,594,117; 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124,246; and 5,681,697. The target nucleic acid may be prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that
30 allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be

controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding. See US Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with several embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the soft tissue sarcoma cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition, screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a soft tissue sarcoma cancer expression pattern leading to a normal expression pattern, or to modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to

identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated soft tissue sarcoma cancer tissue reveals genes that are not expressed in normal tissue or soft tissue sarcoma cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated soft tissue sarcoma cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of cancer cells, that have an associated soft tissue sarcoma cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is achieved. See PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., soft tissue sarcoma cancer tissue may be screened for agents that modulate, e.g., induce or suppress the cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on the cancer activity. By defining such a signature for the soft tissue sarcoma cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In one embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done.

The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In one embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the cancer modulatory protein is a fragment of approximately 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In one embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA

Measurements of soft tissue sarcoma cancer polypeptide activity, or of soft tissue sarcoma cancer or cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the soft tissue sarcoma cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects associated with tumors, tumor growth, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian soft tissue sarcoma cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a soft tissue sarcoma cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from about 0.5-

48 hours. In one embodiment, the soft tissue sarcoma cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the soft tissue sarcoma cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are included. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a soft tissue sarcoma cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In one embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "soft tissue sarcoma cancer proteins." The soft tissue sarcoma cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In another embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of

protein present. Alternatively, cells comprising the soft tissue sarcoma cancer proteins can be used in the assays.

Thus, in one embodiment, the methods comprise combining a soft tissue sarcoma cancer protein and a candidate compound, and determining the binding of the compound to the soft tissue sarcoma cancer protein. Other embodiments utilize the human soft tissue sarcoma cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative soft tissue sarcoma cancer proteins may be used.

Generally, in one embodiment of the methods herein, the soft tissue sarcoma cancer protein or the candidate agent is non-diffusibly bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon, or nitrocellulose, TEFLON[®] (synthetic resinous fluorine-containing polymers), etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusible. Other methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In one embodiment, the soft tissue sarcoma cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include

specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

The determination of the binding of the test modulating compound to the cancer protein may be done in many ways. In one embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a soft tissue sarcoma cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between about 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In one embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially

modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

5 In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test
10 compound is capable of binding to the cancer protein.

In one embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second sample comprises a test compound, a cancer protein, and a
15 competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

20 Alternatively, differential screening is used to identify drug candidates that bind to the native soft tissue sarcoma cancer protein, but cannot bind to modified soft tissue sarcoma cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of the cancer protein are also identified by screening
25 drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-
30 specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may

be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In one embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Useful cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a cancer protein. In one embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate soft tissue sarcoma cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting soft tissue sarcoma cancer cell division is provided. The method comprises administration of a soft tissue sarcoma cancer inhibitor. In another embodiment, a method of inhibiting soft tissue sarcoma cancer is provided. The method may comprise administration of a soft tissue sarcoma cancer inhibitor. In a further embodiment, methods of treating cells or individuals with soft tissue sarcoma cancer are provided, e.g., comprising administration of a soft tissue sarcoma cancer inhibitor.

In one embodiment, a soft tissue sarcoma cancer inhibitor is an antibody as discussed above. In another embodiment, the soft tissue sarcoma cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of soft tissue sarcoma cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) *Culture of Animal Cells: A Manual of Basic Technique* (3d ed.) Wiley-Liss; Freshney (2000) *Culture of Animal Cells: A Manual of Basic Technique* (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) *Nature Genet.* 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells.

Alternatively, labeling index with (^3H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^3H)-thymidine at saturation density is a method of measuring density limitation of growth. Transformed host cells are transfected with a soft tissue sarcoma cancer-associated sequence and are grown for

24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), *supra*.

5 Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts. See, e.g., Temin (1966) *J. Nat'l Cancer Inst.* 37:167-175; Eagle, et al. (1970) *J. Exp. Med.* 131:836-879; Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence
10 of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen
15 activator (PA) is released from human glioma at a higher level than from normal brain cells. See, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) *Biological Responses in Cancer Plenum*. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman
20 (1992) "Angiogenesis and Cancer" *Sem Cancer Biol.* 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. See also, Unkeless, et al. (1974) *J. Biol. Chem.* 249:4295-4305; Strickland and Beers (1976) *J. Biol. Chem.* 251:5694-5702; Whur, et al. (1980) *Br. J. Cancer* 42:305-312; Gullino, "Angiogenesis, tumor vascularization, and
25 potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) *Biological Responses in Cancer Plenum*; Freshney (1985) *Anticancer Res.* 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix
30 constituent can be used as an assay to identify compounds that modulate soft tissue sarcoma cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as

host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of soft tissue sarcoma cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted.

Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) *Science* 244:1288-1292. Chimeric targeted mice can be derived according to Hogan, et al. (1988) *Manipulating the Mouse Embryo: A Laboratory Manual* CSH Press; and Robertson (ed. 1987) *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach* IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) *J. Natl. Cancer Inst.* 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) *Br. J. Cancer* 38:263-272;

Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a soft tissue sarcoma cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

10

Polynucleotide modulators of soft tissue sarcoma cancer Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a soft tissue sarcoma cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a soft tissue sarcoma cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

15

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the soft tissue sarcoma cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

20

25

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

30

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise

a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for soft tissue sarcoma cancer molecules. An antisense molecule is for a soft tissue sarcoma cancer sequence in Tables 1A-11C, or for a ligand or activator thereof. Antisense or sense

5 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) *Cancer Res.* 48:2659-2668; and van der Krol, et al. (1988) *BioTechniques* 6:958-976.

10 RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) *Sciencexpress* (21March2002); Sharp (1999) *Genes Dev.* 13:139-141; and Cathew (2001) *Curr. Op. Cell Biol.* 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, 15 e.g., Elbashir, et al. (2001) *Nature* 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

20 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of soft tissue sarcoma cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes. See, 25 e.g., Castanotto, et al. (1994) *Adv. in Pharmacology* 25:289-317.

General features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) *Nuc. Acids Res.* 18:299-304; European Patent Publication No. 0 360 257; US Patent No. 5,254,678. Methods of preparation are available. See, e.g., WO 94/26877; Yu, et al. (1993) *Proc. Nat'l Acad. Sci. USA* 90:6340-6344; Yamada, et al. (1994) 30 *Human Gene Therapy* 1:39-45; Leavitt, et al. (1995) *Proc. Nat'l Acad. Sci. USA* 92:699-703; Leavitt, et al. (1994) *Human Gene Therapy* 5:1151-120; and Yamada, et al. (1994) *Virology* 205: 121-126.

Polynucleotide modulators of soft tissue sarcoma cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with

a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the
5 ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of soft tissue sarcoma cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood
10 that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating soft tissue sarcoma cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-soft tissue sarcoma cancer antibody that reduces or
15 eliminates the biological activity of an endogenous soft tissue sarcoma cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a soft tissue sarcoma cancer protein. This may be accomplished in many ways. In one embodiment, e.g., when the soft tissue sarcoma cancer sequence is down-regulated in soft tissue sarcoma cancer, such state may be
20 reversed by increasing the amount of soft tissue sarcoma cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous soft tissue sarcoma cancer gene or administering a gene encoding the soft tissue sarcoma cancer sequence, using known gene-therapy techniques. In one embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced
25 homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the soft tissue sarcoma cancer sequence is up-regulated in soft tissue sarcoma cancer, the activity of the endogenous soft tissue sarcoma cancer gene is decreased, e.g., by the administration of a soft tissue sarcoma cancer antisense nucleic acid or other inhibitor,
30 such as RNAi.

In one embodiment, the soft tissue sarcoma cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to soft tissue sarcoma cancer proteins. Similarly, the soft tissue sarcoma cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These

columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic purposes. In one embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The soft tissue sarcoma cancer antibodies may be coupled
5 to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

Methods of identifying variant soft tissue sarcoma cancer-associated sequences

10 Without being bound by theory, expression of various soft tissue sarcoma cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant soft tissue sarcoma cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant soft tissue sarcoma cancer genes, e.g., determining all or part of the sequence of at least one
15 endogenous soft tissue sarcoma cancer gene in a cell. This may be accomplished using known sequencing techniques. In one embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one soft tissue sarcoma cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the
20 evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced soft tissue sarcoma cancer gene to a known soft tissue sarcoma cancer gene, e.g., a wild-type gene.

The sequence of all or part of the soft tissue sarcoma cancer gene can then be compared to the sequence of a known soft tissue sarcoma cancer gene to determine if
25 differences exist. This can be done using known homology programs, such as Bestfit, etc. In another embodiment, the presence of a difference in the sequence between the soft tissue sarcoma cancer gene of the patient and the known soft tissue sarcoma cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

30 In one embodiment, the soft tissue sarcoma cancer genes are used as probes to determine the number of copies of the soft tissue sarcoma cancer gene in the genome.

In another embodiment, the soft tissue sarcoma cancer genes are used as probes to determine the chromosomal localization of the soft tissue sarcoma cancer genes. Information such as chromosomal localization finds use in providing a

diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the soft tissue sarcoma cancer gene locus.

Administration of pharmaceutical and vaccine compositions

5 In one embodiment, a therapeutically effective dose of a soft tissue sarcoma cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and can be ascertained using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical
10 Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for soft tissue sarcoma cancer degradation, systemic versus
15 localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary. U.S. Patent Application N. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and
20 other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In one embodiment the patient is a mammal, preferably a primate, including humans.

The administration of the soft tissue sarcoma cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above,
25 including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally topically, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the soft tissue sarcoma cancer proteins and modulators may be directly applied as a solution, spray, or ointment.

30 The pharmaceutical compositions of the present invention comprise a soft tissue sarcoma cancer protein in a form suitable for administration to a patient. In one embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to

those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like.

"Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly useful are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules, and lozenges. It is recognized that soft tissue sarcoma cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a soft tissue sarcoma cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of

undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g.,
5 sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs. See, e.g., (1980) Remington's Pharmaceutical Science (18th
10 ed.) Mack; and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from about 0.1 to 100 mg per patient per day may be used, particularly when the drug is administered to a
15 secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of soft tissue sarcoma cancer
20 proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the
25 severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. The composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the
30 development of soft tissue sarcoma cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular stage or form of soft tissue sarcoma cancer disorder being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc.

Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer, based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present soft tissue sarcoma cancer protein-modulating compounds can be administered alone or in combination with additional soft tissue sarcoma cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1A-11C, such as RNAi, antisense polynucleotides, or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of soft tissue sarcoma cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo, or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) *Guide to Molecular Cloning Techniques from Methods in Enzymology* (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) *Current Protocols Lippincott*; and Sambrook, et al. (2001) *Molecular Cloning: A Laboratory Manual* (3d ed., Vol. 1-3) CSH Press.

In one embodiment, soft tissue sarcoma cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Soft tissue sarcoma cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) *J. Clin. Invest.* 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) *Molec. Immunol.* 28:287-294; Alonso, et al. (1994) *Vaccine* 12:299-306; Jones, et al. (1995) *Vaccine* 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) *Nature* 344:873-875; Hu, et al. (1998) *Clin. Exp. Immunol.* 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) *Proc. Nat'l Acad. Sci. USA* 85:5409-5413; Tam (1996) *J. Immunol. Meth.* 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) *Concepts in Vaccine Development* de Gruyter; Chakrabarti, et al. (1986) *Nature* 320:535-537; Hu, et al. (1986) *Nature* 320:537-540; Kieny, et al. (1986) *Bio/Technology* 4:790-795; Top, et al. (1971) *J. Infect. Dis.* 124:148-154; Chanda, et al. (1990) *Virology* 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) *J. Immunol. Meth.* 192:25-35; Eldridge, et al. (1993) *Sem. Hematol.* 30:16-24; Falo, et al. (1995) *Nature Med.* 1:649-653), adjuvants (Warren, et al. (1986) *Ann. Rev. Immunol.* 4:369-388; Gupta, et al. (1993) *Vaccine* 11:293-306), liposomes (Reddy, et al. (1992) *J. Immunol.* 148:1585-1589; Rock (1996) *Immunol. Today* 17:131-137), or naked or particle absorbed cDNA (Ulmer, et al. (1993) *Science* 259:1745-1749; Robinson, et al. (1993) *Vaccine* 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) *Concepts in Vaccine Development* de Gruyter; Cease and Berzofsky (1994) *Ann. Rev. Immunol.* 12:923-989; and Eldridge, et al. (1993) *Sem. Hematol.* 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, MA) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA);

aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A; and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. See, e.g., Wolff, et al. (1990) *Science* 247:1465-1468 as well as US Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., US Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described, e.g., in US Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). See Stover, et al. (1991) *Nature* 351:456-460. A wide variety of other vectors are available for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) *Mol. Med. Today* 6:66-71; Shedlock, et al. (2000) *J. Leukoc. Biol.* 68:793-806; and Hipp, et al. (2000) *In Vivo* 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a soft tissue sarcoma cancer patient. The soft tissue sarcoma cancer gene used for DNA vaccines can encode full-length soft tissue sarcoma cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one

embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a soft tissue sarcoma cancer gene. For example, soft tissue sarcoma cancer-associated genes or sequence encoding subfragments of a soft tissue sarcoma cancer protein are introduced into expression vectors and tested
5 for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In one embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that
10 increase the immunogenic response to the soft tissue sarcoma cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another embodiment soft tissue sarcoma cancer genes find use in generating animal models of soft tissue sarcoma cancer. When the soft tissue sarcoma cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology,
15 e.g., wherein antisense RNA directed to the soft tissue sarcoma cancer gene will also diminish or repress expression of the gene. Animal models of soft tissue sarcoma cancer find use in screening for modulators of a soft tissue sarcoma cancer-associated sequence or modulators of soft tissue sarcoma cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous
20 recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the soft tissue sarcoma cancer protein. When desired, tissue-specific expression or knockout of the soft tissue sarcoma cancer protein may be necessary.

It is also possible that the soft tissue sarcoma cancer protein is overexpressed
25 in soft tissue sarcoma cancer. As such, transgenic animals can be generated that overexpress the soft tissue sarcoma cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals
30 generated by such methods find use as animal models of soft tissue sarcoma cancer and are additionally useful in screening for modulators to treat soft tissue sarcoma cancer or to evaluate a therapeutic entity.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, soft tissue sarcoma cancer-specific nucleic acids or antibodies, hybridization probes and/or
5 primers, antisense polynucleotides, ribozymes, dominant negative soft tissue sarcoma cancer polypeptides or polynucleotides, small molecules inhibitors of cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

10 In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are
15 not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of soft tissue sarcoma cancer-associated sequences. Such kits can be prepared from
20 readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a soft tissue sarcoma cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated activity. Optionally, the kit contains biologically active soft tissue sarcoma cancer protein. A wide variety of kits and components can be prepared according to the
25 present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1

Tissue Preparation, Labeling Chips, and Fingerprints

Purify total RNA from tissue using TRIZOL[®] Reagent

Estimate tissue weight. Homogenize tissue samples in 1ml of TRIZOL[®] (chemical reagents for use in isolating biological material from organic tissue) per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.

HOMOGENIZATION

Before using generator, it should have been cleaned after last usage by running it through soapy H₂O and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIZOL[®] directly to frozen tissue then homogenize.

Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.

PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature. Add 0.2ml of chloroform per 1ml of TRIZOL[®] reagent used in the original homogenization. Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.

Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

RNA PRECIPITATION

Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of isopropyl alcohol per 1ml of TRIZOL[®] reagent used in the original homogenization. Cap tubes securely and invert to mix.

Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

RNA WASH

Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C.

Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC H₂O. Try for 2-5ug/ul. Take absorbance readings.

Purify poly A⁺ mRNA from total RNA or clean up total RNA with Qiagen's RNeasy kit

Purification of poly A⁺ mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature.

Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A⁺ mRNA has occurred. Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low.

Read absorbance, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA must be precipitated.

Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

5 *Ethanol Precipitation*

Add 0.4 vol. of 7.5 M NH_4OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C . Wash pellet with 0.5ml of 80% ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash.

- 10 Dry the last bit of ethanol from the pellet in the hood. (Do not speed vacuum dry). Suspend pellet in DEPC H_2O at 1ug/ul concentration.

Clean up total RNA using Qiagen's RNeasy kit

- 15 Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at $>10,000\text{rpm}$. If concerned about yield, re-apply flowthrough to column and centrifuge again.

- 20 Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at $>10,000\text{rpm}$. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at $>10,000\text{rpm}$. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at $>10,000\text{rpm}$. Repeat elution.

- 25 Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

First Strand cDNA Synthesis

- 30 Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70°C . On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37°C for 2 min then add SuperScript RT. Incubate at 37°C for 1 hour.

Second Strand Synthesis

Place 1st strand reactions on ice.

Add: 91ul DEPC H₂O

30ul 5X 2nd Strand Buffer

5 3ul 10mM dNTP mix

1ul 10U/ul *E.coli* DNA Ligase

4ul 10U/ul *E.coli* DNA Polymerase

1ul 2U/ul RNase H

10 Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C.

Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

Clean up cDNA

15 Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel (PLG) tubes.

Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isoamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate: add 7.5X 5M NH₄Oac and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

25 *In vitro* Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

Make NTP labeling mix:

Combine at room temperature: 2ul T7 10xATP (75mM) (Ambion)
2ul T7 10xGTP (75mM) (Ambion)
30 1.5ul T7 10xCTP (75mM) (Ambion)
1.5ul T7 10xUTP (75mM) (Ambion)
3.75ul 10mM Bio-11-UTP (Boehringer-
Mannheim/Roche or Enzo)
3.75ul 10mM Bio-16-CTP (Enzo)

2ul 10x T7 transcription buffer (Ambion)

2ul 10x T7 enzyme mix (Ambion)

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

RNeasy clean-up of IVT product

- 5 Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

Fragmentation

- 10 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer.

- 15 Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

5 x Fragmentation buffer:

200 mM Tris-acetate, pH 8.1

500 mM KOAc

150 mM MgOAc

20

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

Hybridization

- 25 200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

Hybridization Mix: fragment labeled RNA (50ng/ul final conc.)

- 30 50 pM 948-b control oligo
1.5 pM BioB
5 pM BioC
25 pM BioD
100 pM CRE
0.1mg/ml herring sperm DNA

0.5mg/ml acetylated BSA
to 300 ul with 1xMES hyb. buffer

The instruction manuals for the products used herein are incorporated herein in their entirety.

5 *Labeling Protocol*

Hybridization reaction:

Start with non-biotinylated IVT (purified by RNeasy columns)
(see example 1 for steps from tissue to IVT)

	IVT antisense RNA; 4 µg:	µl
10	Random Hexamers (1 µg/µl):	4 µl
	H ₂ O:	µl

14 µl

- Incubate 70°C, 10 min. Put on ice.

15 Reverse transcription:

5X First Strand (BRL) buffer: 6 µl

0.1 M DTT: 3 µl

50X dNTP mix: 0.6 µl

H₂O: 2.4 µl

20 Cy3 or Cy5 dUTP (1mM): 3 µl

SS RT II (BRL): 1 µl

16 µl

- Add to hybridization reaction.

25 - Incubate 30 min., 42°C.

- Add 1 µl SSII and let go for another hour.

Put on ice.

- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 µl each of 100mM dATP, dCTP, and dGTP; 10 µl of 100mM dTTP to 15 µl H₂O. dNTPs from Pharmacia)

30 *RNA degradation:*

86 µl H₂O

- Add 1.5 µl 1M NaOH/ 2mM EDTA, incubate at 65°C, 10 min.

10 µl 10N

NaOH

4 μ l 50mM

EDTA

U-Con 30

500 μ l TE/sample spin at 7000g for 10 min, save flow through for purification5 *Qiagen purification:*-suspend u-con recovered material in 500 μ l buffer PB

-proceed w/ normal Qiagen protocol

DNAse digest:

- Add 1 μ l of 1/100 dil of DNAse/30 μ l Rx and incubate at 37°C for 15 min.

10 -5 min 95°C to denature enzyme

Sample preparation:

- Add:

- Cot-1 DNA: 10 μ l50X dNTPs: 1 μ l15 20X SSC: 2.3 μ lNa pyro phosphate: 7.5 μ l10mg/ml Herring sperm DNA 1 μ l of 1/10 dilution

21.8 final vol.

- Dry down in speed vac.

20 - Resuspend in 15 μ l H₂O.- Add 0.38 μ l 10% SDS.

- Heat 95°C, 2 min.

- Slow cool at room temp. for 20 min.

Put on slide and hybridize overnight at 64°C.

25 *Washing after the hybridization:*

3X SSC/0.03% SDS: 2 min. 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls

H₂O1X SSC: 5 min. 12.5 mls 20X SSC in 250mls H₂O0.2X SSC: 5 min. 2.5 mls 20X SSC in 250mls H₂O

30 Dry slides in centrifuge, 1000 RPM, 1min.

Scan at appropriate PMT's and channels.

Example 2: Gene Chip Analysis

Molecular profiles of various normal and soft tissue sarcoma cancer tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described above (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993). The results are shown in the tables and figures that follow. These soft tissue sarcoma (STSD) associated sequences are identified in the tables by Genbank Accession numbers and gene titles. As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in one embodiment herein, genes within an expression profile, also termed expression profile genes, include ESTs and are not necessarily full length.

TABLE 1A

5	Pkey:	Unique Eos probeset identifier number
	Gene name:	Unigene gene title
	Accession:	Exemplar Accession number, Genbank accession number
10	UniGene:	Unigene number
	RATIO:	95th percentile of chondrosarcomas AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator
	SEQ ID #:	Nucleic acid and protein sequences provided on CD for search purposes

15	Pkey	Gene Name	Accession	UniGene	RATIO	SEQ ID #
	424687	matrix metalloproteinase 9 (gelatinase	J05070	Hs.151738	48.5	1986 1987 6289
	417153	collagen, type II, alpha 1 (primary ost	X57010	Hs.81343	43.3	1084 1085 5625
	422867	cartilage oligomeric matrix protein (ps	L32137	Hs.1584	29.0	1751 1752 6122
20	428305	cartilage linking protein 1	AA446628	Hs.2799	22.1	2426 6607
	422871	collagen, type XI, alpha 2	AL031228	Hs.121509	21.9	1753 1754 6123
	424800	MyoD family inhibitor	AL035588	Hs.153203	21.5	2002 2003 6300
	413778	myosin, light polypeptide 2, regulatory	AA090235	Hs.75535	17.6	740 5356
	441134	cellular retinoic acid-binding protein	W29092	Hs.346950	17.0	3500 7475
25	431553	cartilage linking protein 1	X78075	Hs.2799	16.7	2792 6874
	417866	collagen, type XI, alpha 1	AW067903	Hs.82772	15.7	1162 5685
	425154	collagen, type IX, alpha 1	NM_001851	Hs.154850	15.3	2055 2056 6339
	428748	Ksp37 protein	AW593206	Hs.98785	15.2	2468 6638
	417070	titin	Z19077	Hs.172004	15.0	1070 5614
30	425545	Homo sapiens, clone MGC:12401, mRNA, co	N98529	Hs.158295	13.9	2114 6379
	403088	NM_003319*:Homo sapiens titin (TTN), mR			13.7	4707
	428087	troponin C2, fast	AA100573	Hs.182421	13.4	2396 6582
	440274	scraple responsive protein 1	R24595	Hs.7122	13.2	3464 7443
	404977	Insulin-like growth factor 2 (somatomed			13.1	4766
35	412519	troponin T1, skeletal, slow	AA196241	Hs.73980	12.7	598 5244
	407245	titin	X90568	Hs.172004	12.7	132 133 4881
	427474	aggrecan 1 (chondroitin sulfate proteog	U13192	Hs.2159	12.6	2334 6532
	435013	NM_020142:Homo sapiens NADH:ubiquinone	H91923	Hs.110024	12.5	3096 7115
	452838	preferentially expressed antigen in mel	U65011	Hs.30743	12.5	4357 4358 8188
40	410621	titin	AA194329	Hs.172004	12.2	481 5149
	422887	ESTs	AI751848	Hs.49215	12.1	1755 6124
	432239	matrix metalloproteinase 13 (collagenas	X81334	Hs.2936	12.0	2856 2857 6921
	427335	G antigen 7B	AA448542	Hs.278444	11.6	2317 6520
	432481	intron of collagen, type XI, alpha 1	AW451645	Hs.151504	11.4	2876 6938
45	432268	3'-phosphoadenosine 5'-phosphosulfate s	BE311856	Hs.274230	11.4	2861 6925
	405704	NM_001844*:Homo sapiens collagen, type			11.4	4794
	448204	ESTs	AI475124	Hs.170561	11.2	3988 7887
	456115	titin	F01082	Hs.172004	10.8	4515 8320
	440042	ESTs	AI073387	Hs.133898	10.5	3448 7430
50	427747	serine/threonine kinase 12	AW411425	Hs.180655	10.5	2365 6557
	429329	Homo sapiens pannexin 3 (PANX3)	AA456140	Hs.99235	10.4	2547 6699
	408349	homeo box C10	BE546947	Hs.44276	10.2	213 4949
	416373	ESTs, Weakly similar to S12658 cysteine	AA195845	Hs.73680	10.1	996 5559
	446619	secreted phosphoprotein 1 (osteopontin,	AU076643	Hs.313	9.9	3861 7782
55	443802	KIAA1291 protein	AW504924	Hs.9805	9.9	3647 7609
	437330	Homo sapiens mRNA; cDNA DKFZp761J1112 (AL353944	Hs.50115	9.9	3253 7250
	428698	KIAA1866 protein	AA852773	Hs.334838	9.9	2463 6635
	409200	KIAA0076 gene product	AL042914	Hs.51039	9.8	325 5037
	416491	parathyroid hormone receptor 1	U17418	Hs.1019	9.8	1005 1006 5567
60	406707	myosin, heavy polypeptide 2, skeletal m	S73840	Hs.931	9.4	61 62 4829
	424408	collagen, type V, alpha 1	AI754813	Hs.146428	9.4	1943 6260
	413011	biglycan	AW068115	Hs.821	9.4	669 5302
	414152	thrombospondin 4	NM_003248	Hs.75774	9.1	782 783 5391
	426752	titin	X69490	Hs.172004	9.1	2266 2267 6482
65	426300	delta-like homolog (Drosophila)	U15979	Hs.169228	9.1	2196 2197 6437
	426370	sortilin 1	R98288	Hs.281706	8.8	2215 6449
	421552	secreted frizzled-related protein 4	AF026692	Hs.105700	8.8	1559 1560 5982
	444381	hypothetical protein BC014245	BE387335	Hs.283713	8.7	3697 7652
	417308	KIAA0101 gene product	H60720	Hs.81892	8.7	1094 5634
70	452242	glycosyltransferase	R50956	Hs.159993	8.7	4305 8145
	406704	myosin, heavy polypeptide 7, cardiac mu	M21665	Hs.929	8.6	55 56 4826
	417930	Homo sapiens mRNA for KIAA1870 protein,	H81136	Hs.334604	8.4	1169 5691
	432874	melanoma inhibitory activity	W94322	Hs.279651	8.3	2913 6968
	433513	ESTs	AI566356	Hs.171437	8.2	2985 7024
75	409858	trinucleotide repeat containing 5	NM_006586	Hs.56828	8.2	391 392 5084
	443426	chromosome 20 open reading frame 1	AF098158	Hs.9329	8.2	3621 3622 7586

5	453665	ESTs, Weakly similar to SFRB_HUMAN SPLI	AA626250	Hs.326184	8.1	4434	8253
	407619	collagen, type IX, alpha 2	AL050341	Hs.37165	8.1	146	147 4892
	417849	nidogen 2	AW291587	Hs.82733	8.0	1161	5684
	421967	interleukin 17B	AA476704	Hs.110040	8.0	1621	6027
	412129	troponin T3, skeletal, fast	M21984	Hs.73454	8.0	571	572 5222
	429921	collagen, type XI, alpha 1	AA526911	Hs.82772	7.9	2620	6749
	419875	proenkephalin	AA853410	Hs.93557	7.9	1391	5859
	419741	ubiquitin carrier protein E2-C	NM_007019	Hs.93002	7.9	1379	1380 5850
10	429166	KIAA1270 protein	AB033096	Hs.197668	7.8	2522	2523 6679
	431103	pleiotrophin (heparin binding growth fa	M57399	Hs.44	7.8	2748	2749 6840
	408482	adenosine A2b receptor	NM_000676	Hs.45743	7.7	226	227 4959
	406964	FGENES predicted novel secreted protein	M21305		7.7	87	88 4847
	434449	hypothetical protein FLJ22041 similar t	AW953484	Hs.3849	7.7	3057	7083
	450778	soluble carrier family 29 (nucleoside tr	U81375	Hs.25450	7.6	4191	4192 8055
15	422640	troponin C, slow	M37984	Hs.118845	7.6	1718	1719 6099
	409327	collagen, type IX, alpha 3	L41162	Hs.53563	7.6	341	342 5047
	416658	fibrillin 2 (congenital contractural ar	U03272	Hs.79432	7.5	1020	1021 5577
	412978	homeo box C6	AI431708	Hs.820	7.5	665	5298
20	409169	(clone PWHL2-24) myosin light chain 2	F00991	Hs.50889	7.5	316	5029
	449378	ESTs	AW664026	Hs.59892	7.5	4085	7967
	418883	acid phosphatase 5, tartrate resistant	BE387036	Hs.1211	7.5	1281	5774
	432538	male-enhanced antigen	BE258332	Hs.278362	7.4	2884	6945
	453060	hypothetical protein MGC15754	AW294092	Hs.21594	7.3	4386	8213
25	420462	chondromodulin I precursor	AF050147	Hs.97932	7.3	1454	1455 5908
	403071	NM_003319*:Homo sapiens titin (TTN), mR			7.3	4702	
	426991	Homo sapiens cDNA FLJ10674 fis, clone N	AK001536	Hs.214410	7.3	2294	6502
	417435	carbonic anhydrase III, muscle specific	NM_005181	Hs.82129	7.2	1121	1122 5655
	438913	ESTs	AI380429	Hs.172445	7.2	3364	7347
	453935	ESTs	AI633770	Hs.42572	7.2	4470	8281
30	422684	H2A histone family, member Z	BE561617	Hs.119192	7.2	1726	6105
	444784	ectonucleotide pyrophosphatase/phosphod	D12485	Hs.11951	7.2	3724	3725 7673
	444232	hypothetical protein DKFZp761H221	W56010	Hs.347297	7.1	3687	7644
	425071	deiodinase, iodothyronine, type II	NM_013989	Hs.154424	7.1	2043	2044 6330
	422633	enolase 3, (beta, muscle)	X56832	Hs.118804	7.0	1716	1717 6098
35	453271	ESTs	AA903424	Hs.6786	7.0	4409	8232
	452402	peroxisome proliferative activated rece	AI138530	Hs.22216	7.0	4327	8162
	421579	stem cell growth factor; lymphocyte sec	NM_002975	Hs.105927	7.0	1567	1568 5987
	425397	topoisomerase (DNA) II alpha (170kD)	J04088	Hs.156346	7.0	2099	2100 6369
40	449969	Homo sapiens cDNA FLJ14337 fis, clone P	AW295142	Hs.180187	6.9	4123	8001
	419926	DKFZP586D2223 protein	AW900992	Hs.93796	6.9	1396	5863
	432596	matrilin 3	AJ224741	Hs.278461	6.9	2889	2890 6950
	419452	PTK7 protein tyrosine kinase 7	U33635	Hs.90572	6.9	1340	1341 5821
	448721	ESTs	AI632123	Hs.371431	6.9	4029	7921
45	437352	hypothetical protein DKFZp434P0531	AL353957	Hs.284181	6.8	3255	3256 7252
	408831	endocrine regulator	AF090114	Hs.48433	6.8	266	267 4992
	426935	collagen, type I, alpha 1	NM_000088	Hs.172928	6.7	2288	2289 6498
	434906	Homo sapiens, clone IMAGE:4053965, mRNA	BE410573	Hs.283636	6.7	3090	7110
	405946	Target Exon			6.7	4798	
50	450701	hypothetical protein XP_098151 (leucine	H39960	Hs.288467	6.7	4183	8048
	403074	NM_003319*:Homo sapiens titin (TTN), mR			6.6	4703	
	411296	growth suppressor 1	BE207307	Hs.10114	6.6	524	5183
	452281	Homo sapiens cDNA FLJ11041 fis, clone P	T93500	Hs.28792	6.6	4309	8149
	421535	phosphoribosylformylglycinamide synth	AB002359	Hs.105478	6.5	1557	1558 5981
55	427585	collagen, type X, alpha 1 (Schmid metap	D31152	Hs.179729	6.5	2349	6543
	428981	ESTs, Weakly similar to ALU2_HUMAN ALU	BE313077	Hs.93135	6.5	2497	6660
	428342	Homo sapiens cDNA FLJ13458 fis, clone P	AI739168	Hs.349283	6.5	2432	6611
	436608	down syndrome critical region protein D	AA628980	Hs.192371	6.5	3205	7207
	444165	hypothetical protein FLJ11236	AL137443	Hs.10441	6.5	3682	7639
60	419745	slug (chicken homolog), zinc finger pro	AF042001	Hs.93005	6.4	1381	1382 5851
	438746	Human melanoma-associated antigen p97 (AI885815	Hs.184727	6.4	3353	7337
	449048	similar to S68401 (cattle) glucose indu	Z45051	Hs.22920	6.4	4061	7945
	441553	ESTs	AA281219	Hs.121296	6.4	3525	7498
	437696	hypothetical protein dJ37E16.5	Z83844	Hs.5790	6.4	3281	7274
	410929	ESTs	H47233	Hs.30643	6.4	504	5166
65	443105	chondroitin sulfate proteoglycan 4 (mel	X96753	Hs.9004	6.3	3600	3601 7568
	446051	ephrin-A3	BE048061	Hs.37054	6.3	3816	7744
	400440	nebulin	X83957	Hs.83870	6.3	24	25 4627
	429359	matrix metalloproteinase 14 (membrane-I	W00482	Hs.2399	6.3	2551	6702
	433001	clone HQ0310 PRO0310p1	AF217513	Hs.279905	6.3	2923	2924 6977
70	415989	ESTs	AI267700	Hs.351201	6.3	962	5530
	452826	peroxisomal biogenesis factor 6	BE245286	Hs.301636	6.3	4353	8184
	434352	small muscle protein, X-linked	AF129505	Hs.86492	6.3	3047	3048 7075
	409142	SMC4 (structural maintenance of chromos	AL136877	Hs.50758	6.3	312	313 5027
	412709	KIAA0027 protein	AL022327	Hs.74518	6.2	631	632 5269
75	411789	Adican	AF245505	Hs.72157	6.2	553	554 5207
	453392	SRY (sex determining region Y)-box 11	U23752	Hs.32964	6.2	4416	4417 8239

	440028	ESTs, Weakly similar to T17227 hypothet	AW473675	Hs.367649	6.2	3446 7428
	416768	regenerating islet-derived 1 alpha (pan	AA363733	Hs.1032	6.2	1030 5583
	422627	transforming growth factor, beta-induce	BE336857	Hs.118787	6.2	1715 6097
	443610	mitochondrial ribosomal protein S18A	AW248314	Hs.9622	6.2	3628 7591
5	421307	Homo sapiens mRNA; cDNA DKFZp434B0425 (BE539976	Hs.103305	6.1	1528 5963
	426413	gb:EST90805 Synovial sarcoma Homo sapie	AA377823		6.1	2219 6453
	424086	lysyl oxidase	AI351010	Hs.102267	6.1	1896 6227
	450087	MUM2 protein	BE293180	Hs.24379	6.1	4133 8008
	421155	lysyl oxidase	H87879	Hs.102267	6.1	1512 5950
10	407604	collagen, type VIII, alpha 2	AW191962	Hs.353001	6.1	145 4891
	437033	RNA polymerase I subunit	AW248364	Hs.5409	6.1	3231 7230
	427427	lectin, superfamily member 1 (cartilage	AF077345	Hs.177936	6.0	2328 2329 6528
	420005	ESTs	AW271106	Hs.133294	6.0	1407 5871
	453331	ESTs	AI240665	Hs.352537	6.0	4413 8236
15	423785	Homo sapiens WWp2-like mRNA complete cd	BE467186	Hs.333382	6.0	1849 6195
	412719	ESTs	AW016610	Hs.816	6.0	633 5270
	425462	Homo sapiens cDNA: FLJ22382 fis, clone	AI491852	Hs.46783	5.9	2106 6373
	437898	ESTs	W81260	Hs.43410	5.9	3293 7286
	417944	collagen, type V, alpha 2	AU077196	Hs.82985	5.9	1172 5693
20	439737	Homo sapiens mRNA full length insert cD	AI751438	Hs.41271	5.9	3427 7410
	420162	cyclin-dependent kinase 4	BE378432	Hs.95577	5.9	1422 5883
	449722	cyclin B1	BE280074	Hs.23960	5.9	4112 7990
	412140	RAB6 interacting, kinesin-like (rabkine	AA219691	Hs.73625	5.8	573 5223
	421823	ESTs	N40850	Hs.28625	5.8	1600 6011
25	451149	RNA binding motif protein 8B	AL047586	Hs.10283	5.8	4214 8073
	444371	forkhead box M1	BE540274	Hs.239	5.8	3696 7651
	427157	thymine-DNA glycosylase	U51166	Hs.173824	5.8	2305 2306 6511
	429415	procollagen C-endopeptidase enhancer	NM_002593	Hs.202097	5.8	2557 2558 6706
	431556	sarcospan (Kras oncogene-associated gen	AF016028	Hs.183428	5.8	2793 2794 6875
30	419987	osteomodulin	NM_005014	Hs.94070	5.8	1402 1403 5868
	412646	transmembrane protein (63kD), endoplasm	NM_006825	Hs.74368	5.8	623 624 5262
	412939	eukaryotic translation elongation facto	AW411491	Hs.75069	5.8	657 5292
	443184	ESTs	AI638728	Hs.135159	5.8	3607 7574
	426462	dermatan sulphate proteoglycan 3	U59111	Hs.169993	5.7	2230 2231 6460
35	428269	ESTs, Moderately similar to ZN91_HUMAN	W35195	Hs.95659	5.7	2416 6598
	444301	asporin (LRR class 1)	AK000136	Hs.10760	5.7	3691 3692 7647
	439253	ESTs	AF086064	Hs.337696	5.7	3387 7370
	409731	thymosin, beta, identified in neuroblas	AA125985	Hs.56145	5.7	386 5080
	422087	matrix metalloproteinase 2 (gelatinase	X58968	Hs.111301	5.7	1641 6040
40	414477	amplified in osteosarcoma	U41635	Hs.76228	5.7	822 823 5425
	410102	ESTs; homologue of PEM-3 [Ciona savigny	AW248508	Hs.279727	5.7	422 5107
	407740	ESTs	AA295547	Hs.353519	5.7	156 4900
	452973	ESTs	H88409	Hs.40527	5.7	4375 8203
	417900	CDC20 (cell division cycle 20, S. cerev	BE250127	Hs.82906	5.7	1165 5688
45	414219	ALL1-fused gene from chromosome 1q	W20010	Hs.75823	5.7	789 5397
	409686	Homo sapiens mRNA; cDNA DKFZp434L0827 (AK000002	Hs.55879	5.7	376 377 5073
	426067	ESTs	AW664691	Hs.97053	5.6	2169 6416
	417160	proteolipid protein 1 (Pelizaeus-Merzba	N76497	Hs.355807	5.6	1086 5626
50	423961	periostrin (OSF-2os)	D13666	Hs.136348	5.6	1878 1879 6215
	427871	Homo sapiens, clone IMAGE:3507281, mRNA	AW992405	Hs.352406	5.6	2380 6568
	431089	ESTs, Weakly similar to unknown protein	BE041395	Hs.374629	5.6	2745 6838
	410491	Homo sapiens clone 25218 mRNA sequence	AA465131	Hs.64001	5.6	465 5138
	433075	sortilin 1	NM_002959	Hs.351872	5.6	2936 2937 6987
	407896	Zic family member 1 (odd-paired Drosoph	D76435	Hs.41154	5.5	176 177 4919
55	428862	SRY (sex determining region Y)-box 9 (c	NM_000346	Hs.2316	5.5	2483 2484 6650
	443883	serine (or cysteine) proteinase inhibit	AA114212	Hs.9930	5.5	3653 7614
	452862	ADAMTS2 (a disintegrin-like and metall	AW378065	Hs.8687	5.5	4360 8190
	452471	gb:RC-BT029-090199-079 BT029 Homo sapie	AI903332		5.5	4335 8169
	423073	MAD (mothers against decapentaplegic, D	BE252922	Hs.123119	5.5	1777 6142
60	409893	minichromosome maintenance deficient [S	AW247090	Hs.57101	5.5	397 5088
	453597	myo-inositol 1-phosphate synthase A1	BE281130	Hs.381118	5.5	4429 8249
	439456	hypothetical protein FLJ20980	AI752409	Hs.109314	5.5	3400 7383
	418533	myosin-binding protein C, fast-type	NM_004533	Hs.85937	5.5	1253 1254 5754
	437446	ESTs, Moderately similar to CA1C RAT CO	AA788946	Hs.101302	5.5	3264 7259
65	419073	Homo sapiens cDNA FLJ12797 fis, clone N	AW372170	Hs.183918	5.5	1296 5786
	439108	synaptogyrin 3	AW163034	Hs.6467	5.5	3377 7360
	436476	bHLH protein DEC2	AA326108	Hs.33829	5.4	3190 7195
	414117	proteolipid protein 1 (Pelizaeus-Merzba	W88559	Hs.355807	5.4	777 5386
70	441362	RAD51 (S. cerevisiae) homolog (E coli R	BE614410	Hs.23044	5.4	3512 7486
	417796	ESTs	AA206141	Hs.367818	5.4	1159 5682
	406687	matrix metalloproteinase 11 (stromelysi	M31126	Hs.352054	5.4	49 50 4823
	418054	lysyl oxidase-like 2	NM_002318	Hs.83354	5.4	1184 1185 5702
	432691	mitogen-activated protein kinase 7	U29725	Hs.3080	5.4	2897 2898 6956
	410687	lysyl oxidase-like 1	U24389	Hs.65436	5.4	485 486 5153
75	453941	Bloom syndrome	U39817	Hs.36820	5.4	4471 4472 8282
	432731	fibronectin 1	R31178	Hs.287820	5.4	2904 6961

	430209	collagen, type V, alpha 3	AF177941	Hs.235368	5.3	2659 2660 6778
	409041	Hypothetical protein, XP_051860 (KIAA11	AB033025	Hs.50081	5.3	299 300 5017
	408901	hypothetical protein FLJ10468	AK001330	Hs.48855	5.3	272 273 4997
5	411078	CocoaCrisp	AI222020	Hs.182364	5.3	512 5172
	457211	ESTs, Weakly similar to S51797 vasodila	AW972565	Hs.32399	5.3	4543 8344
	426058	Nedd4-like ubiquitin-protein ligase	U96114	Hs.333382	5.3	2166 2167 6414
	431247	matrilin 4	AL021578	Hs.278489	5.3	2768 2769 6855
	418140	microfibrillar-associated protein 2	BE613836	Hs.83551	5.3	1196 5713
10	452214	hypothetical protein FLJ10567	AK001429	Hs.380887	5.3	4300 4301 8141
	422043	retinoic acid induced 1	AL133649	Hs.110953	5.3	1629 1630 6033
	452683	progesterone membrane binding protein	AI089575	Hs.374574	5.3	4341 8175
	423811	homeo box C4	AW299598	Hs.50895	5.3	1854 6198
	423225	Thy-1 cell surface antigen	AA852604	Hs.125359	5.2	1786 6148
	424308	minichromosome maintenance deficient (S	AW975531	Hs.154443	5.2	1932 6250
15	436907	ESTs	AA737171	Hs.131809	5.2	3226 7225
	430393	estrogen-responsive B box protein	BE185030	Hs.241305	5.2	2688 6798
	433612	Homo sapiens Ku70-binding protein (KUB3	AF078164	Hs.61188	5.2	2991 2992 7030
	441356	ESTs, Weakly similar to JC5024 UDP-gala	BE384361	Hs.182885	5.2	3511 7485
20	447343	ESTs, Highly similar to S02392 alpha-2-	AA256641	Hs.236894	5.2	3916 7828
	445826	Homo sapiens mRNA; cDNA DKFZp586D0918 (BE313754	Hs.13350	5.2	3800 7730
	452873	hypothetical protein FLJ10385	AK001247	Hs.30922	5.2	4362 4363 8192
	408202	DKFZP586L151 protein	AA227710	Hs.43658	5.2	202 4942
	435256	cytokine-like protein C17	AF193766	Hs.13872	5.2	3116 3117 7133
25	412641	heat shock 90kD protein 1, beta	M16660	Hs.74335	5.2	620 621 5260
	430890	glypican 1	X54232	Hs.2699	5.2	2735 2736 6831
	414358	ESTs	AA476456	Hs.98969	5.2	807 5412
	442573	branched chain aminotransferase 1, cyto	H93366	Hs.7567	5.2	3570 7541
	412564	cardiac ankyrin repeat protein	X83703	Hs.355934	5.2	606 607 5251
30	417791	ESTs	AW965339	Hs.44269	5.1	1158 5681
	422765	baculoviral IAP repeat-containing 5 (su	AW409701	Hs.1578	5.1	1734 6110
	416391	mesoderm specific transcript (mouse) ho	AI878927	Hs.79284	5.1	999 5562
	421295	DC2 protein	AW081061	Hs.103180	5.1	1524 5960
	445564	KIAA1034 protein	AB028957	Hs.12896	5.1	3784 3785 7718
35	417675	similar to murine leucine-rich repeat p	AI808607	Hs.3781	5.1	1144 5670
	447149	TAR (HIV) RNA-binding protein 2	BE299857	Hs.326	5.1	3893 7809
	435284	Homo sapiens cDNA FLJ11492 fis, clone H	AA879470	Hs.96849	5.1	3118 7134
	419488	nucleophosmin/nucleoplasmin 3	AA316241	Hs.90691	5.1	1342 5822
	408829	heparan sulfate (glucosamine) 3-O-sulfo	NM_006042	Hs.48384	5.1	264 265 4991
40	409262	hypothetical protein FLJ20624	AK000631	Hs.52256	5.1	333 334 5042
	446142	ESTs	AI754693	Hs.145968	5.1	3820 7748
	418927	ESTs	BE349635	Hs.190284	5.1	1284 5776
	418283	cathepsin K (pseudosclerosis)	S79895	Hs.83942	5.1	1210 1211 5724
	428957	WNT1 inducible signaling pathway protei	NM_003881	Hs.194679	5.1	2491 2492 6656
45	416322	pyrroline-5-carboxylate reductase 1	BE019494	Hs.79217	5.1	989 5554
	409361	sine oculis homeobox (Drosophila) homol	NM_005982	Hs.54416	5.1	344 345 5049
	414733	minichromosome maintenance deficient (S	BE514535	Hs.77171	5.1	860 5454
	415885	KIAA0161 gene product	D79983	Hs.78894	5.1	953 954 5524
	444912	putative prostate cancer susceptibility	AW247380	Hs.12124	5.0	3733 7679
50	448425	ESTs	AI500359	Hs.371249	5.0	4004 7901
	423292	nuclear RNA export factor 2	AK000423	Hs.306209	5.0	1791 1792 6152
	437430	gene predicted from cDNA with a complet	W44671	Hs.124	5.0	3261 7256
	451999	DEAD/H (Asp-Glu-Ala-Asp/His) box polype	AW176401	Hs.380623	5.0	4268 8115
	418113	SRV (sex determining region Y)-box 4	AI272141	Hs.83484	5.0	1194 5711
55	445160	sine oculis homeobox (Drosophila) homol	AI299144	Hs.101937	5.0	3748 7692
	431411	hypothetical protein FLJ20343	AI929382	Hs.252692	5.0	2782 6866
	431347	insulin-like growth factor 2 (somatomed	AI133461	Hs.251664	5.0	2774 6859
	452907	ESTs, Moderately similar to I54374 gene	BE256966	Hs.31652	5.0	4368 8197
	440211	ESTs	AA872730	Hs.125229	5.0	3463 7442
60	436895	carbonic anhydrase XII	AF037335	Hs.5338	5.0	3224 3225 7224
	414883	CDC28 protein kinase 1	AA926960	Hs.348669	5.0	885 5471
	408135	methyltransferase-like 1	AA317248	Hs.42957	5.0	194 4936
	414038	hypothetical protein FLJ22439	BE242722	Hs.180040	5.0	773 5382
	411102	triadin	AA401295	Hs.23926	5.0	515 5175
65	433659	hypothetical protein FLJ10439	AK001301	Hs.3487	4.9	2998 2999 7035
	433092	WAS protein family, member 2	AI936829	Hs.288908	4.9	2939 6989
	433430	ESTs	AI863735	Hs.369982	4.9	2977 7018
	417605	regulator of G-protein signalling 3	AF006609	Hs.82294	4.9	1138 1139 5665
	412490	Homo sapiens cDNA: FLJ22528 fis, clone	AW803564	Hs.288850	4.9	595 5242
70	437206	ESTs, Weakly similar to I38344 titin, c	AW975934	Hs.172004	4.9	3245 7242
	413434	Homo sapiens cDNA FLJ11416 fis, clone H	N41759	Hs.287331	4.9	718 5337
	406706	myosin, heavy polypeptide 1, skeletal m	X03740	Hs.231581	4.9	59 60 4828
	410611	KIAA1628 protein	AW954134	Hs.20924	4.9	480 5148
	442295	Homo sapiens cDNA FLJ11469 fis, clone H	AI827248	Hs.224398	4.9	3555 7527
75	439717	ESTs, Moderately similar to ALU1_HUMAN	W94472	Hs.59529	4.9	3423 7406
	451766	ephrin-B3	NM_001406	Hs.26988	4.9	4255 4256 8104
	409243	KIAA1340 protein	AB037761	Hs.51743	4.9	328 329 5039

	407690	hypothetical protein FLJ14281	R47799	Hs.266957	4.9	150 4895
	407025	Human unknown protein mRNA within the p	U58658	Hs.356460	4.9	96 97 4852
	414812	monokine induced by gamma interferon	X72755	Hs.77367	4.9	874 875 5464
5	424162	ESTs, Weakly similar to ALU2_HUMAN ALU	AA336229	Hs.93135	4.9	1907 6235
	446157	Homo sapiens cDNA: FLJ22562 fis, clone	BE270828	Hs.131740	4.9	3821 7749
	441944	Homo sapiens clone 23767 and 23782 mRNA	AW855861	Hs.8025	4.9	3541 7513
	411742	eukaryotic translation initiation facto	AW247593	Hs.71819	4.9	549 5204
	415702	gb:HSPD18414 HM3 Homo sapiens cDNA clon	F28877	Hs.73680	4.9	942 5515
10	429500	hexabrachion (tenascin C, cytotoactin)	X78565	Hs.289114	4.9	2574 2575 6718
	431183	KDEL (Lys-Asp-Glu-Leu) endoplasmic reti	NM_008855	Hs.250696	4.8	2756 2757 6845
	428409	ESTs	AW117207	Hs.98523	4.8	2438 6616
	451404	ESTs, Weakly similar to T17248 hypothet	AA460775	Hs.6295	4.8	4229 8084
	453115	ESTs, Moderately similar to JC5238 gala	AW772041	Hs.18439	4.8	4392 8218
	448950	CGI-152 protein	AF288687	Hs.9275	4.8	4050 4051 7936
15	426509	pentaxin-related gene, rapidly induced	M31166	Hs.2050	4.8	2243 2244 6468
	451684	CDA14	AF216751	Hs.26813	4.8	4246 4247 8098
	425196	carbonic anhydrase II	AL037915	Hs.155097	4.8	2064 6345
	412755	ESTs, Weakly similar to P4HA_HUMAN PROL	BE144306	Hs.179891	4.8	637 5274
	453393	ESTs	AW956392	Hs.110376	4.8	4418 8240
20	428977	cyclin B2	AK001404	Hs.194698	4.8	2496 6659
	419086	Kallmann syndrome 1 sequence	NM_000216	Hs.89591	4.8	1300 1301 5789
	447519	ESTs	U46258	Hs.339665	4.8	3936 7844
	414359	cadherin 11, type 2, OB-cadherin (osteo	M62194	Hs.75929	4.8	808 5413
25	438093	COP9 (constitutive photomorphogenic, Ar	BE206885	Hs.6076	4.8	3303 7296
	444670	hypothetical protein MGC5370	H58373	Hs.332938	4.8	3714 7666
	409103	XAGE-1 protein	AF251237	Hs.112208	4.7	304 305 5021
	422809	hypothetical protein FLJ10549	AK001379	Hs.121028	4.7	1741 1742 6115
	419762	ESTs	AI608647	Hs.32374	4.7	1387 5855
30	421057	Homo sapiens cDNA: FLJ22063 fis, clone	T58283	Hs.120638	4.7	1501 5940
	419575	topoisomerase (DNA) III alpha	U43431	Hs.91175	4.7	1355 1356 5831
	408196	SRY (sex determining region Y)-box 22	AL034548	Hs.43627	4.7	199 200 4940
	402408	NM_030920*:Homo sapiens hypothetical pr			4.7	4681
	421778	actin related protein 2/3 complex, subu	AA428000	Hs.283072	4.7	1591 6003
35	411894	GLI-Kruppel family member GLI3 (Greig c	M57609	Hs.72916	4.7	559 560 5212
	403285	Target Exon			4.7	4712
	435099	flap structure-specific endonuclease 1	AC004770	Hs.4756	4.7	3104 3105 7123
	413658	A kinase (PRKA) anchor protein 10	AA055369	Hs.372446	4.7	734 5351
	454119	uncoupling protein 4	BE549773	Hs.40510	4.7	4492 8300
40	415667	developmentally regulated GTP-binding p	F11582	Hs.78582	4.7	935 5509
	402672	Target Exon			4.7	4686
	446517	phosphatidylethanolamine N-methyltransf	BE382714	Hs.15192	4.7	3849 7772
	437623	chromosome condensation-related SMC-ass	D63880	Hs.5719	4.7	3275 3276 7269
	447377	transcription factor AP-2 alpha	X77343	Hs.334334	4.7	3920 3921 7831
45	425848	valyl-HRNA synthetase 2	BE242709	Hs.159637	4.7	2150 6402
	448121	hypothetical protein DKFZp564F013	AL045714	Hs.128653	4.7	3979 7881
	414961	myosin-binding protein H	U27266	Hs.927	4.6	896 897 5479
	403903	C5001632*:gil10645308[gb]AAG21430.1[AC0			4.6	4731
	444719	ESTs, Weakly similar to GGE1_HUMAN GAGE	N40147	Hs.43879	4.6	3717 7668
50	418036	latent transforming growth factor beta	Z37976	Hs.83337	4.6	1180 1181 5699
	406976	gb:Human alpha-1 collagen type II gene,	M60299		4.6	92 93 4850
	411852	ESTs, Weakly similar to T00329 hypothet	AA528140	Hs.107515	4.6	555 5208
	421506	thymidine kinase 1, soluble	BE302796	Hs.105097	4.6	1550 5976
	428344	Homo sapiens cDNA FLJ12425 fis, clone M	AW449466	Hs.9299	4.6	2433 6612
55	448734	Homo sapiens mRNA; cDNA DKFZp564H1916 (BE614070	Hs.326416	4.6	4031 7923
	412014	ESTs, Weakly similar to A46010 X-linked	AI620650	Hs.43761	4.6	566 5218
	452436	ESTs, Moderately similar to A46010 X-li	BE077546	Hs.31447	4.6	4330 8164
	445373	ESTs, Weakly similar to DIA1_HUMAN DIAP	AW962886	Hs.199316	4.6	3764 7703
	413004	interleukin enhancer binding factor 2,	T35901	Hs.75117	4.6	667 5300
60	442426	hypothetical protein MGC5370	AI373062	Hs.332938	4.6	3562 7534
	408920	fibronectin leucine rich transmembrane	AL120071	Hs.48998	4.6	276 4999
	425259	Homo sapiens mRNA; cDNA DKFZp564K143 (f	AL 049280	Hs.145010	4.6	2075 6353
	409096	sarcomeric muscle protein	AA194412	Hs.50550	4.6	302 5019
	428279	ESTs, Weakly similar to A47582 B-cell g	AA425310	Hs.155766	4.6	2417 6599
65	449510	ESTs	AI653154	Hs.328147	4.6	4092 7974
	422112	Lsm1 protein	BE540240	Hs.111783	4.5	1649 6046
	427217	ESTs	AA399272	Hs.144341	4.5	2310 6514
	412537	nuclear transcription factor Y, alpha	AL031778	Hs.348999	4.5	601 5247
	430411	bone gamma-carboxyglutamate (gla) prote	X51699	Hs.2558	4.5	2691 2692 6800
70	407204	ESTs, Weakly similar to ALU1_HUMAN ALU	R41933	Hs.140237	4.5	121 4873
	421114	ESTs, Weakly similar to I78885 serine/t	AW975051	Hs.293156	4.5	1507 5946
	408197	ESTs, Weakly similar to A46010 X-linked	AA282262	Hs.107410	4.5	201 4941
	436291	protein regulator of cytokinesis 1	BE568452	Hs.344037	4.5	3180 7185
	414416	hypothetical protein MGC2721	AW409985	Hs.76084	4.5	813 5417
75	407792	putative secreted ligand homologous to	AI077715	Hs.39384	4.5	162 4906
	452461	transcription factor	N78223	Hs.108106	4.5	4333 8167
	436252	Homo sapiens cDNA FLJ11562 fis, clone H	AI539519	Hs.142827	4.5	3179 7184

	422034	Ets2 repressor factor	AC006486	Hs.333069	4.5	1627 1628 6032
	432917	PRO0327 protein	NM_014125	Hs.241517	4.5	2915 2916 6970
	453299	ESTs	W44626	Hs.30627	4.5	4411 8234
5	424265	hair/enhancer-of-split related with YR	AF173901	Hs.144287	4.5	1927 1928 6247
	436481	HSPC150 protein similar to ubiquitin-co	AA379597	Hs.5199	4.5	3192 7197
	420197	ESTs, Weakly similar to A57291 cytokine	AW139647	Hs.88134	4.5	1429 5889
	420576	KIAA1858 protein	AA297634	Hs.54925	4.5	1463 5914
	409012	DKFZP434I216 protein	AL117435	Hs.49725	4.5	293 294 5013
10	419552	gb:zd30a08.s1 Soares_fetal_heart_NbHH19	W63730	Hs.379098	4.4	1350 5828
	407239	leukocyte immunoglobulin-like receptor,	AA076350	Hs.67846	4.4	129 4879
	424330	Homo sapiens cDNA FLJ13596 fis, clone P	AW073953	Hs.34054	4.4	1936 6253
	417933	thymidylate synthetase	X02308	Hs.82962	4.4	1170 1171 5692
	447630	lymphoid enhancer-binding factor 1	AI660149	Hs.44865	4.4	3944 7851
15	404567	NM_015902*:Homo sapiens progesteron induc			4.4	4752
	439053	chaperonin containing TCP1, subunit 2 (BE244588	Hs.6456	4.4	3374 7357
	438982	ESTs, Weakly similar to A47582 B-cell g	AW979101	Hs.291980	4.4	3372 7355
	423575	Intron of periostin (OSF-2os)	C18863	Hs.163443	4.4	1820 6173
	458816	hypothetical protein FLJ10647	AK001509	Hs.144391	4.4	4531 4532 8334
20	443778	Homo sapiens cDNA FLJ14207 fis, clone N	AW964139	Hs.9741	4.4	3642 7605
	430681	ESTs	AW969675	Hs.291232	4.4	2719 6819
	434652	bladder cancer overexpressed protein	AF148713	Hs.125830	4.4	3066 3067 7092
	435937	ESTs	AA830893	Hs.119769	4.4	3164 7172
	447381	Homo sapiens cDNA FLJ14459 fis, clone H	AI377119	Hs.295362	4.4	3922 7832
25	427647	Homo sapiens cDNA FLJ20653 fis, clone K	W19744	Hs.180059	4.4	2354 6548
	424084	hypothetical protein FLJ23056	AI940675	Hs.20914	4.4	1895 6226
	425274	minichromosome maintenance deficient (m	BE281191	Hs.155462	4.4	2079 6356
	412935	tubulin-specific chaperone c	BE267045	Hs.75064	4.4	656 5291
	422599	non-metastatic cells 1, protein (NM23A)	BE387202	Hs.118638	4.4	1710 6092
30	426363	transforming growth factor, beta 3	M58524	Hs.2025	4.4	2210 2211 6446
	418156	nuclear receptor subfamily 1, group I,	W17056	Hs.83623	4.4	1198 5715
	453880	ESTs, Weakly similar to I38022 hypothet	AI803166	Hs.135121	4.4	4458 8272
	423739	ESTs	AA398155	Hs.97600	4.4	1842 6190
	439688	hypothetical protein FLJ12921	AW445181	Hs.209637	4.4	3418 7401
35	449037	Homo sapiens mRNA; cDNA DKFZp586F071 (f	AL050125	Hs.22907	4.4	4060 7944
	418677	SRY (sex determining region Y)-box 5	S83308	Hs.87224	4.4	1267 1268 5764
	433446	ESTs	AW469546	Hs.122116	4.3	2979 7020
	420044	ESTs	AA253164	Hs.136294	4.3	1410 5873
	417124	ESTs	BE122762	Hs.25338	4.3	1082 5623
40	421777	HSPC037 protein	BE562088	Hs.108196	4.3	1590 6002
	430044	ESTs	AA464510	Hs.152812	4.3	2642 6765
	429973	ESTs	AI423317	Hs.164680	4.3	2628 6756
	410366	hypothetical protein	AI267589	Hs.302689	4.3	457 5133
	425308	receptor tyrosine kinase-like orphan re	M97639	Hs.155585	4.3	2087 2088 6362
45	442052	ESTs	AW450515	Hs.128381	4.3	3546 7518
	421848	collagen, type VI, alpha 1	X15880	Hs.108885	4.3	1602 1603 6013
	424840	extra spindle poles, S. cerevisiae, hom	D79987	Hs.153479	4.3	2011 2012 6306
	417788	nuclear transcription factor Y, beta	AI436699	Hs.84928	4.3	1157 5680
	404561	trichorhinophalangeal syndrome I gene (4.3	4751
50	433447	neuronal pentraxin II	U29195	Hs.3281	4.3	2980 2981 7021
	428280	sarcospan (Kras oncogene-associated gen	H05541	Hs.183428	4.3	2418 6600
	406850	collagen, type I, alpha 1	AI624300	Hs.172928	4.3	70 4837
	407730	splicing factor, arginine/serine-rich 9	AI457482	Hs.77608	4.3	155 4899
	426487	variable charge, Y chromosome	AF000979	Hs.170076	4.3	2240 2241 6466
55	410036	calsequestrin 2 (cardiac muscle)	R57171	Hs.57975	4.3	412 5100
	422452	Homo sapiens mRNA; cDNA DKFZp566J1846 (AL110255	Hs.116808	4.3	1685 6073
	421016	transcription factor 3 (E2A immunogloblu	AA504583	Hs.101047	4.3	1497 5937
	427458	ESTs, Weakly similar to LKHU proteoglyc	BE208364	Hs.29283	4.3	2332 6530
	442117	ESTs; hypothetical protein for IMAGE:44	AW664964	Hs.128899	4.3	3551 7523
60	425516	ESTs	BE000707	Hs.353519	4.3	2110 6376
	425398	hypothetical protein similar to tenasci	AL049689	Hs.156369	4.3	2101 2102 6370
	413053	ESTs, Moderately similar to KIAA1399 pr	AW963263	Hs.65377	4.3	674 5306
	406837	immunoglobulin kappa constant	R70292	Hs.156110	4.3	69 4836
	423072	solute carrier family 12 (sodium/potass	AI792946	Hs.123116	4.3	1776 6141
65	435124	ESTs	AA725362	Hs.75514	4.3	3107 7125
	410169	hypothetical protein MGC3047	AI373741	Hs.59384	4.3	428 5112
	436878	ESTs	BE465204	Hs.47448	4.3	3223 7223
	429638	kinectin 1 (kinesin receptor)	AI916662	Hs.211577	4.3	2595 6731
	425532	KIAA0446 gene product	AB007915	Hs.158286	4.3	2112 2113 6378
70	424905	NIMA (never in mitosis gene a)-related	NM_002497	Hs.153704	4.3	2022 2023 6315
	451448	homolog of yeast MOG1	AW952599	Hs.13605	4.3	4231 8086
	432101	EphA3	AI918950	Hs.123642	4.3	2841 6909
	410701	RNA binding motif protein 8A	AF198620	Hs.10283	4.3	487 488 5154
	426817	Homo sapiens mRNA; cDNA DKFZp564C0671 (AL122088	Hs.172627	4.3	2276 6488
	424560	protein predicted by clone 23733	AA158727	Hs.150555	4.2	1972 6279
75	417404	pleckstrin homology-like domain, family	NM_007350	Hs.82101	4.2	1110 1111 5648
	454090	gb:MR0-CT0064-100899-002-h09 CT0064 Hom	AW062462		4.2	4490 8298

	405452	Target Exon		4.2	4784
	406947	DNA-binding protein amplifying expressi	L10403	Hs.3134	4.2
	414312	ESTs	AA155694	Hs.191060	4.2
	435373	ESTs	AW665538	Hs.117689	4.2
5	425514	integrin, alpha 10 2QQ	AF112345	Hs.158237	4.2
	419341	ESTs, Weakly similar to ALU1_HUMAN ALU	N71463	Hs.118888	4.2
	418407	nuclear transcription factor Y, beta	AL044818	Hs.84928	4.2
	435520	HNOEL-iso protein	AA297990	Hs.9315	4.2
	409877	zinc finger protein 106	AW502498	Hs.15220	4.2
10	435523	membrane-spanning 4-domains, subfamily	T62849	Hs.11090	4.2
	449077	ESTs	AW262836	Hs.252844	4.2
	411666	neurofilament 3 (150kD medium)	AF106564	Hs.71346	4.2
	410011	PFTAIRe protein kinase 1	AB020641	Hs.57856	4.2
	435370	ESTs	AI964074	Hs.225838	4.2
15	421917	KIAA1020 protein	AB028943	Hs.109445	4.2
	435818	ESTs	AA700553		4.2
	452110	Homo sapiens cDNA FLJ11309 fis, clone P	T47667	Hs.28005	4.2
	421458	carbohydrate (keratan sulfate Gal-6) su	NM_003654	Hs.104576	4.2
	410286	DKFZP586N2124 protein	AI739159	Hs.61898	4.2
20	417358	KIAA0094 protein	D42084	Hs.82007	4.2
	427239	ubiquitin carrier protein	BE270447	Hs.356512	4.2
	407140	ESTs, Weakly similar to I38022 hypothet	AA059106	Hs.271780	4.2
	406923	gb:G1 phase-specific gene (3' region) [S70622		4.2
	434629	glioma-amplified sequence-41	AA789081	Hs.4029	4.2
25	446238	SCO (cytochrome oxidase deficient, yeas	T95143	Hs.14511	4.2
	433047	methionine-tRNA synthetase	M86135	Hs.279946	4.2
	445413	CGI-147 protein	AA151342	Hs.12677	4.2
	425428	DKFZP586B0621 protein	AL110261	Hs.157211	4.2
	419911	BN51 (BHK21) temperature sensitivity co	L15301	Hs.1276	4.2
30	436856	ESTs	AI469355	Hs.127310	4.2
	411529	Homo sapiens cDNA FLJ12927 fis, clone N	AA430348	Hs.28229	4.1
	417259	chondroitin sulfate proteoglycan 2 (ver	AW903838	Hs.81800	4.1
	451489	amyloid beta (A4) precursor protein-bin	NM_005503	Hs.26468	4.1
	450300	ESTs, Highly similar to ITH4_HUMAN INTE	AL041440	Hs.58210	4.1
35	425688	NGFI-A binding protein 2 (ERG1 binding	U48361	Hs.159223	4.1
	424066	ESTs, Weakly similar to I38022 hypothet	Z99348	Hs.112461	4.1
	440129	ESTs, Weakly similar to S71886 Ste20-li	AA865818	Hs.369523	4.1
	417115	small nuclear ribonucleoprotein polypep	AW952792	Hs.334612	4.1
	453922	budding uninhibited by benzimidazoles 1	AF053306	Hs.36708	4.1
40	429005	lymphocyte antigen 95 (activating NK-re	AJ225109	Hs.194721	4.1
	439755	B7 homolog 3	AW748482	Hs.77873	4.1
	434608	hypothetical protein FLJ22995	AA805443	Hs.179909	4.1
	424378	neural cell adhesion molecule 1	W28020	Hs.167988	4.1
	410813	gb:QV4-NN0039-040500-196-g04 NN0039 Hom	AW895909		4.1
45	435538	low density lipoprotein receptor-relate	AB011540	Hs.4930	4.1
	446444	ESTs	AI743737	Hs.24370	4.1
	437789	ESTs, Weakly similar to T17330 hypothet	AI581344	Hs.127812	4.1
	412677	ESTs	AW029608	Hs.17384	4.1
	453833	cytochrome P450, subfamily VIIIb (stero	AF090320	Hs.35718	4.1
50	414591	ESTs, Weakly similar to ALU8_HUMAN ALU	AI888490	Hs.248107	4.1
	421686	KIAA0584 protein	AB011156	Hs.106794	4.1
	422737	collagen, type III, alpha 1 (Ehlers-Dan	M26939	Hs.119571	4.1
	429317	Homo sapiens cDNA: FLJ21243 fis, clone	AA831552	Hs.268016	4.1
	428134	ESTs	AA421773	Hs.161008	4.1
55	419625	nuclear factor of kappa light polypepti	U91616	Hs.182885	4.1
	450835	hypothetical protein FLJ10767	BE262773	Hs.25584	4.1
	444901	ESTs	AA357543	Hs.250829	4.1
	409585	mitochondrial ribosomal protein L2	R62410	Hs.55041	4.1
	445730	ESTs	AI624342	Hs.179082	4.1
60	413125	glyoxalase I	BE244589	Hs.75207	4.1
	437786	polymerase (DNA directed), eta	BE142681	Hs.155573	4.0
	448719	trinucleotide repeat containing 3	AA033627	Hs.21858	4.0
	411704	hypothetical protein FLJ10074	AI499220	Hs.71573	4.0
	430287	ESTs, Weakly similar to LEU5_HUMAN LEUK	AW182459	Hs.125759	4.0
65	426075	ESTs, Weakly similar to 2109260A B cell	AW513691	Hs.270149	4.0
	411263	kinesin-like 6 (mitotic centromere-asso	BE297802	Hs.69360	4.0
	439092	gb:cc44f08.s1 NCL CGAP_GCB1 Homo sapien	AA 830149		4.0
	443957	hypothetical protein FLJ23412	AA521049	Hs.353013	4.0
	429150	smoothened (Drosophila) homolog	AF120151	Hs.197366	4.0
70	444412	Homo sapiens clone HH409 unknown mRNA	AI147652	Hs.216381	4.0
	429290	neurofilament, heavy polypeptide (200kD	AF203032	Hs.198760	4.0
	432335	ESTs	AA534039	Hs.377990	4.0
	409132	protein kinase, AMP-activated, beta 2 n	AJ224538	Hs.50732	4.0
	423880	DKFZP564C186 protein	BE278111	Hs.134200	4.0
75	452097	a disintegrin-like and metalloprotease	AB002364	Hs.27916	4.0
	407137	gb:ye53h05.s1 Soares fetal liver spleen	T97307		4.0

5	419690	Homo sapiens cDNA FLJ11223 fis, clone P	AK002085	Hs.92308	4.0	1370 5843
	429134	ESTs	AA446953	Hs.99004	4.0	2514 6673
	430130	Homo sapiens mRNA; cDNA DKFZp761G02121	AL137311	Hs.234074	4.0	2650 2651 6772
	428839	Homo sapiens cDNA FLJ14814 fis, clone N	AI767756	Hs.82302	4.0	2480 6648
	447924	ESTs, Weakly similar to T23110 hypothet	AI817226	Hs.313413	4.0	3967 7869
	436637	ESTs	AI783629	Hs.26766	4.0	3206 7208
	442328	ESTs, Weakly similar to ALU4_HUMAN ALU	AI952430	Hs.150614	4.0	3556 7528

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TABLE 1B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

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Pkey	CAT Number	Accession
426413	372468_1	AW954494 AA377823 BG219617 BG195685 BG616269 AI022688
452471	3144769_1	AI903332 AI903301 AI903476 AI903379 AI903351 AI903262 AI903258
454090	579894_1	AW062465 AW062462 BF333918 AW176554 AW062482 AW062481 AW062468 AW062467
435818	136148_1	AA700553 AI241378 AI247835
410813	353225_1	AW895702 BG003544 BG003539 BF994824 BF986640 AW895909 AW805882 AW805813 AW805808 BE176767 BI049482 BI064061
AW895888		
439092	919640_1	AW978407 AA830149 M85983 AW503637 BF352096

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TABLE 1C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NI_position:	Indicates nucleotide positions of predicted exons.

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Pkey	Ref	Strand	NI_position
403088	8954241	Plus	169894-170193,170504-170806
404977	3738341	Minus	43081-43229
405704	4204244	Plus	138842-139051
403071	8954241	Plus	136688-137096
405946	6758796	Plus	28296-28830
403074	8954241	Plus	143375-143561
402408	9796239	Minus	110326-110491
403285	7230870	Minus	73908-74168,74914-75174,75295-75555
402672	8077089	Minus	65791-66596
403903	7710671	Minus	101165-102597
404567	7249169	Minus	101320-101501
404561	9795980	Minus	69039-70100
405452	7656638	Minus	93876-94275

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TABLE 2A

Pkey:	Unique Eos probeset identifier number
Gene name:	Unigene gene title
Accession:	Exemplar Accession number, Genbank accession number
UniGene:	Unigene number
RATIO:	95th percentile of dermatofibrosarcoma protuberans AIs divided by the 95th percentile of normal tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator
SEQ ID #:	nucleic acid and protein sequences provided on CD for search purposes

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Pkey	Gene Name	Accession	UniGene	RATIO	SEQ ID #
419875	proenkephalin	AA853410	Hs.93557	10.4	1391 5859
449048	similar to S68401 (cattle) glucose indu	Z45051	Hs.22920	9.3	4061 7945
441134	cellular retinoic acid-binding protein	W29092	Hs.346950	8.7	3500 7475
439979	hypothetical protein FLJ10430	AW600291	Hs.6823	8.5	3442 7424
424326	ADAM-like disintegrin protease, decysin	NM_014479	Hs.1 45296	7.6	1934 1935 6252
421920	gamma-aminobutyric acid (GABA) receptor	BE551245	Hs.1438	6.0	1614 6022
423236	keratocan	NM_007035	Hs.1 25750	5.9	1788 1789 6150
441636	Homo sapiens mRNA; cDNA DKFZp566E183 (f	AA081846	Hs.7921	5.5	3530 7502
420931	small inducible cytokine B subfamily (C	AF044197	Hs.100431	5.1	1493 1494 5935
420376	protocadherin 18	AL137471	Hs.97266	5.0	1447 1448 5903
426027	platelet-derived growth factor beta pol	NM_002608	Hs.1 976	4.8	2161 2162 6411
428405	cholinergic receptor, nicotinic, alpha	Y00762	Hs.2266	4.7	2436 2437 6615
450375	a disintegrin and metalloproteinase dom	AA009647	Hs.352537	4.7	4159 8028
414085	aldehyde dehydrogenase 1 family, member	AA114016	Hs.75746	4.6	775 5384
413566	sprouty (Drosophila) homolog 4	AW604451	Hs.381153	4.6	730 5347
453033	KIAA0281 gene product	AA325869	Hs.31463	4.6	4383 8210
417153	collagen, type II, alpha 1 (primary ost	X57010	Hs.81343	4.6	1084 1085 5625
440151	gb:ak38e07.s1 Soares_testis_NHT Homo sa	AA868167		4.6	3457 7437
413199	ELAV (embryonic lethal, abnormal vision	M62843	Hs.75236	4.4	687 688 5317
409698	short stature homeobox 2	AF022654	Hs.55967	4.3	378 379 5074
426300	delta-like homolog (Drosophila)	U15979	Hs.169228	4.3	2196 2197 6437
417866	collagen, type XI, alpha 1	AW067903	Hs.82772	4.3	1162 5685
451698	endothelin converting enzyme-like 1	Y16187	Hs.26880	4.2	4249 4250 8100
434747	ESTs	AA837085	Hs.372254	4.1	3073 7097
430896	spinal cord-derived growth factor-B	AW968905	Hs.112885	4.1	2739 6833
424162	ESTs, Weakly similar to ALU2_HUMAN ALU	AA336229	Hs.93135	4.0	1907 6235
418007	matrix metalloproteinase 1 (interstitia	M13509	Hs.83169	3.9	1177 1178 5697

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	429500	hexabrachion (lanscin C, cytolaclin)	X78565	Hs.289114	3.9	2574 2575 6718
	412755	ESTs, Weakly similar to P4HA_HUMAN	PROL BE144306	Hs.179891	3.9	637 5274
	421458	carbohydrate (keratan sulfate Gal-6) su	NM_003654	Hs.1 04576	3.9	1543 1544 5972
5	426287	calpain 6	AF029232	Hs.169172	3.8	2194 2195 6436
	425256	collapsin response mediator protein 1	BE297611	Hs.155392	3.8	2074 6352
	453331	ESTs	AI240665	Hs.352537	3.8	4413 8236
	416658	fibrillin 2 (congenital contractural ar	U03272	Hs.79432	3.7	1020 1021 5577
	425071	diiodinase, iodothyronine, type II	NM_013989	Hs.1 54424	3.7	2043 2044 6330
10	418113	SRY (sex determining region Y)-box 4	AI272141	Hs.83484	3.7	1194 5711
	415989	ESTs	AI267700	Hs.351201	3.7	962 5530
	421566	early growth response 2 (Krox-20 (Droso	NM_000399	Hs.1 395	3.6	1563 1564 5984
	426457	chimerin (chimaerin) 1	AW894667	Hs.380138	3.6	2229 6459
	448731	ESTs	AI522273	Hs.173179	3.6	4030 7922
15	411852	ESTs, Weakly similar to T00329 hypothet	AA528140	Hs.107515	3.6	555 5208
	447033	Predicted gene: Eos cloned; secreted w/	AI357412	Hs.157601	3.6	3885 7802
	406687	matrix metalloproteinase 11 (stromelysi	M31126	Hs.352054	3.6	49 50 4823
	454071	ESTs	AI041793	Hs.42502	3.6	4487 8295
	452944	ESTs	AI266750	Hs.135261	3.6	4371 8199
20	447584	ESTs, Weakly similar to A53531 oncofeta	W48664	Hs.263561	3.5	3940 7847
	408938	ESTs	AA059013	Hs.22607	3.5	279 5002
	446544	ESTs, Weakly similar to Unknown (H.sapi	AI631932	Hs.7047	3.5	3855 7776
	454755	gb:CM1-ST0283-071299-061-h03 ST0283	Hom AW819204		3.5	4503 8309
	449595	ESTs	AW293799	Hs.255238	3.5	4098 7979
25	429139	ESTs	F09092	Hs.66087	3.4	2517 6675
	433645	ESTs, Moderately similar to ALU6_HUMAN	AI821746	Hs.190258	3.4	2995 7033
	452888	ephrin-B2	AW955454	Hs.30942	3.4	4366 8195
	439783	hypothetical protein FLJ14594	AI125760	Hs.24835	3.4	3431 7414
	420067	Homo sapiens mRNA; cDNA DKFZp564O222 (f	T52431	Hs.94795	3.4	1414 5876
30	414821	Fc fragment of IgG, high affinity Ia, r	M63835	Hs.77424	3.4	876 877 5465
	404145	ENSP00000229781: cDNA FLJ12078 fis, clo			3.4	4738
	425262	GS3955 protein	D87119	Hs.155418	3.4	2076 2077 6354
	456967	T-box 2	AW004056	Hs.168357	3.4	4535 8337
	420173	ESTs	AA256151	Hs.22999	3.4	1426 5886
35	421785	Homo sapiens cDNA FLJ11946 fis, clone H	T11937	Hs.323231	3.3	1593 6005
	416539	epithelial membrane protein 1	Y07909	Hs.79368	3.3	1010 1011 5570
	423922	H1 histone family, member 0	Z97630	Hs.226117	3.3	2621 2622 6750
	429524	KIAA1211 protein	AB033037	Hs.205293	3.3	2577 2578 6720
	414467	copline II	AW903820	Hs.85752	3.3	821 5424
40	453960	ESTs	N62791	Hs.231883	3.3	4475 8285
	417333	bromodomain and PHD finger containing,	AL157545	Hs.173179	3.3	1096 5636
	428865	BarH-like homeobox 1	BE544095	Hs.164960	3.3	2485 6651
	425065	Homo sapiens, clone IMAGE:3603836, mRNA	AA371906	Hs.294151	3.3	2042 6329
	435793	KIAA1313 protein	AB037734	Hs.4993	3.2	3152 3153 7162
45	408762	ESTs	BE395364	Hs.118032	3.2	255 7984
	448719	trinucleotide repeat containing 3	AA033627	Hs.21858	3.2	4028 7920
	452291	CDC7 (cell division cycle 7, S. cerevis	AF015592	Hs.28853	3.2	4310 4311 8150
	424498	hypothetical protein DKFZp761L0424	AB033043	Hs.149377	3.2	1963 1964 6274
	407785	ESTs, Weakly similar to A43932 mucin 2	AW207285	Hs.98279	3.1	160 4904
50	408934	ESTs	AI268324	Hs.146050	3.1	278 5001
	435370	ESTs	AI964074	Hs.225838	3.1	3120 7136
	431089	ESTs, Weakly similar to unknown protein	BE041395	Hs.374629	3.1	2745 6838
	426991	Homo sapiens cDNA FLJ10674 fis, clone N	AK001536	Hs.214410	3.1	2294 6502
	414175	hypothetical protein DKFZp761D112	AI308876	Hs.103849	3.1	786 5394
55	424287	hypothetical protein DKFZp434F2322	AL133105	Hs.144633	3.1	1929 1930 6248
	429262	spinal cord-derived growth factor-B	AW503454	Hs.112885	3.1	2536 6690
	416932	ESTs	N20884	Hs.269039	3.1	1049 5598
	417689	KIAA0128 protein; septin 2	AA828347	Hs.90998	3.1	1148 5673
	408915	hepatocellular carcinoma novel gene-3 pr	NM_016651	Hs.4 8950	3.1	274 275 4998
60	423401	coagulation factor II (thrombin) recept	NM_001992	Hs.1 28087	3.0	1803 1804 6160
	400419	Target	AF084545		3.0	22 23 4626
	447471	sprouty (Drosophila) homolog 2	AF039843	Hs.18676	3.0	3930 3931 7839
	438960	ESTs	H26514	Hs.167506	3.0	3370 7353
	446259	hypothetical protein FLJ13391	AA425204	Hs.334721	3.0	3831 7758
65	428305	cartilage linking protein 1	AA446628	Hs.2799	3.0	2426 6607
	421268	ESTs	AI126821	Hs.193513	3.0	1522 5958
	429006	hypothetical protein FLJ13842	AA443143	Hs.50929	3.0	2501 6663
	432994	ESTs	AA573452	Hs.150941	3.0	2922 6976
	443709	ESTs	AI082692	Hs.134662	3.0	3637 7600
70	421666	endothelin 3	AL035250	Hs.1408	3.0	1574 1575 5991
	418054	lysyl oxidase-like 2	NM_002318	Hs.8 3354	2.9	1184 1185 5702
	413474	Homo sapiens cDNA FLJ14438 fis, clone H	T86312	Hs.334485	2.9	726 5343
	401973	NM_018896: Homo sapiens calcium channel			2.9	4671
	449885	ESTs, Weakly similar to JC2025 hexokina	AI673121	Hs.161610	2.9	4119 7997
75	451598	ESTs	N29102	Hs.79658	2.9	4241 8093
	412453	ESTs	R20205	Hs.75236	2.9	589 5237
	449677	gb:zh85d01.s1 Soares_fetal_liver_spleen	AA002071		2.9	4105 7985
	414482	endothelin receptor type A	S57498	Hs.76252	2.9	824 825 5426
	423778	flavin containing monooxygenase 2	Y09267	Hs.132821	2.9	1846 1847 6193
80	400920	NM_025208: Homo sapiens spinal cord-der			2.9	4640
	448672	ESTs	AI955511	Hs.89582	2.9	4025 7917
	457869	Homo sapiens, alpha-1 (VI) collagen	AU077186	Hs.108885	2.9	4561 8359
	451195	mesenchyme homeo box 1	U10492	Hs.438	2.9	4218 4219 8077
	415773	ESTs, Moderately similar to A47582 B-ce	R21651	Hs.324725	2.9	947 5519
85	422674	ESTs, Weakly similar to JW0079 heteroge	AI498100	Hs.103512	2.9	1724 6103
	405889	ENSP00000240003: HYPOTHETICAL 37.3 kDa			2.9	4797
	439130	ESTs	AA306090	Hs.345588	2.9	3378 7361

	429492	ESTs	W21183	Hs.13205	2.9	2572	6716
	422222	hypothetical protein DKFZp434A171	AI699372	Hs.374343	2.9	1661	6056
	417675	similar to murine leucine-rich repeat p	AI808607	Hs.3781	2.9	1144	5670
5	409728	ESTs	AW883968	Hs.321190	2.9	385	5079
	416083	ESTs, Weakly similar to ALU1_HUMAN ALU	R53487	Hs.269122	2.9	971	5539
	431553	cartilage linking protein 1	X78075	Hs.2799	2.9	2792	6874
	450661	ESTs	AW952160	Hs.270753	2.8	4178	8043
	421912	Homo sapiens clone 24775 mRNA sequence	AW021958	Hs.109438	2.8	1610	6019
10	429327	prostaglandin E receptor 4 (subtype EP4)	AA283981	Hs.199248	2.8	2546	6698
	445016	reslin	U79716	Hs.12246	2.8	3738	3739 7684
	428981	ESTs, Weakly similar to ALU2_HUMAN ALU	BE313077	Hs.93135	2.8	2497	6660
	425525	ESTs	AA358883	Hs.23871	2.8	2111	6377
	448493	ESTs	AI524124	Hs.270307	2.8	4006	7903
15	419221	ESTs, Weakly similar to T46428 hypothet	T65460	Hs.21192	2.8	1317	5802
	428626	ESTs	T95297	Hs.17551	2.8	2457	6630
	428392	secretory granule, neuroendocrine prote	H10233	Hs.2265	2.8	2434	6613
	408988	Homo sapiens clone TUA8 Cri-du-chat reg	AL119844	Hs.49476	2.8	289	5009
	456364	Homo sapiens, clone IMAGE:3163559, mRNA	AA234315	Hs.58093	2.8	4520	8324
20	434203	hypothetical protein PRO1855	BE262677	Hs.283558	2.8	3033	7066
	413064	gb:RC1-HT0268-280200-015-b09 HT0268 Hom	BE150462		2.8	677	5309
	424633	bromodomain and PHD finger containing, T71491		Hs.173179	2.8	1980	6284
	452866	Homo sapiens cDNA: FLJ21243 fis, clone	R26969	Hs.268016	2.8	4361	8191
	423308	Homo sapiens mRNA for KIAA1755 protein, AI365680		Hs.114085	2.8	1793	6153
25	411324	gb:QV1-LT0036-150200-070-c11 LT0036 Hom	AWB36835		2.8	525	5184
	437450	Homo sapiens mRNA: cDNA DKFZp762G123 (f	AL390154	Hs.26954	2.8	3265	7260
	408172	phosphoglycerate mutase 2 (muscle)	W02488	Hs.46039	2.8	196	4938
	451090	hypothetical protein	AF175409	Hs.25924	2.8	4210	4211 8070
	439628	ESTs	W81007	Hs.323780	2.8	3412	7395
30	411035	gb:PM0-CT0263-201099-003-f06 CT0263 Hom	AW854930		2.8	511	5171
	430147	hair/enhancer-of-split related with YR	R60704	Hs.234434	2.8	2652	6773
	429484	sera domain, immunoglobulin domain (Ig)	L26081	Hs.2414	2.7	2569	2570 6714
	453931	ESTs	AL121278	Hs.25144	2.7	4469	8280
	406387	Target Exon			2.7	4805	
35	421509	ESTs	AA292223	Hs.137459	2.7	1553	5978
	429359	matrix metalloproteinase 14 (membrane-i	W00482	Hs.2399	2.7	2551	6702
	403372	slit/lin (silent mating type information			2.7	4716	
	414959	Homo sapiens cDNA FLJ12284 fis, clone M	D59968	Hs.45184	2.7	895	5478
	400263	Eos Control		Hs.75309	2.7	4613	
40	451669	Homo sapiens, clone IMAGE:3603836, mRNA	AA349726	Hs.294151	2.7	4243	8095
	420028	carbohydrate (N-acetylglucosamine-6-O)	AB014680	Hs.8786	2.7	1408	1409 5872
	410910	gb:MR4-ST0125-021199-017-d08 ST0125 Hom	AW810204		2.7	503	5165
	413802	ESTs, Weakly similar to S65657 alpha-1C	AW964490	Hs.255938	2.7	744	5359
	423680	Homo sapiens cDNA: FLJ23137 fis, clone	H01345	Hs.24139	2.7	1838	6187
45	423044	protocadherin 18	AA320829	Hs.97266	2.7	1772	6138
	429187	ESTs, Weakly similar to S65657 alpha-1C	AA447648	Hs.163872	2.7	2529	6683
	434276	leucine zipper, putative tumor suppress	AF123659	Hs.93605	2.7	3039	3040 7070
	447749	ESTs	T53260	Hs.8297	2.7	3959	7862
	440168	ESTs	AA868507	Hs.126141	2.7	3458	7438
50	408643	hypothetical protein FLJ21610	F06427	Hs.12727	2.7	246	4976
	427700	dual specificity phosphatase 6	AA262294	Hs.180383	2.7	2361	6554
	438549	trinucleotide repeat containing 3	BE386801	Hs.21858	2.7	3331	7320
	417709	KIAA0247 gene product	D87434	Hs.82426	2.7	1149	1150 5674
	408431	Homo sapiens cDNA: FLJ22536 fis, clone	AI338631	Hs.43266	2.7	220	4954
55	440818	ESTs	AI147060	Hs.146726	2.7	3487	7463
	414359	cadherin 11, type 2, OB-cadherin (osteo	M62194	Hs.75929	2.7	808	5413
	436936	ESTs	AL134451	Hs.197478	2.7	3227	7226
	411789	Adican	AF245505	Hs.72157	2.7	553	554 5207
	429194	ESTs	AA447745	Hs.371421	2.6	2530	6684
60	450141	ESTs	Z44619	Hs.13205	2.6	4135	8010
	434553	hypothetical protein FLJ21687	AW514302	Hs.193170	2.6	3060	7086
	446019	histone deacetylase 3	AI362520	Hs.302718	2.6	3810	7739
	445102	ESTs	AW204610	Hs.22270	2.6	3743	7688
	432812	ESTs	AI935412	Hs.302718	2.6	2910	6965
65	448595	KIAA0644 gene product	AB014544	Hs.21572	2.6	4015	4016 7910
	425717	retinoic acid receptor, beta	X07282	Hs.171495	2.6	2131	2132 6390
	406964	FGFES predicted novel secreted protein M21305			2.6	87	88 4847
	429709	diclkop1 (Xenopus laevis) homolog 2	BE047680	Hs.211869	2.6	2607	6739
	458422	DnaJ (Hsp40) homolog, subfamily C, memb	AI344782	Hs.9683	2.6	4574	8371
70	402354	ENSP00000221785*:Hypothetical 117.0 kDa			2.6	4680	
	402636	Target Exon			2.6	4685	
	415046	ESTs	R40018	Hs.56400	2.6	903	5484
	419550	KIAA0128 protein; septin 2	D50918	Hs.90998	2.6	1348	1349 5827
	429973	ESTs	AI423317	Hs.164680	2.6	2628	6756
75	453876	ESTs, Weakly similar to I38022 hypothet	AW021748	Hs.110406	2.6	4457	8271
	439070	ESTs	AI733278	Hs.7621	2.6	3375	7358
	409723	ESTs	AW885757	Hs.257862	2.6	384	5078
	424153	MAGE-like 2	AA451737	Hs.141496	2.5	1904	6233
	424962	TRAM-like protein	NM_012288	Hs.153954	2.5	2033	2034 6323
80	418140	microfibrillar-associated protein 2	BE613836	Hs.83551	2.5	1196	5713
	404627	NM_001401*:Homo sapiens endothelial dif			2.5	4753	
	446142	ESTs	AI754693	Hs.145968	2.5	3820	7748
	445252	Homo sapiens clone 23927 mRNA sequence	AF052109	Hs.12473	2.5	3752	7695
	422152	solute carrier family 30 (zinc transpor	AA909249	Hs.112282	2.5	1653	6049
	441005	Homo sapiens mRNA: cDNA DKFZp547G133 (f	Z141305	Hs.303172	2.5	3493	7469
85	447253	ESTs	AW250196	Hs.103512	2.5	3907	7822
	400352	taste receptor, type 2, member 7	AF227133		2.5	138	139 4622

433292	gb:PM3-HT0344-281299-008-a12 HT0344 Hom BE154829 Hs.182366 2.5	2968	7009
450842	ESTs AA011358 Hs.103316 2.5	4200	8061
424025	Homo sapiens cDNA: FLJ23131 fis, clone AJ701852 Hs.301296 2.5	1887	6220
420842	hypothetical protein MGC10986 AI083668 Hs.50601 2.5	1485	5929
426933	ESTs AA621076 Hs.179694 2.5	2287	6497
440974	KIAA0700 protein AW450345 Hs.13999 2.5	3492	7468
400608	C10001899:gil7508633 pir JT25392 hypoth 2.5	4633	
404234	Target Exon 2.5	4741	
405521	C8001409*:gil7441226 pir S31212 collag 2.5	4786	
446617	ESTs N41529 Hs.176013 2.5	3859	7780
436045	DKFZP564O0423 protein AB037723 Hs.5028 2.5	3169	3170 7176
404030	NM_015669*:Homo sapiens protocadherin b 2.5	4735	
452734	Homo sapiens mRNA; cDNA DKFZp434O1311 [AL137616 Hs.30483 2.5	4349	8181
435056	glycoprotein M6B AW023337 Hs.5422 2.5	3100	7119
403134	C2000555*:gil6330407 dbj BAA86514.1 (A 2.5	4709	
434891	ESTs AA814309 Hs.123583 2.5	3089	7109
417632	glycoprotein M6B R20855 Hs.379090 2.5	1141	5667
444035	ESTs AW073319 Hs.135067 2.5	3673	7632
433842	ESTs AI652156 Hs.26346 2.5	3009	7044
412792	gb:IL2-HT0449-100100-033-A09 HT0449 Hom BE162129 2.5	642	5279
401357	tumor protein D52-like 1 2.5	4650	
434067	Homo sapiens cDNA FLJ14218 fis, clone N H18913 Hs.124023 2.5	3026	7059
443996	retinal degeneration B beta H17822 Hs.333212 2.5	3666	7625
409921	gb:EST00009 pGEM-T library Homo sapiens AW600239 Hs.285885 2.5	398	5089
422982	ESTs, Weakly similar to A46010 X-linked AA346147 Hs.43143 2.5	1765	6132
414402	gb:601172959F1 NIH_MGC_17 Homo sapiens BE294186 Hs.164680 2.5	812	5416
428211	ESTs AA424211 Hs.183176 2.5	2407	6591
421483	hypothetical protein MGC11333 NM_003388 Hs.1 04717 2.5	1545	1546 5973
455811	gb:MR0-HT0080-011099-002-b03 HT0080 Hom BE141468 2.5	4508	8314
410534	gb:QV0-NN1071-280400-207-g07 NN1071 Hom AW905138 Hs.13291 2.5	471	5142
410642	gb:CMD-UM0001-010300-258-h11 UM0001 Hom AW792784 2.4	484	5152
433430	ESTs AI863735 Hs.369982 2.4	2977	7018
419093	spinal cord-derived growth factor-B AI804054 Hs.112885 2.4	1304	5792
419073	Homo sapiens cDNA FLJ12797 fis, clone N AW372170 Hs.183918 2.4	1296	5786
451820	ESTs AW058357 Hs.199248 2.4	4260	8107
428771	KIAA1069 protein AB028992 Hs.193143 2.4	2471	2472 6641
438944	KIAA1444 protein AA302517 Hs.92732 2.4	3368	7351
401441	Target Exon 2.4	4652	
405523	C8001409*:gil7441226 pir S31212 collag 2.4	4788	
410781	ESTs AJ375672 Hs.165028 2.4	495	5159
453174	ESTs AI633529 Hs.135238 2.4	4399	8224
451507	ESTs, Weakly similar to T31611 hypothet AW291109 Hs.332563 2.4	4236	8090
400829	C11000244:gil11056030 ref NP_061738.1 2.4	4639	
408530	LUC7 (S. cerevisiae)-like BE143941 Hs.16803 2.4	235	4966
438305	gb:yI79c09.s1 Soares infant brain 1NIB H06377 2.4	3315	7306
440209	neurexin 3 H05049 Hs.247837 2.4	3461	7440
438703	ESTs AI803373 Hs.31599 2.4	3348	7333
420547	gonadotropin-regulated testicular RNA h AF155140 Hs.98738 2.4	1460	1461 5912
451752	KIAA1171 protein AB032997 Hs.353087 2.4	4252	4253 8102
437249	hypothetical protein FLJ21347 AA432202 Hs.103147 2.4	3250	7247
422667	ESTs H25642 Hs.132821 2.4	1723	6102
420489	ESTs AA815089 Hs.193513 2.4	1458	5910
446947	polycythemia rubra vera 1; cell surface AF146747 Hs.232165 2.4	3881	3882 7799
441544	ESTs AW300043 Hs.127137 2.4	3523	7496
409633	ESTs AW449822 Hs.55200 2.4	371	5068
404681	C9001188*:gil12738842 ref NP_073725.1 2.4	4756	
420888	dihydropyrimidinase-like 4 AB006713 Hs.100058 2.4	1486	1487 5930
441689	ESTs AI123705 Hs.289068 2.4	3533	7505
414933	ESTs, Weakly similar to I38022 hypothet D60141 Hs.270977 2.4	893	5476
406107	C11002500*:gil3298456 dbj BAA31514.1 (2.4	4801	
446509	protocadherin 20 AF169693 Hs.132892 2.4	3845	3846 7769
423556	dynlcn, cytoplasmic, heavy polypeptide R72694 Hs.356692 2.4	1816	6170
450278	ESTs AW205234 Hs.201587 2.4	4151	8021
439873	ESTs BE159253 Hs.300638 2.4	3436	7419
441389	endocytic receptor (macrophage mannose AF134838 Hs.7835 2.4	3514	3515 7488
455215	ESTs AW867003 Hs.278344 2.4	4506	8312
415314	glycoprotein M6B N88802 Hs.5422 2.4	921	5497
450282	ESTs AA007655 Hs.93523 2.4	4152	8022
444292	ESTs AI139794 Hs.146569 2.4	3690	7646
410333	ras association (RafGDS/AF-6) domain co AL049538 Hs.62349 2.4	451	452 5128
438662	cleavage and polyadenylation specific f AA223599 Hs.6351 2.4	3345	7330
401929	C17001690:gil6005701 ref NP_009099.1 A 2.4	4668	
422578	caudal type homeo box transcription fac AF239666 Hs.1545 2.4	1707	1708 6090
433600	ESTs R42833 Hs.22232 2.4	2990	7029
424870	ESTs T15545 Hs.244624 2.4	2014	6308
431961	Homo sapiens cDNA FLJ11300 fis, clone P AK002162 Hs.272249 2.4	2836	6905
447357	ESTs AI375922 Hs.132821 2.4	3917	7829
402687	Target Exon 2.4	4688	
415892	ESTs, Moderately similar to JC5238 gala H08267 Hs.125979 2.3	955	5525
443749	ESTs R38828 Hs.143463 2.3	3641	7604
427669	ESTs, Moderately similar to KIAA1200 pr AW451832 Hs.255938 2.3	2358	6552
450203	L-kynurenine/alpha-aminoadipate aminotr AF097994 Hs.301528 2.3	4141	4142 8015
400207	Eos Control Hs.76847 2.3	4599	
429030	gb:IL2-UM0079-030300-048-F01 UM0079 Hom AW803288 2.3	2503	6665
458956	gb:h19811.x1 NCI_CGAP_Lu24 Homo sapien BE220675 2.3	4587	8383
451952	ESTs AW078832 Hs.226806 2.3	4266	8113

	434635	Homo sapiens cDNA FLJ11934 fis, clone H H47794	Hs.261699	2.3	3065 7091	
	450701	hypothetical protein XP_098151 (leucine H39950	Hs.288467	2.3	4183 8048	
	419087	hypothetical protein FLJ14594	AI671245	Hs.24835	2.3 1302 5790	
5	410244	ESTs	N62178	Hs.48472	2.3 438 5118	
	441469	ESTs	AW451400	Hs.127019	2.3 3520 7493	
	457455	gb:EST384956 MAGE resequences, MAGL Hom AW972861		2.3	4551 8350	
	440516	cadherin 2, type 1, N-cadherin (neurona S42303	Hs.161	2.3	3472 3473 7451	
	457085	ESTs	AA412446	Hs.365809	2.3 4540 8341	
10	417231	ESTs	R40739	Hs.166351	2.3 1090 5630	
	409348	ESTs	AI401535	Hs.146090	2.3 343 5048	
	402741	NM_002508:Homo sapiens nidogen (enactin		2.3	4689	
	414259	integrin, beta-like 1 (with EGF-like re W44633	Hs.301296	2.3	792 5400	
	433235	contactin 3 (plasmacytoma associated) AB040929	Hs.35089	2.3	2963 2964 7006	
	425863	Human unidentified mRNA, partial sequen U43604	Hs.159901	2.3	2152 6404	
15	452036	sema domain, seven thrombospondin repea NM_003966	Hs.27621	2.3	4273 4274 8119	
	426320	transforming growth factor, beta 2 W47595	Hs.169300	2.3	2205 6442	
	420058	Homo sapiens cDNA FLJ10561 fis, clone N AK001423	Hs.94694	2.3	1411 5874	
	423782	ESTs	AI472209	Hs.323117	2.3	1848 6194
20	418678	cancer/testis antigen (NY-ESO-1) NM_001327	Hs.8 7225	2.3	1269 1270 5765	
	430060	roundabout (axon guidance receptor, Dro NM_002941	Hs.3 01198	2.3	2645 2646 6768	
	444561	c-fos induced growth factor (vascular e NM_004469	Hs.1 1392	2.3	3705 3706 7658	
	437696	hypothetical protein dJ37E16.5 ZB3844	Hs.5790	2.3	3281 7274	
	424893	Homo sapiens cDNA FLJ13303 fis, clone O AW295112	Hs.153648	2.3	2020 6313	
25	443785	basic-helix-loop-helix-PAS protein AW449952	Hs.190125	2.3	3645 7607	
	409041	Hypothetical protein, XP_051860 (KIAA11 AB033025	Hs.50081	2.3	299 300 5017	
	454410	gb:RC3-ST0186-181099-012-c09 ST0186 Hom AW612744		2.3	4499 8305	
	456068	RGC32 protein	AI677897	Hs.76640	2.3	4513 8318
	410126	KIAA0036 gene product	BE169274	Hs.167	2.3	424 5109
30	440129	ESTs, Weakly similar to S71886 Ste20-li AA865818	Hs.369523	2.3	3456 7436	
	452352	X11L-binding protein 51	BE301921	Hs.324104	2.3	4319 8156
	411642	neuroligin 1	NM_014932	Hs.7 1132	2.3	544 545 5200
	425801	gb:HSC14H051 normalized infant brain cD Z43151	Hs.343666	2.3	2144 6397	
	419133	protein tyrosine phosphatase, receptor U46116	Hs.89627	2.3	1307 1308 5795	
35	401961	NM_021626:Homo sapiens serine carboxype		2.3	4669	
	453751	Homo sapiens cDNA: FLJ21238 fis, clone R36762	Hs.101282	2.3	4436 8255	
	425398	hypothetical protein similar to tenasci AL049689	Hs.156369	2.3	2101 2102 6370	
	443916	hypothetical protein DKFZp434C2322 AV647043	Hs.131433	2.3	3658 7619	
	426322	transcobalamin I (vitamin B12 binding p J05068	Hs.2012	2.3	2206 2207 6443	
40	417337	ESTs	AW292905	Hs.128770	2.3	1098 5638
	408015	epidermal differentiation complex prote AW136771	Hs.244349	2.3	184 4926	
	430850	gb:MRO-HT0165-060200-006-e02 HT0165 Hom BE144152		2.3	2734 6830	
	408513	ESTs	AW206468	Hs.103118	2.3	234 4965
	419940	ESTs	AW611903	Hs.144585	2.3	1397 5864
45	410581	tumor endothelial marker 7 precursor AA018982	Hs.125036	2.3	478 5146	
	409098	pleckstrin homology, Sec7 and coiled/co AA132672	Hs.7984	2.3	303 5020	
	434741	ESTs, Weakly similar to ALU1_HUMAN ALU AI762825	Hs.270538	2.3	3072 7096	
	433372	hypothetical protein FLJ23132	AI625577	Hs.287727	2.3	2974 7015
	445526	A kinase (PRKA) anchor protein 7	AA223447	Hs.12835	2.3	3779 7715
50	414110	gb:601112444F1 NIH_MGC_16 Homo sapiens BE251752		2.3	776 5385	
	403574	Target Exon		2.3	4724	
	425227	ESTs	H84455	Hs.40639	2.3	2069 6348
	452339	ESTs	R31567	Hs.97169	2.3	4316 8154
	416857	FGENESH predicted TM containing protein AA188775	Hs.292453	2.3	1042 5592	
55	425781	class-I MHC-restricted T cell associate AF001622	Hs.159523	2.3	2140 2141 6395	
	450513	ESTs	N27780	Hs.374621	2.3	4172 8038
	406064	Target Exon		2.3	4799	
	434269	similar to murine leucine-rich repeat p AK001991	Hs.3781	2.3	3037 3038 7069	
	412218	gb:QVC-NN1020-170400-195-h02 NN1020 Hom AW901809		2.3	578 5227	
60	402742	NM_002508:Homo sapiens nidogen (enactin		2.3	4690	
	433927	small nuclear protein PRAC	AI557019	Hs.116467	2.3	3015 7049
	434728	Homo sapiens cDNA: FLJ22749 fis, clone AA544655		2.3	3071 7095	
	411893	ESTs	R82845	Hs.273789	2.3	558 5211
	444649	ESTs	AW207523	Hs.371001	2.2	3710 7662
65	413457	ESTs	AW974787	Hs.114956	2.2	724 5341
	427297	Homo sapiens, clone MGC:17333, mRNA, co AW292593	Hs.334907	2.2	2315 6518	
	446189	ESTs	H85224	Hs.214013	2.2	3822 7750
	401974	NM_018896*:Homo sapiens calcium channel		2.2	4672	
	424578	hypothetical protein	AK001973	Hs.150890	2.2	1973 1974 6280
70	438555	Homo sapiens mRNA for FLJ00024 protein, AI222089	Hs.143878	2.2	3334 7322	
	452188	ESTs	AI864208	Hs.176275	2.2	4294 8136
	423629	Homo sapiens cDNA: FLJ21909 fis, clone AW021173	Hs.18612	2.2	1828 6180	
	429424	thiopurine S-methyltransferase	BE621985	Hs.381154	2.2	2559 6707
	422611	fucosyltransferase 8 (alpha (1,6) fucos AA158177	Hs.118722	2.2	1712 6094	
75	406483	NM_003059*:Homo sapiens solute carrier		2.2	4807	
	423632	gb:EST32358 Embryo, 12 week I Homo sapi AA328824	Hs.188490	2.2	1829 6181	
	411880	gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapien AW872477		2.2	556 5209	
	448664	splicing factor 3a, subunit 1, 120kD	AI879317	Hs.334691	2.2	4024 7916
	453197	ESTs, Weakly similar to ALU5_HUMAN ALU AI916269	Hs.127804	2.2	4402 8226	
80	423337	axin 2 (conductin, axil)	NM_004655	Hs.1 27337	2.2	1796 1797 6156
	408049	desmoplakin (DPI, DP11)	AW076098	Hs.345588	2.2	187 4929
	410929	ESTs	H47233	Hs.30643	2.2	504 5166
	415400	ESTs	Z42803	Hs.23772	2.2	925 5501
	413059	gb:RC0-HT0295-291199-031-E11 HT0295 Hom BE151498		2.2	675 5307	
85	453041	Homo sapiens cDNA FLJ11918 fis, clone H AI680737	Hs.289068	2.2	4384 8211	
	452834	KIAA1688 protein	AI638627	Hs.105685	2.2	4356 8187
	412591	ESTs, Weakly similar to T26845 hypothet BE217736	Hs.292653	2.2	614 5256	

	434997	ESTs	AW975155	Hs.146014	2.2	3095 7114
	449461	ESTs	AI652043	Hs.195363	2.2	4090 7972
	436761	ESTs	AI817776	Hs.236557	2.2	3213 7214
5	429470	guanine nucleotide binding protein (G p	AI878901	Hs.203862	2.2	2564 6711
	427129	sine oculis homeobox (Drosophila) homol	H29990	Hs.356340	2.2	2304 6510
	405078	Target Exon			2.2	4770
	404682	ortholog of mouse polydomain protein			2.2	4757
	402864	Target Exon			2.2	4696
10	407803	ESTs, Weakly similar to T42689 hypothet	AW081681	Hs.269064	2.2	163 4907
	404673	Target Exon			2.2	4755
	444579	ESTs, Weakly similar to A56194 thrombox	AI168336	Hs.301564	2.2	3708 7660
	424375	Homo sapiens clone 24820 mRNA sequence	AF070547	Hs.146312	2.2	1939 6256
	424442	ESTs, Weakly similar to ZN91_HUMAN ZINC	AW051949	Hs.90035	2.2	1954 6268
15	441746	ESTs	H59955	Hs.127829	2.2	3535 7507
	404735	cofilin 1 (non-muscle)			2.2	4760
	408604	ESTs	D51408	Hs.21925	2.2	243 4973
	447623	Homo sapiens cDNA: FLJ23020 fis, clone	AA350235	Hs.6127	2.2	3942 7849
	431285	ESTs	AW301205	Hs.189422	2.2	2770 6856
20	401851	NM_002401*:Homo sapiens mitogen-activat			2.2	4666
	419157	ESTs	AA234540	Hs.23871	2.2	1313 5798
	439696	ESTs	W95298	Hs.171882	2.2	3419 7402
	446645	ESTs	AI336596	Hs.97266	2.2	3864 7785
	438552	type I transmembrane receptor (seizure-	AJ245820	Hs.6314	2.2	3332 3333 7321
	445363	tubulin-specific chaperone d	NM_005993	Hs.1 2570	2.2	3762 3763 7702
25	421680	Human DNA sequence from clone CTA-984G1	AL031186	Hs.289106	2.2	1576 1577 5992
	414701	gb:HTM1-811F HTM1 Homo sapiens cDNA, mR	BE440040	Hs.193632	2.2	851 5447
	400504	Target Exon			2.2	4629
	407438	gb:Homo sapiens candidate taste recepto	AF227133		2.2	138 139 4886
30	412148	gb:yp82c03.s1 Soares fetal liver spleen	R83307		2.2	574 5224
	453872	ESTs	R59989	Hs.176539	2.2	4455 8269
	442204	ESTs	AI635450	Hs.21914	2.2	3553 7525
	411027	leukocyte immunoglobulin-like receptor,	AF072099	Hs.67846	2.2	509 510 5170
	437230	ESTs	AL133065	Hs.48996	2.2	3248 7245
35	400632	C10001871*:g 1705533 sp P32018 CA1E_CH			2.2	4635
	409549	phospholipase C, epsilon 2	AB029015	Hs.54886	2.2	357 358 5059
	405522	C8001409*:g 7441226 pir S31212 collag			2.2	4787
	425247	matrix metalloproteinase 11 (stromelysi	NM_005940	Hs.1 55324	2.2	2072 2073 6351
	416031	ESTs, Weakly similar to T00329 hypothet	T30290	Hs.107515	2.2	963 5531
40	422311	cytokine receptor-like factor 1	AF073515	Hs.114948	2.2	1669 1670 6062
	425856	hypothetical protein FLJ13993	AA364908	Hs.98927	2.1	2151 6403
	405401	C12001565*:g 11067002 gb AAG02570.1			2.1	4780
	419049	ESTs	AI278445	Hs.43334	2.1	1292 5783
	406796	ribosomal protein L6	AI890167	Hs.349961	2.1	66 4833
45	419584	F-box only protein 24	AF053356	Hs.283764	2.1	1357 1358 5832
	409672	ESTs	AW971226	Hs.298893	2.1	375 5072
	431189	ESTs	AI627353	Hs.126120	2.1	2758 6846
	455813	gb:QV2-HT0083-071299-018-a11 HT0083 Hom	BE141577		2.1	4509 8315
	450530	cytochrome P450, subfamily 46 (choleste	NM_006668	Hs.2 5121	2.1	4173 4174 8039
50	456600	DKFZP564O0823 protein	AL080121	Hs.105460	2.1	4524 4525 8328
	446904	DKFZP434H204 protein	AL110226	Hs.16441	2.1	3875 3876 7795
	423956	Homo sapiens clone 25215 mRNA sequence,	W28203	Hs.136169	2.1	1877 6214
	449773	ESTs	R76294	Hs.302383	2.1	4113 7991
	457740	KIAA0460 protein	AW500458	Hs.29956	2.1	4560 8358
55	437219	ESTs	AW975966	Hs.27788	2.1	3246 7243
	453983	ESTs	H94997	Hs.16450	2.1	4476 8286
	423944	phosphodiesterase 10A	T91433	Hs.348762	2.1	1876 6213
	405563	ENSP00000248912*:IG lambda chain V regl			2.1	4790
	404033	C5000413*:g 202800 gb AAA40703.1 (M64			2.1	4736
60	423225	Thy-1 cell surface antigen	AA852604	Hs.125359	2.1	1786 6148
	457458	ESTs	AW972881	Hs.276507	2.1	4552 8352
	436315	hypothetical protein MGC4837	BE390513	Hs.27935	2.1	3182 7187
	438393	Homo sapiens cDNA: FLJ22272 fis, clone	AA351815	Hs.50740	2.1	3319 7309
	449625	odx (odd Oz/ten-m, Drosophila) homolog	NM_014253	Hs.3 49094	2.1	4101 4102 7982
65	448390	hypothetical protein	AL035414	Hs.21068	2.1	3999 7897
	456549	ESTs	AA283740	Hs.89211	2.1	4523 8327
	419694	hypothetical protein FLJ22029	AW293506	Hs.285243	2.1	1372 5845
	426659	ESTs, Weakly similar to T21371 hypothet	AA382928	Hs.16450	2.1	2260 6478
	401628	ENSP00000219101*:WWP2.			2.1	4657
70	430444	ESTs	AW296421	Hs.121035	2.1	2700 6806
	424911	ESTs	AA984364	Hs.7913	2.1	2026 6317
	422810	Ksp37 protein	AA317400	Hs.98785	2.1	1743 6116
	458935	CDP-diacylglycerol synthase (phosphatid	Y16521	Hs.24812	2.1	4585 4586 8382
	459487	gb:z178b05.s1 Soares_fetal_liver_spleen	AA699665		2.1	4593 8389
75	447771	ESTs	BE505004	Hs.25348	2.1	3963 7865
	436748	collagen, type VI, alpha 2	BE159107	Hs.159263	2.1	3212 7213
	433417	Homo sapiens, Similar to RIKEN cDNA 583	AA587773	Hs.8859	2.1	2976 7017
	411101	gb:RC2-CT0298-300100-014-h09 CT0298 Hom	AW856816		2.1	514 5174
	408953	ESTs	AW297144	Hs.335802	2.1	282 5004
80	457067	hypothetical protein FLJ22624	R36022	Hs.179566	2.1	4539 8340
	441405	ESTs	AW136087	Hs.126896	2.1	3517 7490
	400360	Homo sapiens pregnancy-induced hyperten	AF232216		2.1	16 17 4623
	435384	gb:ac29b10.s1 Stralagene ovary (937217)	AA679202	Hs.380314	2.1	3122 7138
	442117	ESTs; hypothetical protein for IMAGE:44	AW664964	Hs.128899	2.1	3551 7523
	422766	heparan sulfate (glucosamine) 3-O-sulfo	AA334108	Hs.159572	2.1	1735 6111
85	408904	gb:Human SEF2-1D protein (SEF2-1D) mRNA	M74720		2.1	75 76 4841
	418383	ESTs	AA218986	Hs.118854	2.1	1224 5733

	401583	Target Exon		2.1	4655
	402236	NM_025040:Homo sapiens hypothetical pro		2.1	4675
	423604	ESTs	AA486585	Hs.258901	1825 6178
5	402888	Target Exon		2.1	4698
	443620	ESTs, Weakly similar to ALU7_HUMAN ALU	AJ079575	Hs.134540	3630 7593
	428046	ESTs, Moderately similar to I38022 hypo	AW812795	Hs.337534	2393 6579
	419198	ESTs	AA234938	Hs.87384	1315 5800
	446918	KIAA1577 protein	AL135125	Hs.13913	3877 7796
10	447720	ESTs	AL038765	Hs.161304	3952 7858
	440483	ESTs	AI200836	Hs.356890	3467 7446
	416406	lipoma HMGIC fusion partner-like 2	D86961	Hs.79299	1001 1002 5564
	446997	hypothetical protein FLJ20898	AA130390	Hs.25549	4057 7941
	425403	Human DNA sequence from clone 1198H6	on AL023753	Hs.156406	2103 6371
15	457646	ESTs	AA725650	Hs.112948	4559 8357
	413482	ESTs	AA129869	Hs.197143	727 5344
	427778	ESTs	AA412323	Hs.105323	2368 6559
	419043	ets variant gene 1	T19167	Hs.89566	1291 5782
	421568	ESTs	W85858	Hs.99804	1565 5985
20	421398	vav 2 oncogene	AW629852	Hs.4248	1540 5970
	424551	KIAA0320 protein	AB002318	Hs.150443	1970 1971 6278
	401754	C17002014*:[gil12740832]ref[XP_008642.2]		2.1	4659
	405230	C2001066:gil10257425[ref]NP_033892.1] C		2.1	4773
	419700	galactokinase 1	AF084935	Hs.92357	1373 1374 5846
25	400135	Eos Control		Hs.118890	4597
	408209	ets variant gene 5 (ets-related molcul	NM_004454	Hs.4 3697	204 205 4944
	404685	NM_022127:Homo sapiens solute carrier f		2.1	4758
	454013	growth hormone releasing hormone	L00137	Hs.37023	4479 4480 8289
	446048	KIAA1811 protein	AI272364	Hs.182081	3815 7743
30	433323	ESTs	AA805132	Hs.159142	2970 7011
	436773	PC4 and SFRS1 interacting protein 1	AW078629	Hs.351305	3215 7216
	415345	gb:HSC11C121 normalized Infant brain cD	F06228	2.1	924 5500
	452997	ESTs	N64777	Hs.44656	4377 8205
	423582	Homo sapiens cDNA FLJ11812 fis, clone H	BE000831	Hs.23837	1821 6174
35	423508	hepatitis A virus cellular receptor 1	AW604297	Hs.129711	1814 6168
	437544	EST	AL037786	Hs.210786	3269 7263
	448211	PRO0659 protein	BE384592	Hs.6451	3989 7888
	421100	Homo sapiens cDNA: FLJ21763 fis, clone	AW351839	Hs.124660	1505 5944
	414611	Homo sapiens cDNA FLJ13656 fis, clone P	AA149955	Hs.85077	837 5437
40	400098	Eos Control		2.1	4596
	414443	platelet-derived growth factor receptor	AU077268	Hs.76144	817 5421
	429091	ESTs	AA935658	Hs.374241	2512 6671
	410295	nidogen (enactin)	AA741357	Hs.356624	450 5127
	435397	ESTs	AI809920	Hs.199676	3123 7139
45	430228	ESTs, Highly similar to T00391 hypothet	AW950939	Hs.6382	2663 6780
	451302	ESTs	H39006	2.1	4223 8080
	414633	gb:z107b07.s1 Soares_pregnant_uterus_Nb	AA150238	2.1	839 5439
	450408	ESTs	AI694959	Hs.202340	4164 8032
	452328	ESTs	AA805679	Hs.61271	4315 8153
50	421197	gb:z121g02.r1 Soares ovary tumor NbHOT	AA284739	Hs.344806	1516 5953
	438816	gb:PMO-LT0017-031299-001-c07 LT0017	Hom AW835829	2.1	3354 7338
	439791	ESTs	H77774	Hs.35755	3432 7415
	440326	ESTs	AW630250	Hs.132161	3466 7445
	458846	ESTs	AI589615	Hs.185602	4582 8379
55	403433	NM_001622:Homo sapiens alpha-2-HS-glyco		2.1	4720
	426773	KIAA0440 protein	NM_015556	Hs.1 72180	2269 2270 6484
	404917	Target Exon		2.1	4764
	417272	ESTs	AA343751	Hs.85992	1093 5633
	428433	ESTs	AA521410	Hs.41371	2442 6620
60	449634	ESTs	AI656553	Hs.197715	4103 7983
	434241	Homo sapiens PRO3077 mRNA, complete cds	AF119913	2.0	3034 3035 7067
	402001	Target Exon		2.0	4673
	427876	ESTs	AI494291	Hs.369171	2381 6569
	409112	quinone oxidoreductase homolog	BE243971	Hs.50649	306 5022
65	445289	ESTs	AW275575	Hs.371247	3756 7698
	408870	ESTs	AA058586	Hs.129907	271 4996
	419536	gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	AA603305	2.0	1347 5826
	413305	Homo sapiens cDNA: FLJ23176 fis, clone	NM_000426	Hs.75279	697 698 5324
	455046	gb:PMO-CT0237-141099-001-c06 CT0237	Hom AW852480	2.0	4504 8310
70	424291	ephrin-B1	AL120051	Hs.144700	1931 6249
	440966	ESTs, Weakly similar to MCAT_HUMAN MITO	AI401006	Hs.376694	3491 7467
	423469	DKFZP586N1922 protein	AA326213	Hs.7357	1811 6166
	402945	Target Exon		2.0	4699
	419587	ESTs, Weakly similar to T2D3_HUMAN TRAN	AI638859	Hs.227699	1369 5842
75	405651	Target Exon		2.0	4791
	423925	Human clone 23629 mRNA sequence	AW003668	Hs.135587	1873 6211
	429955	ESTs, Weakly similar to ZN91_HUMAN ZINC	AA461317	Hs.247150	2625 6753
	426514	bone morphogenetic protein 7 (osteogeni	BE616633	Hs.170195	2246 6470
	448019	ESTs, Moderately similar to I38022 hypo	AW947164	Hs.195641	3970 7872
80	412902	gb:QVO-BN0147-290400-214-c01 BN0147	Hom BE008018	2.0	654 5289
	427400	hypothetical protein FLJ11939	AW245084	Hs.94229	2325 6525
	423648	hypothetical protein FLJ20449	AK000456	Hs.130546	1833 1834 6184
	450785	Homo sapiens, alpha-1 (VI) collagen	AA852713	Hs.108885	4193 8056
	420743	ESTs	AA279885	Hs.99745	1475 5921
	449851	ESTs	AW207738	Hs.231946	4118 7996
85	419437	neogenin (chicken) homolog 1	U61262	Hs.90408	1338 1339 5820
	430891	G protein-coupled receptor 8	U22492	Hs.248118	2737 2738 6832

	434011	clone FLB5214	AW953437	Hs.5486	2.0	3023 7056
	401972	NM_018896*:Homo sapiens calcium channel			2.0	4670
	450271	ESTs	AI693900	Hs.87224	2.0	4150 8020
	431475	putative nuclear protein	AI567669	Hs.40342	2.0	2791 6873
5	406673	major histocompatibility complex, class	M34996	Hs.198253	2.0	90 91 4821
	438251	ESTs	AI435502	Hs.14931	2.0	3310 7302
	402285	sclerostin			2.0	4677
	423940	SEC14 (S. cerevisiae)-like 2	NM_012429	Hs.2 77728	2.0	1874 1875 6212
	454050	ESTs	AW022889	Hs.233176	2.0	4484 8293
10	428664	similar to SALL1 (sal (Drosophila)-like	AK001666	Hs.189095	2.0	2461 6633
	428878	ESTs	AA436884	Hs.48926	2.0	2486 6652
	439668	frizzled (Drosophila) homolog 8	AI091277	Hs.302634	2.0	3414 7397
	448882	protease, serine, 12 (neurotrypsin, mot	AJ001531	Hs.22404	2.0	4045 4046 7933
	407915	ESTs, Weakly similar to JC5256 adipocyl	AI342364	Hs.313515	2.0	181 4923
15	435977	brain-specific membrane-anchored protel	AL138079	Hs.5012	2.0	3166 7174
	417563	gb:zx52a10.r1 Soares_fetal_liver_spleen	AA203701		2.0	1133 5661
	426666	CD22 antigen	AW500131	Hs.171763	2.0	2261 6479
	419200	EST	AW966405	Hs.313342	2.0	1316 5801
	415079	hypothetical protein FLJ23548	R43179	Hs.22895	2.0	908 5487
20	446205	ESTs	AW172662	Hs.149479	2.0	3823 7751
	457207	tryptophan rich basic protein	H56585	Hs.198308	2.0	4541 8342
	442414	ribonuclease 6 precursor	BE408758	Hs.8297	2.0	3560 7532
	401356	tumor protein D52-like 1			2.0	4649
	411171	gb:QV2-ST0296-150200-040-c10 ST0296 Hom	AW820260		2.0	518 5178
25	458202	ESTs	C14215	Hs.102572	2.0	4568 8365
	453118	ESTs	AW195849	Hs.252757	2.0	4393 8219
	445517	hypothetical protein	AF208855	Hs.12830	2.0	3777 3778 7714
	420762	dolichyl-phosphate (UDP-N-acetylglucosa	U51699	Hs.143509	2.0	1477 5923
	454074	ESTs	R63503	Hs.159795	2.0	4488 8296
30	425741	Homo sapiens clone 24628 mRNA sequence	AF052152	Hs.129997	2.0	2133 6391
	442609	selenoprotein N	AL020996	Hs.8518	2.0	3574 7544
	412806	L-kynurenine/alpha-aminoadipate aminotr	W05694	Hs.352546	2.0	648 5284
	403226	C2001193*:gi 9966829 ref NP_065091.1			2.0	4711
	434539	ESTs, Weakly similar to MUC2_HUMAN MUCI	AW748078	Hs.214410	2.0	3059 7085
35	427647	Homo sapiens cDNA FLJ20653 fis, clone K W19744		Hs.180059	2.0	2354 6548
	450823	complement-c1q tumor necrosis factor-re	T81223	Hs.22011	2.0	4198 8059
	446254	Homo sapiens cDNA FLJ12832 fis, clone N BE179829		Hs.179852	2.0	3830 7767
	443888	hypothetical protein FLJ12752	AI434150	Hs.237146	2.0	3654 7615
	444121	ESTs	AI124734	Hs.40866	2.0	3678 7636
40	411536	gb:IL3-CT0219-280100-062-B11 CT0219 Hom	AW850510		2.0	540 5197
	447949	EST	AI446820	Hs.165839	2.0	3969 7871
	412275	gb:QV2-NN1073-220400-159-h12 NN1073 Hom	AW905372		2.0	579 5228
	456103	ESTs	Z39430	Hs.213248	2.0	4514 8319
	401111	Target Exon			2.0	4642
45	404156	C6002456:gi 6755268 ref NP_036008.1 RA			2.0	4739
	404293	ligand of neuronal nitric oxide synthas			2.0	4745
	432525	ESTs, Weakly similar to YQ42_CAEEL HYPO	AI796096	Hs.109414	2.0	2882 6943
	437845	ESTs	AA769578	Hs.90488	2.0	3290 7283
	456805	empty spiracles (Drosophila) homolog 1	AW771596	Hs.140400	2.0	4530 8333
50	458560	hypothetical protein MGC16202	AI699099	Hs.246914	2.0	4576 8373
	458676	ESTs	AI692464	Hs.202263	2.0	4578 8375
	426363	transforming growth factor, beta 3	M58524	Hs.2025	2.0	2210 2211 6446
	420324	prostate androgen-regulated transcript	AF163474	Hs.96744	2.0	1445 1446 5902
	406634	GDP dissociation inhibitor 1	AA386235	Hs.74576	2.0	31 4813
55	433365	ESTs	AF026944	Hs.293797	2.0	2973 7014
	422627	transforming growth factor, beta-induce	BE336857	Hs.118787	2.0	1715 6097
	449579	ESTs, Weakly similar to T46425 hypothet	AW207260	Hs.134014	2.0	4097 7978
	440037	ESTs	AA851611	Hs.130643	2.0	3447 7429
	409200	KIAA0076 gene product	AL042914	Hs.51039	2.0	325 5037
60	412104	Homo sapiens, Similar to RIKEN cDNA 221	AW205197	Hs.240951	2.0	569 5220
	416110	hypothetical protein DKFZp564A176	Z42262	Hs.322844	2.0	974 5541
	445644	ESTs, Moderately similar to A47582 B-ce	R77768	Hs.271593	2.0	3788 7720
	407604	collagen, type VIII, alpha 2	AW191962	Hs.353001	2.0	145 4891
65	426919	ELAV (embryonic lethal, abnormal vision	AL041228	Hs.166109	2.0	2284 6495
	428949	hypothetical protein DKFZp434J0617	AA442153	Hs.104744	2.0	2490 6655
	456034	gb:UL-H-B13-ala-a-12-0-UL.s1 NCI_CGAP_S	AW450979		2.0	4510 8316
	434149	hypothetical protein MGC5469	Z43829	Hs.244624	2.0	3030 7063
	452119	ESTs	AI656378	Hs.33461	2.0	4291 8133
	447499	protocadherin beta 16	AW262580	Hs.147674	2.0	3934 7842
70	416201	ESTs	AA467752	Hs.195161	2.0	980 5547
	423568	growth arrest-specific 2	NM_005256	Hs.1 29818	2.0	1818 1819 6172
	431103	pleiotrophin (heparin binding growth fa	M57399	Hs.44	2.0	2748 2749 6840
	433972	cisplatin resistance-associated overexp	AI878910	Hs.278670	1.9	3021 7054
	400235	NM_005336:Homo sapiens high density lip		Hs.177516	1.9	4604
75	440652	ESTs	AI216751	Hs.143977	1.9	3478 7456
	412782	ESTs, Weakly similar to I38022 hypothet	AI189211	Hs.259347	1.9	640 5277
	403857	Target Exon			1.9	4730
	450258	chimerin (chimaerin) 2	R94862	Hs.286055	1.9	4149 8019
	431242	KIAA1201 protein	AA987742	Hs.347534	1.9	2766 6853
80	432952	Homo sapiens cDNA FLJ12187 fis, clone M	AA813887	Hs.188173	1.9	2918 6972
	408212	hypothetical protein	AA297567	Hs.43728	1.9	206 4945
	442694	ESTs, Weakly similar to T13476 hypothet	AI217992	Hs.255938	1.9	3577 7547
	401797	Target Exon			1.9	4563
	403489	C7002058:gi 585761 sp P38024 PUR6_CHICK			1.9	4722
85	452965	Human DNA sequence from clone RP11-524D	AI904779	Hs.247525	1.9	4374 8202
	433859	ESTs	AW896758	Hs.273789	1.9	3010 7045

	436252	Homo sapiens cDNA FLJ11562 fis, clone HAI539519	Hs.142827	1.9	3179 7184	
	430110	gb:aa24c01.r1 NCL_CGAP_GCB1 Homo sapien	AA465314	1.9	2649 6771	
	403404	Target Exon		1.9	4718	
5	407753	ESTs	AL045916	Hs.179972	1.9	157 4901
	436838	ESTs	AW978101	Hs.291787	1.9	3219 7220
	429150	smoothed (Drosophila) homolog	AF120103	Hs.197366	1.9	2519 2520 6677
	420103	aldehyde dehydrogenase 1 family, member	AA382259	Hs.95197	1.9	1416 5878
	446936	ESTs	H10207	Hs.47314	1.9	3880 7798
	423961	perlestin (OSF-2os)	D13668	Hs.136348	1.9	1878 1879 6215
10	440704	insulin-like growth factor binding prot	M69241	Hs.162	1.9	3482 3483 7459
	414764	ESTs	AW013887	Hs.31522	1.9	868 5460
	435931	RNA binding motif protein 9	AI077464	Hs.351478	1.9	3163 7171
	426138	Homo sapiens clone 23798 and 23825 mRNA	D81871	Hs.167036	1.9	2178 6423
15	426054	ELAV (embryonic lethal, abnormal vision	U12431	Hs.166109	1.9	2164 2165 6413
	427375	metallocarboxypeptidase CPX-1	AL035460	Hs.177536	1.9	2320 2321 6522
	423600	ESTs	AI633559	Hs.310359	1.8	1824 6177
	420705	fetal Alzheimer antigen	AB032251	Hs.99872	1.8	1471 1472 5919
	448379	KIAA1130 protein	AI097463	Hs.21035	1.8	3995 7894
20	431457	integrin, alpha 11	NM_012211	Hs.2 56297	1.8	2787 2788 6870
	413195	protease, serine, 12 (neurotrypsin, mol	AA127382	Hs.22404	1.8	686 5316
	425064	ESTs	AW953237	Hs.193513	1.8	2041 6328
	411737	hypothetical protein	AW160339	Hs.71791	1.8	548 5203
	440293	ESTs	AI004193	Hs.238889	1.8	3465 7444
25	434355	ESTs	AA630865	Hs.186556	1.8	3049 7076
	401849	Target Exon		1.8	4665	
	442420	ESTs	AI024834	Hs.131729	1.8	3561 7533
	414142	hemiscentin (fibulin 6)	AW368397	Hs.334485	1.8	781 5390
	441149	ESTs	AI569766	Hs.13205	1.8	3501 7476
30	452862	ADAMTS2 (a disintegrin-like and metal	AW378065	Hs.8687	1.8	4360 8190
	429910	5-hydroxytryptamine (serotonin) recepto	NM_000867	Hs.2 507	1.8	2617 2618 6747
	424077	Homo sapiens mRNA; cDNA DKFZp564G1162 (AL080082	Hs.139006	1.8	1892 6224
	433455	ESTs	AA360439	Hs.49476	1.8	2982 7022
	437327	Homo sapiens mRNA; cDNA DKFZp761L23121	AL353942	Hs.306504	1.8	3252 7249
35	435908	Homo sapiens mRNA for KIAA1755 protein,	AI569989	Hs.114085	1.8	3162 7170
	422213	ESTs	AA306385	Hs.133160	1.8	1660 6055
	415910	chemokine (C-X3-C) receptor 1	U20350	Hs.78913	1.8	957 958 5527
	425297	gb:EST63062 Jurkat T-cells V Homo sapie	AA354685		1.8	2086 6361
	448425	ESTs	AI500359	Hs.371249	1.8	4004 7901
40	410345	gb:hi29d09.x1 NCL_CGAP_Co14 Homo sapien	AW662559		1.8	454 5130
	423013	secreted modular calcium-binding protel	AW875443	Hs.22209	1.8	1769 6135
	447691	sperm acrosome associated 1	AI809484	Hs.161241	1.8	3948 7855
	421044	Human DNA sequence from clone RP1-238D1	AF051871	Hs.101302	1.8	1499 1500 5939
	445718	ESTs	H79791	Hs.15227	1.7	3794 7725
45	450676	ESTs	AI147155	Hs.279727	1.7	4180 8045
	403451	Target Exon		1.7	4721	
	421016	transcription factor 3 (E2A immunoglobu	AA504583	Hs.101047	1.7	1497 5937
	432842	hypothetical protein MGC4485	AW674093	Hs.334822	1.7	2911 6966
	446782	ESTs	AI653048	Hs.144006	1.7	3872 7792
50	412182	Splicing factor, arginine/serine-rich,	AA205588	Hs.73737	1.7	577 5226
	419745	slug (chicken homolog), zinc finger pro	AF042001	Hs.93005	1.7	1381 1382 5851
	404394	ENSP00000241075:TRRAP PROTEIN.			1.7	4747
	436605	ESTs	AI187742	Hs.125562	1.7	3204 7206
	405387	NM_022170*:Homo sapiens Williams-Beuren			1.7	4779
55	440676	LIM and senescent cell antigen-like dom	NM_004987	Hs.1 12378	1.7	3479 3480 7457
	404208	C6001282:g[4504223]ref[NP_000172.1] g[1.7	4740
	437118	CD9 partner 1	AB037857	Hs.300591	1.7	3236 3237 7235
	403790	NM_001334*:Homo sapiens cathepsin O (CT			1.7	4728
	431467	Homo sapiens mRNA; cDNA DKFZp434E0528 (N71831	Hs.256398	1.7	2789 6871
60	432439	Homo sapiens cDNA FLJ12394 fis, clone M	AW972926	Hs.209209	1.7	2875 6937
	405203	NM_002086*:Homo sapiens growth factor r			1.7	4772
	426413	gb:EST90805 Synovial sarcoma Homo sapie	AA377823		1.7	2219 6453
	443813	Homo sapiens mRNA; cDNA DKFZp667D095 (f	AA876372	Hs.93961	1.7	3648 7610
	440650	Human DNA sequence from PAC 75N13 on ch	R44692	Hs.326801	1.7	3477 7455
65	412454	ESTs	R55745	Hs.75236	1.7	590 5238
	447198	ESTs	D61523	Hs.283435	1.6	3898 7814
	432975	chimerin (chimaerin) 2	AA331517	Hs.286055	1.6	2920 6974
	445139	synaptotagmin XIII	AB037848	Hs.12365	1.6	3746 3747 7691
	433212	ESTs	BE218049	Hs.121820	1.6	2956 7001
70	442739	cytosolic acyl coenzyme A thioester hyd	NM_007274	Hs.8 679	1.6	3581 3582 7550
	420208	silver (mouse homolog) like	BE276055	Hs.95972	1.6	1431 5891
	425841	ESTs	BE262951	Hs.99052	1.6	2148 6400
	404977	Insulin-like growth factor 2 (somatomed			1.6	4766
	447565	chromosome 12 open reading frame	AF052105	Hs.18879	1.6	3939 7846
75	433013	axin 2 (conductin, axil)	AI697890	Hs.127337	1.6	2927 6979
	425082	inositol 1,4,5-triphosphate receptor, t	N44238	Hs.102991	1.6	2048 6333
	448299	hypothetical protein FLJ10392	AA497044	Hs.20887	1.6	3992 7891
	432682	ESTs	AI376400	Hs.159588	1.6	2896 6955
	407054	gb:H.sapiens NOS2 gene, exon 27.	X85781		1.6	101 4855
80	430238	hydroxyacid oxidase 2 (long chain)	N72519	Hs.236545	1.6	2665 6782
	421917	KIAA1020 protein	AB028943	Hs.109445	1.6	1612 1613 6021
	445537	EGF-like-domain, multiple 6	AJ245671	Hs.12844	1.6	3780 3781 7716
	421948	keratin 6A	L42583	Hs.334309	1.6	1618 1619 6025
	428418	ESTs	AI368826	Hs.8768	1.6	2441 6619
	405674	NM_022775:Homo sapiens hypothetical pro			1.5	4792
85	455629	histone deacetylase 3	AW891965	Hs.367942	1.5	4526 8329
	433577	ESTs	AW007080	Hs.284192	1.5	2989 7028

429686	Homo sapiens cDNA: FLJ21086 fis, clone	AI871613	Hs.159066	1.5	2604 6736
421187	KIAA0680 gene product	NM_014721	Hs.1 02471	1.5	1514 1515 6952
400333	ATP7B	S77447		1.5	10 11 4620
415705	collin	U06632	Hs.966	1.5	943 944 5516
444083	gb:oo17a10.x1 Soares_NSF_F8_SW_OT_PA_P_	AI123195	Hs.47783	1.5	3674 7633
443184	ESTs	AE38728	Hs.135159	1.5	3607 7574
433209	KIAA1474 protein	AB040907	Hs.278436	1.4	2953 2954 6999
449969	Homo sapiens cDNA FLJ14337 fis, clone P	AW295142	Hs.180187	1.4	4123 8001
400220	Eos Control		Hs.155560	1.4	4600
418819	ESTs	AA228776	Hs.191721	1.4	1274 5769
425176	TEA domain family member 1 (SV40 transc	AW015644	Hs.42458	1.4	2063 6344
417366	small proline-rich protein 1B (cornifin	BE185289	Hs.1076	1.4	1104 5642
418154	nuclear receptor subfamily 1, group I,	BE165866	Hs.352403	1.4	1197 5714
433075	sortilin 1	NM_002959	Hs.3 51872	1.4	2936 2937 6987
451166	ESTs	T98171	Hs.185675	1.4	4216 8075
401914	Target Exon			1.4	4667
446619	secreted phosphoprotein 1 (osteopontin,	AU076643	Hs.313	1.4	3861 7782
430390	KIAA0969 protein	AB023186	Hs.343666	1.4	2666 2667 6797
454478	superoxide dismutase 2, mitochondrial	AW805749	Hs.372783	1.3	4501 8307
443271	ESTs	BE568568	Hs.159066	1.3	3616 7582
428748	Ksp37 protein	AW593206	Hs.98785	1.3	2468 6638
417258	gb:yy60a09.s1 Soares_multiple_sclerosis	N58885	Hs.166361	1.3	1091 5631
403830	NM_001328*:Homo sapiens C-terminal bind			1.3	4729
419301	tenomodulin protein	AA236166	Hs.132957	1.3	1328 5811
423325	hypothetical protein FLJ22427	R55565	Hs.334691	1.3	1794 6154
431566	J domain containing protein 1	AF176012	Hs.260720	1.3	2797 2798 6877
432078	hypothetical protein FLJ12541 similar t	BE314877	Hs.24553	1.3	2838 6907
435886	hepatocellular carcinoma-associated ant	BE265839	Hs.12126	1.3	3159 7167
407100	gb:F1-1179D 22 week old human fetal liv	R29657		1.3	108 4860
444015	ESTs	AI472865	Hs.135534	1.3	3669 7628
400252	NM_004651*:Homo sapiens ubiquitin spec		Hs.171501	1.3	4609
422567	glypican 6	AF111178	Hs.118407	1.3	1702 1703 6087
408784	ESTs	AW971350	Hs.63386	1.3	257 4986
431759	G protein pathway suppressor 1	U20285	Hs.268530	1.2	2818 2819 6893
439343	hypothetical protein FLJ11808	AF086161	Hs.114611	1.2	3394 7377
433058	Homo sapiens, Similar to CG8405 gene pr	H86865	Hs.380962	1.2	2933 6985
422168	S100 calcium-binding protein A7 (psoria	AA586894	Hs.112408	1.2	1654 6050
400259	NM_017432*:Homo sapiens prostate tumor		Hs.19555	1.2	4610
431725	Norrie disease (pseudoglioma)	X65724	Hs.2839	1.2	2812 2813 6888
419418	luberos scleriosis 2	X75621	Hs.90303	1.2	1335 1336 5818
433220	ESTs	AI076192	Hs.131933	1.1	2957 7002
428698	KIAA1866 protein	AA852773	Hs.334838	1.1	2463 6635
401203	Target Exon			1.1	4647
420798	keratin 10 (epidermolytic hyperkeratosis	W93774	Hs.99936	1.1	1479 5925
431393	ESTs, Highly similar to cytokine recept	AW971493	Hs.134269	1.1	2780 6864
406885	gb:Human mRNA for pre-mRNA splicing fac	D28423		1.1	73 74 4840
427666	calmodulin-like skin protein (CLSP)	AI791495	Hs.180142	1.0	2356 6550
457211	ESTs, Weakly similar to S51797 vasodila	AW972565	Hs.32399	1.0	4543 8344

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TABLE 2B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

440151	1879911_1	AA868167 F21558 F31418 F35624
454755	1070995_1	AW819203 AW819204 AW819197 AW819202 AW819211 BE158469 AW819221 BE158473 AW819235 AW819207 AW819220 AW819208 AW819238 AW819198 AW819234
449677	79505_1	AA002232 T99209 AA002071
413064	1101606_1	BE150469 BE150462 BE063366 BE150799 BE063378 BG952296
411324	1076104_1	AW836835 AW836833 T02838
411035	352355_1	BF697879 BG984482 AW854930 AW854941 AW814115 AW814431 AW814190 BF325887 BF325890 BF985536
410910	1063929_1	AW810196 AW810555 AW810507 AW810204 AW810619 AW810534
412792	7586_19	BE162129 AW997959
455811	124024_1	BE141466 BE141531 BF336589 BF336571 BE141527 BF368787 BE141530 AA663234 BE141468 BE141484
410642	1044044_1	AW792784 H06639 Z44444
438305	999803_1	H06377 AW628008
429030	1058507_1	AA443446 AW803288 AW803356 BE349897 AW803287 BI015966
458956	81880_1	BE873716 BE907282 AA009992 BE220675 AA345621
457455	1077062_1	AW838069 AW972861 AA523684 T05725
454410	6852_9	AW812744 AW581974 BG985054 AW812725
430850	296806_1	BE144152 AA487799 BF916865 AA937952
414110	1634167_1	BE253764 BE250764 BE255757 BE251752 BE251925
412218	1159394_1	AW901809 AW901787 AW901792 AW901744 AW901753 AW901807 AW901798 AW901795
434728	36765_8	AV733124 AW630740 AA644655
411880	1139083_1	BE088101 T05990 AW872477
413059	1488711_1	BE063078 BE151503 BE151498
412148	1155069_1	R83307 AW895776 AW895655
455813	1515590_1	BE141577 BE141585 BE141587
459487	135353_1	AA699665 R84889
411101	1232297_1	AW856816 AW856814 AW817559 AW856813 AW856810 AW817561 AW861130 AW861132 AW856811 AW861135 AW934798 AW817558
415345	1870623_1	R60302 F06228 R18381
451302	84753_1	AA017069 H39010 H39006
414633	3280746_1	AA150368 AA150238
438816	1075247_1	AW835829 R01759 AA826305

85

	434241	63414_1	AF119913 AJ207698 R57074
	419536	251846_1	AA244095 AA603305 AA244183
	455046	1092261_1	AW852480 AW852484 AW852493
5	412902	1476802_1	BE008024 BE008022 BE008026 BE008029 BE008025 BE008027 BE008020 BE008018 BE008019 BE008021 BE008015
			BE008023 BE008030 BE007959 BE008016 BE008014 BE008028 BE007994
	417563	2243443_1	AA203701 R86895
	411171	1071787_1	AW820332 AW820260 R94405
	411536	1089425_1	AW850510 BE143820 BF349605 BE143792
10	412275	319144_1	BF952703 BF952683 BF952777 BF952870 BF952880 BF952714 BF947615 AW905341 AW905312 AW905371 BF952646
			BF952879 AW905391 AW905372
	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	430110	1233222_1	AW968358 AA465314 AA465464 AW976324 AA465465
	425297	1227439_1	AW962101 AA354685 H85269 R55281 F11427
	410345	1007452_1	AW662569 R92204 R92309
15	426413	372468_1	AW954494 AA377823 BG219617 BG195685 BG616269 AJ022688

TABLE 2C:

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
		sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NI_position:	Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	NI_position
	404145	9863643	Plus	30607-31266
	401973	3126777	Plus	82036-82187,82950-83059,84113-84246,8453
	400920	7547222	Minus	129895-130075,133882-134086
30	405889	7677717	Plus	53701-53825
	406387	9256180	Plus	116229-116371,117512-117651
	403372	9087278	Minus	130002-130131
	402354	8886964	Plus	54039-54154
	402636	9958122	Minus	108409-108893
	404627	9796589	Plus	65191-65388
35	400608	9887666	Minus	96756-97558
	404234	8247273	Plus	27209-27380
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,8424
	404030	7671252	Plus	149362-151749
40	403134	9211444	Plus	76642-76800
	401357	9931663	Plus	143295-143425
	401441	8248727	Plus	139505-139628
	405523	9454643	Plus	114550-114688,117265-117407,119490-11959
	400829	8570385	Plus	152176-152616
45	404681	9797231	Minus	40430-40549
	406107	9126889	Plus	33807-33931
	401929	3810670	Minus	3167-3286,4216-4310
	402687	8318556	Plus	160550-160705,161161-161349
	402741	9212200	Minus	18603-18760,19719-19890
50	401961	4581193	Minus	124054-124209
	403574	8101156	Plus	5542-6176
	406064	9111535	Minus	110744-111133
	402742	9212200	Minus	23487-23613
	401974	3126777	Plus	85330-85683
55	406483	7711304	Plus	49021-49147
	405078	7798783	Plus	111012-111208
	404682	9797231	Minus	40977-41150
	402864	5881341	Plus	93475-93648,101571-101743,102803-102937,
	404673	9797204	Minus	26201-26391,26768-27034,27467-27564,2865
60	404735	4190944	Plus	137269-138200
	401851	7770425	Minus	148443-146684,147794-147971,148351-14848
	400504	9796369	Minus	156301-157005
	400632	3818355	Plus	72875-73447,75874-76425
	405522	9454643	Plus	103664-103803,111740-111863,112064-11220
65	405401	6850244	Minus	5753-5866,11177-11294,12712-12817
	405563	2114222	Plus	15385-15752
	404033	8122195	Plus	7976-8156
	401628	8575954	Minus	210617-210796
	401583	9800594	Minus	22044-22120,22887-23029
70	402236	7690107	Plus	54636-55502
	402888	9930892	Minus	54727-54901
	401754	9838215	Minus	50722-50883,51021-51134,51261-51324
	405230	7249032	Minus	97493-97682
	404685	9797437	Minus	153217-153315,154043-154124,159185-15935
75	403433	9719611	Minus	72225-72437
	404917	7341851	Plus	49330-49498
	402001	9501818	Plus	68052-68223
	402945	9368458	Minus	100591-100710
	405651	4926905	Minus	80289-80357,116604-116672,118630-118698,
80	401972	3126777	Plus	67726-67849,69495-69563,69690-69874,7083
	402285	2689079	Minus	92386-92634
	401356	9931663	Minus	110335-110442,110581-110739,111294-11146
	403226	7630996	Plus	114887-115301
	401111	9966191	Minus	188185-188986
	404156	9886577	Plus	127319-127754
85	404293	3046744	Minus	85067-85654
	403857	7708910	Minus	2524-3408

	401797	6730720	Plus	6973-7118
	403489	7331314	Minus	38897-39212
	403404	9438460	Plus	22392-22598, 22967-23148
5	401849	7770425	Plus	129375-129483, 129597-129720
	403451	9838240	Plus	77382-78300
	404394	3135305	Minus	37121-37205, 37491-37762, 41053-41140, 4132
	405387	6587915	Minus	3769-3833, 5708-5895
	404208	3080468	Minus	105346-105573
10	403790	8084957	Minus	87826-87947, 89835-90002
	405203	7230116	Plus	125295-125463
	404977	3738341	Minus	43081-43229
	405674	4589984	Plus	68302-68429
	401914	9369520	Plus	62537-62945, 63155-63308
15	403830	9887814	Minus	20687-20893
	401203	9743387	Minus	172961-173056, 173868-173928

TABLE 3A

20	Pkey: Unique Eos probeset identifier number					
	Gene name: Unigene gene title					
	Accession: Exemplar Accession number, Genbank accession number					
	UniGene: Unigene number					
25	RATIO: 95th percentile of fibrosarcoma AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator					
	SEQ ID #: nucleic acid and protein sequences provided on CD for search purposes					
	Pkey	Gene Name	Accession	UniGene	RATIO	SEQ ID #
30	428087	troponin C2, fast	AA100573	Hs.182421	37.1	2396 6582
	407245	titin	X90568	Hs.172004	36.1	132 133 4881
	413778	myosin, light polypeptide 2, regulatory	AA090235	Hs.75535	33.6	740 5356
	425545	Homo sapiens, clone MGC:12401, mRNA, co N98529	Hs.158295	30.2	2114 6379	
	426752	titin	X69490	Hs.172004	30.2	2266 2267 6482
35	409169	(clone PWHLC2-24) myosin light chain 2	F00991	Hs.50889	27.6	316 5029
	400440	nebulin	X83957	Hs.83870	24.6	24 25 4627
	407013	gb:Human nebulin mRNA, partial cds	U35637	Hs.83870	23.4	94 95 4851
	422867	cartilage oligomeric matrix protein (ps	L32137	Hs.1584	22.6	1751 1752 6122
	428221	ATPase, Ca transporting, cardiac muscle	U96781	Hs.183075	22.3	2408 2409 6592
40	412129	troponin T3, skeletal, fast	M21984	Hs.73454	22.0	571 572 5222
	406704	myosin, heavy polypeptide 7, cardiac mu	M21665	Hs.929	20.7	55 56 4826
	406707	myosin, heavy polypeptide 2, skeletal m	S73840	Hs.931	20.6	61 62 4829
	412519	troponin T1, skeletal, slow	AA196241	Hs.73980	18.4	598 5244
	405001	interleukin enhancer binding factor 1			18.3	4767
45	417435	carbonic anhydrase III, muscle specific	NM_005181	Hs.8 2129	18.2	1121 1122 5655
	418205	troponin I, skeletal, fast	L21715	Hs.83760	17.4	1204 1205 5720
	452838	preferentially expressed antigen in mel	U65011	Hs.30743	17.0	4357 4358 8188
	422633	enolase 3, (beta, muscle)	X56832	Hs.118804	16.9	1716 1717 6098
	406706	myosin, heavy polypeptide 1, skeletal m	X03740	Hs.231581	16.9	59 60 4828
50	422640	troponin C, slow	M37984	Hs.118845	16.9	1718 1719 6099
	410223	calsequestrin 1 (fast-twitch, skeletal	S73775	Hs.60708	15.7	433 434 5115
	418391	troponin I, skeletal, slow	NM_003281	Hs.8 4673	13.9	1228 1229 5736
	414152	thrombospondin 4	NM_003248	Hs.7 5774	13.7	782 783 5391
	416373	ESTs, Weakly similar to S12658 cysteine	AA195845	Hs.73680	13.7	996 5559
55	417070	titin	Z19077	Hs.172004	13.5	1070 5614
	446523	sarcolipin	NM_003063	Hs.3 34629	13.4	3852 3853 7774
	422069	titin-cap (telethonin)	AJ010063	Hs.343603	13.4	1635 1636 6037
	431204	cytochrome c oxidase subunit VIa polype	F28841	Hs.250760	13.4	2760 6848
	428405	cholinergic receptor, nicotinic, alpha	Y00762	Hs.2266	13.2	2436 2437 6615
60	421566	early growth response 2 (Krox-20 (Droso	NM_000399	Hs.1 395	12.9	1563 1564 5984
	409096	sarcomeric muscle protein	AA194412	Hs.50550	12.8	302 5019
	418533	myosin-binding protein C, fast-type	NM_004533	Hs.8 5937	12.5	1253 1254 5754
	424982	phosphorylase, glycogen; muscle (McArdl	U94777	Hs.351580	12.4	2036 2037 6325
	431205	tropomodulin 4 (muscle)	AA194560	Hs.250763	12.4	2761 6849
65	408915	hepatocellular carcinoma novel gene-3 pr	NM_016651	Hs.4 8950	12.3	274 275 4998
	419138	ryanodine receptor 1 (skeletal)	U48508	Hs.89631	12.3	1309 1310 5796
	418390	titin immunoglobulin domain protein (my	AF133820	Hs.84665	11.6	1226 1227 5735
	450701	hypothetical protein XP_098151 (leucine	H39960	Hs.288467	11.5	4183 8048
	400499	C10001858:gij6679124[ref]NP_032759.1)n			11.4	4628
70	430681	ESTs	AW969675	Hs.291232	11.3	2719 6819
	426429	myosin-binding protein C, slow-type	X73114	Hs.169849	11.1	2224 2225 6456
	444381	hypothetical protein BC014245	BE387335	Hs.283713	11.1	3697 7652
	420103	aldehyde dehydrogenase 1 family, member	AA382259	Hs.95197	11.1	1416 5878
	428398	ESTs	AI249368	Hs.98558	10.8	2435 6614
75	426300	delta-like homolog (Drosophila)	U15979	Hs.169228	10.8	2196 2197 6437
	420197	ESTs, Weakly similar to A57291 cytokine	AW139647	Hs.88134	10.6	1429 5889
	400651	ENSP00000228031*:COPPER CHAPERONE FOR S			10.6	4636
	434352	small muscle protein, X-linked	AF129505	Hs.86492	10.5	3047 3048 7075
	453331	ESTs	AI240665	Hs.352537	10.5	4413 8236
80	429973	ESTs	AI423317	Hs.164680	10.3	2628 6756
	411102	triadin	AA401295	Hs.23926	10.3	515 5175
	416658	fibrillin 2 (congenital contractural ar	U03272	Hs.79432	10.1	1020 1021 5577
	406687	matrix metalloproteinase 11 (stromelysi	M31126	Hs.352054	10.1	49 50 4823
	437206	ESTs, Weakly similar to I38344 titin, c	AW975934	Hs.172004	9.9	3245 7242
	416378	ankyrin repeat domain 2 (stretch respon	AW044467	Hs.73708	9.7	997 5560
85	436519	myozenin	AJ278124	Hs.238756	9.7	3196 3197 7200
	444329	hypothetical protein FLJ12921	W73753	Hs.209637	9.7	3693 7648

	418072	Human DNA sequence from clone RP3-353C1	F35210	Hs.86507	9.7	1190 5707
	410621	titin	AA194329	Hs.172004	9.6	481 5149
	435370	ESTs	AJ964074	Hs.225838	9.5	3120 7136
5	419550	KIAA0128 protein; septin 2	D50918	Hs.90998	9.4	1348 1349 5827
	429997	apolipoprotein B mRNA editing enzyme, c	NM_006789	Hs.2 27457	9.3	2636 2637 6761
	416349	myomesin (M-protein) 2 (165kD)	X69089	Hs.79227	9.2	991 992 5556
	419301	tenomodulin protein	AA236166	Hs.132957	9.2	1328 5811
	421296	perilipin	NM_002666	Hs.1 03253	9.2	1525 1526 5961
10	441134	cellular retinoic acid-binding protein	W29092	Hs.346950	9.2	3500 7475
	450375	a disintegrin and metalloproteinase dom	AA009647	Hs.352537	9.1	4159 8028
	409028	Z-band alternatively spliced PDZ-motif	AB014513	Hs.49998	8.6	296 297 5015
	423961	periostin (OSF-2os)	D13666	Hs.136348	8.6	1878 1879 6215
	421512	myomegalin	AB007923	Hs.265848	8.5	1554 1555 5979
15	444301	asporin (LRR class 1)	AK000136	Hs.10760	8.5	3691 3692 7647
	411789	Adiclan	AF245505	Hs.72157	8.5	553 554 5207
	419050	adenosine monophosphate deaminase 1	(is NM_000036	Hs.89570	8.5	1293 1294 5784
	428698	KIAA1866 protein	AA852773	Hs.334838	8.4	2463 6635
	417689	KIAA0128 protein; septin 2	AA828347	Hs.90998	8.3	1148 5673
20	425065	Homo sapiens, clone IMAGE:3603836, mRNA	AA371906	Hs.294151	8.3	2042 6329
	406964	FGENES predicted novel secreted protein	M21305		8.2	87 88 4847
	429500	hexabrachion (tenascin C, cytotoxicin)	X78565	Hs.289114	8.1	2574 2575 6718
	443727	ESTs	Z25389	Hs.18459	8.1	3640 7603
	422311	cytokine receptor-like factor 1	AF073515	Hs.114948	8.0	1669 1670 6062
25	414219	ALL1-fused gene from chromosome 1q	W20010	Hs.75823	8.0	789 5397
	419875	proenkephalin	AA853410	Hs.93557	8.0	1391 5859
	427674	H2B histone family, member Q	NM_003528	Hs.2 178	7.9	2359 2360 6553
	450300	ESTs, Highly similar to ITH4_HUMAN INTE	AL041440	Hs.58210	7.9	4154 8024
	429134	ESTs	AA446953	Hs.99004	7.9	2514 6673
30	418113	SRY (sex determining region Y)-box 4	AI272141	Hs.83484	7.9	1194 5711
	415672	ESTs	N53097	Hs.193579	7.9	937 5511
	424408	collagen, type V, alpha 1	AI754813	Hs.146428	7.9	1943 6260
	424086	lysyl oxidase	AI351010	Hs.102267	7.8	1896 6227
	424688	myosin, light polypeptide 3, alkali; ve	AA216287	Hs.1815	7.7	1988 6290
35	440704	Insulin-like growth factor binding prot	M69241	Hs.162	7.7	3482 3483 7459
	411852	ESTs, Weakly similar to T00329 hypothet	AA528140	Hs.107515	7.7	555 5208
	451681	ESTs, Weakly similar to AA64_HUMAN 64 K	Z28564	Hs.255950	7.7	4245 8097
	423575	Intron of periostin (OSF-2os)	C18863	Hs.163443	7.5	1820 6173
	425308	receptor tyrosine kinase-like orphan re	M97639	Hs.155585	7.4	2087 2088 6362
40	421458	carbohydrate (keratan sulfate Gal-6) su	NM_003654	Hs.1 04576	7.4	1543 1544 5972
	417333	bromodomain and PHD finger containing,	AL157545	Hs.173179	7.4	1096 5636
	418156	nuclear receptor subfamily 1, group I,	W17056	Hs.83623	7.4	1198 5715
	408493	phosphoglycerate mutase 2 (muscle)	BE206854	Hs.46039	7.3	231 4962
	420212	calcium channel, voltage-dependent, L t	NM_000069	Hs.1 294	7.3	1432 1433 5892
45	416931	adipose most abundant gene transcript 1	D45371	Hs.80485	7.3	1047 1048 5597
	417074	guanidinacetate N-methyltransferase	Z49878	Hs.81131	7.3	1071 1072 5615
	417866	collagen, type XI, alpha 1	AW067903	Hs.82772	7.2	1162 5685
	421552	secreted frizzled-related protein 4	AF026692	Hs.105700	7.2	1559 1560 5982
	448493	ESTs	AI524124	Hs.270307	7.2	4006 7903
50	442376	Homo sapiens cDNA FLJ12228 fis, clone M	W95588	Hs.129982	7.2	3557 7529
	438091	nuclear receptor subfamily 1, group I,	AW373062	Hs.351546	7.2	3302 7295
	438089	nuclear receptor subfamily 1, group I,	W05391	Hs.351546	7.1	3301 7294
	449048	similar to S68401 (cell) glucose indu	Z45051	Hs.22920	7.1	4061 7945
	428957	WNT1 inducible signaling pathway protei	NM_003881	Hs.1 94679	7.0	2491 2492 6656
55	427639	Homo sapiens, clone MGC:18257, mRNA, co	AW444530	Hs.350860	7.0	2353 6547
	418054	lysyl oxidase-like 2	NM_002318	Hs.8 3354	7.0	1184 1185 5702
	440042	ESTs	AI073387	Hs.133898	7.0	3448 7430
	408988	Homo sapiens clone TUA8 Crt-du-chat reg	AL119844	Hs.49476	6.9	289 5009
	407112	ESTs, Weakly similar to ALU7_HUMAN ALU	AA070801	Hs.51615	6.9	111 4863
60	414443	platelet-derived growth factor receptor	AU077268	Hs.76144	6.9	817 5421
	425227	ESTs	H84455	Hs.40639	6.8	2069 6348
	414085	aldehyde dehydrogenase 1 family, member	AA114015	Hs.75746	6.8	775 5384
	422148	histidine-rich calcium-binding protein	M60052	Hs.1480	6.8	1651 1652 6048
	407204	ESTs, Weakly similar to ALU1_HUMAN ALU	R41933	Hs.140237	6.8	121 4873
65	441636	Homo sapiens mRNA; cDNA DKFZp566E183 (f	AA081846	Hs.7921	6.8	3530 7502
	453392	SRY (sex determining region Y)-box 11	U23752	Hs.32964	6.8	4416 4417 8239
	434449	hypothetical protein FLJ22041 similar t	AW953484	Hs.3849	6.8	3057 7083
	431089	ESTs, Weakly similar to unknown protein	BE041395	Hs.374629	6.8	2745 6838
	424375	Homo sapiens clone 24820 mRNA sequence	AF070547	Hs.146312	6.8	1939 6256
70	451698	endothelin converting enzyme-like 1	Y16187	Hs.26880	6.7	4249 4250 8100
	416559	ESTs	AI039195	Hs.128060	6.7	1012 5571
	413011	biglycan	AW068115	Hs.821	6.7	669 5302
	452862	ADAMTS2 (a disintegrin-like and metall	AW378065	Hs.8687	6.7	4360 8190
	420028	carbohydrate (N-acetylglucosamine-6-O)	AB014680	Hs.8786	6.7	1408 1409 5872
75	433577	ESTs	AW007080	Hs.284192	6.7	2989 7028
	423044	protocadherin 18	AA320829	Hs.97266	6.6	1772 6138
	410102	ESTs; homologue of PEM-3 [Ciona savigny	AW248508	Hs.279727	6.6	422 5107
	418045	ESTs	AI972919	Hs.118837	6.6	1183 5701
	419745	slug (chicken homology), zinc finger pro	AF042001	Hs.93005	6.6	1381 1382 5851
80	435905	KIAA0456 protein	AW997484	Hs.5003	6.6	3160 7168
	432408	ESTs, Weakly similar to A46010 X-linked	N39127	Hs.356235	6.5	2872 6934
	439688	hypothetical protein FLJ12921	AW445181	Hs.209637	6.5	3418 7401
	448731	ESTs	AI522273	Hs.173179	6.5	4030 7922
	421143	immunoglobulin superfamily containing I	AB024536	Hs.102171	6.5	1510 1511 5949
85	423778	flavin containing monooxygenase 2	Y09267	Hs.132821	6.5	1846 1847 6193
	429892	myomesin 1 (skelemin) (185kD)	NM_003803	Hs.2 504	6.4	2614 2615 6745
	413566	sprouty (Drosophila) homolog 4	AW604451	Hs.381153	6.4	730 5347

	453575	peptidyl arginine deiminase, type II	AB023211	Hs.33455	6.4	4425 4426 8246
	407656	Homo sapiens mRNA; cDNA DKFZp434B2119 AW747986	Hs.37443	6.4	148 4893	
	420376	protocadherin 18	AL137471	Hs.97266	6.3	1447 1448 5903
5	411296	growth suppressor 1	BE207307	Hs.10114	6.3	524 5183
	423225	Thy-1 cell surface antigen	AA852604	Hs.125359	6.3	1786 6148
	433235	contactin 3 (plasmacytoma associated)	AB040929	Hs.35089	6.3	2953 2964 7006
	421487	serine/threonine kinase Z3	AF027406	Hs.104865	6.3	1548 1549 5975
	402621	Target Exon			6.3	4684
10	420842	hypothetical protein MGC10986	AI083668	Hs.50601	6.3	1485 5929
	409361	sine oculis homeobox (Drosophila) homol	NM_005982	Hs.5 4416	6.3	344 345 5049
	431183	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum	NM_005855	Hs.250696	6.3	2756 2757 6845
	413199	ELAV (embryonic lethal, abnormal vision)	M62843	Hs.75236	6.2	687 688 5317
	418059	gbzn56d05.s1 Stratagene muscle 937209	AA211586		6.2	1186 5703
15	437330	Homo sapiens mRNA; cDNA DKFZp761J1112 (AL353944	Hs.50115	6.2	3253 7250	
	420576	KIAA1858 protein	AA297634	Hs.54925	6.2	1463 5914
	413795	ESTs	AL040178	Hs.142003	6.2	743 5358
	412104	Homo sapiens, Similar to RIKEN cDNA 221	AW205197	Hs.240951	6.2	569 5220
	410611	KIAA1628 protein	AW954134	Hs.20924	6.1	480 5148
20	449595	ESTs	AW293799	Hs.255238	6.1	4098 7979
	418140	microfibrillar-associated protein 2	BE613836	Hs.83551	6.1	1196 5713
	421579	stem cell growth factor, lymphocyte sec	NM_002975	Hs.1 05927	6.1	1567 1568 5987
	414142	hemicanthin (fibulin 6)	AW368397	Hs.334485	6.1	781 5390
	451598	ESTs	N29102	Hs.79658	6.1	4241 8093
25	434326	reticulin 2	NM_005619	Hs.3 803	6.0	3043 3044 7073
	453859	myogenic factor 6 (herculin)	NM_002469	Hs.3 5937	6.0	4451 4452 8267
	417944	collagen, type V, alpha 2	AU077196	Hs.82985	6.0	1172 5693
	417389	midkine (neurite growth-promoting factor)	BE260964	Hs.82045	6.0	1109 5647
	452063	ESTs, Weakly similar to TWST_HUMAN	TWIS R53185	Hs.32366	6.0	4281 8124
30	449717	cerebral cell adhesion molecule	AB040935	Hs.23954	6.0	4110 4111 7989
	412755	ESTs, Weakly similar to P4HA_HUMAN	PROL BE144306	Hs.179891	6.0	637 5274
	421823	ESTs	N40850	Hs.28625	6.0	1600 6011
	426935	collagen, type I, alpha 1	NM_000088	Hs.1 72928	6.0	2288 2289 6498
	424734	ESTs	AI217685	Hs.96844	6.0	1992 6293
35	408349	homeo box C10	BE546947	Hs.44276	6.0	213 4949
	452360	ESTs	AI742082	Hs.98539	6.0	4321 8158
	449238	muscle-specific RING-finger protein 3	AA428229	Hs.331561	5.9	4075 7957
	431457	integrin, alpha 11	NM_012211	Hs.2 56297	5.9	2787 2788 6870
	420067	Homo sapiens mRNA; cDNA DKFZp564O222 (f T52431	Hs.94795	5.9	1414 5876	
40	412472	ESTs	AW975398	Hs.293836	5.9	593 5240
	408486	sodium channel, voltage-gated, type IV,	L04236	Hs.46038	5.9	228 229 4960
	421155	lysyl oxidase	H87879	Hs.102267	5.9	1512 5950
	429823	ESTs	AA459443	Hs.181400	5.9	2613 6744
	439751	Homo sapiens mRNA full length insert cD	AA196090	Hs.50794	5.9	3428 7411
45	415555	ESTs	W05433	Hs.352293	5.9	932 5506
	452223	hypothetical protein MGC2827	AA425467	Hs.8035	5.8	4302 8142
	430223	nephroblastoma overexpressed gene	NM_002514	Hs.2 35935	5.8	2661 2662 6779
	415556	ESTs	W84346	Hs.84673	5.8	933 5507
	417045	Homo sapiens ORF1	F01180	Hs.332030	5.8	1066 5610
50	422667	ESTs	H25642	Hs.132621	5.8	1723 6102
	415702	gb:HSPD18414 HM3 Homo sapiens cDNA clon	F28877	Hs.73680	5.8	942 5515
	435101	ESTs	AI743156	Hs.131064	5.8	3106 7124
	410108	OSBP-related protein 6	AA081659	Hs.318775	5.8	423 5108
	429359	matrix metalloproteinase 14 (membrane-i	W00482	Hs.2399	5.8	2551 6702
55	403081	NM_003319: Homo sapiens titin (TTN), mR			5.7	4704
	442117	ESTs; hypothetical protein for IMAGE:44	AW664964	Hs.128899	5.7	3551 7523
	417027	triadin	AA192306	Hs.23926	5.7	1062 5607
	442295	Homo sapiens cDNA FLJ11469 fis, clone	H AI827248	Hs.224398	5.7	3555 7527
	445417	a disintegrin-like and metalloprotease	AK001058	Hs.12680	5.7	3766 7705
60	410295	ndogen (enactin)	AA741357	Hs.356624	5.7	450 5127
	448595	KIAA0644 gene product	AB014544	Hs.21572	5.7	4015 4016 7910
	450506	fibroblast activation protein, alpha	NM_004460	Hs.4 18	5.7	4170 4171 8037
	414482	endothelin receptor type A	S57498	Hs.76252	5.7	824 825 5426
	411021	titin	F00055	Hs.172004	5.7	508 5169
65	453514	ESTs	AA036675	Hs.50918	5.7	4424 8245
	452023	KIAA1173 protein	AB032999	Hs.27566	5.7	4271 4272 8118
	409944	four and a half LIM domains 3	BE297925	Hs.57687	5.6	399 5090
	439979	hypothetical protein FLJ10430	AW600291	Hs.6823	5.6	3442 7424
	414359	cadherin 11, type 2, OB-cadherin (osteo	M62194	Hs.75929	5.6	808 5413
70	437446	ESTs, Moderately similar to CA1C RAT CO	AA788946	Hs.101302	5.6	3264 7259
	407080	myosin, heavy polypeptide 8, skeletal m	Z38133	Hs.113973	5.6	105 106 4858
	429415	procollagen C-endopeptidase enhancer	NM_002593	Hs.2 02097	5.5	2557 2558 6706
	411396	ESTs	CD4646	Hs.85428	5.5	533 5191
	401566	NM_005159: Homo sapiens actin, alpha, ca			5.5	4654
75	453983	ESTs	H94997	Hs.16450	5.5	4476 8286
	420190	hypothetical protein EST00098	AI816209	Hs.95867	5.5	1428 5888
	447253	ESTs	AW250196	Hs.103512	5.5	3907 7822
	457458	ESTs	R14439	Hs.209194	5.5	4553 8352
	406519	C10001858:g 5679124 ref NP_032759.1 n			5.5	4808
80	443184	ESTs	AI638728	Hs.135159	5.5	3607 7574
	425863	Human unidentified mRNA, partial sequen	U43604	Hs.159901	5.4	2152 6404
	446904	DKFZP434H204 protein	AL110226	Hs.16441	5.4	3875 3876 7795
	448520	doublecortin and CaM kinase-like 1	AB002367	Hs.21355	5.4	4010 4011 7907
	449700	paraneoplastic antigen	L02867	Hs.78358	5.4	4108 4109 7988
	452613	ESTs	AA461599	Hs.23459	5.4	4337 8171
85	451917	Homo sapiens unknown mRNA	AW391351	Hs.50820	5.4	4261 8108
	439039	ESTs	AI656707	Hs.48713	5.4	3373 7356

	446142	ESTs	AI754693	Hs.145968	5.4	3820 7748
	422087	matrix metalloproteinase 2 (gelatinase)	X58968	Hs.111301	5.4	1641 6040
	414002	FBJ murine osteosarcoma viral oncogene	NM_006732	Hs.75678	5.4	763 764 5375
5	430713	eukaryotic translation elongation facto	AA351647	Hs.2642	5.4	2726 6824
	421251	enigma (LIM domain protein)	Z28913	Hs.102948	5.4	1521 5957
	406705	myosin, heavy polypeptide 8, skeletal m	Z38133	Hs.113973	5.4	105 106 4827
	411000	ESTs, Weakly similar to S38383 SEB4B pr	N40449	Hs.201619	5.4	505 5167
	404977	Insulin-like growth factor 2 (somatomed			5.3	4766
10	427863	MLL septin-like fusion	AF189712	Hs.181002	5.3	2378 2379 6567
	413031	phosphofructokinase, muscle	BE515051	Hs.75160	5.3	671 5304
	416982	creatine kinase, mitochondrial 2 (sarco	J05401	Hs.80691	5.3	1055 1056 5602
	453817	ESTs	AW755253	Hs.379638	5.3	4442 8260
	424330	Homo sapiens cDNA FLJ13596 fis, clone P	AW073953	Hs.34054	5.3	1936 6253
	407826	calpain 3, (p94)	AA128423	Hs.40300	5.3	167 4911
15	414285	ESTs	AA312914	Hs.71719	5.3	798 5405
	426485	platelet-derived growth factor receptor	NM_006207	Hs.1 70040	5.3	2238 2239 6465
	445875	Homo sapiens clone 24453 mRNA sequen	AF070524	Hs.13410	5.3	3801 7731
	448106	ESTs	AI800470	Hs.171941	5.2	3977 7879
20	425292	37 kDa leucine-rich repeat (LRR) protei	NM_005824	Hs.1 55545	5.2	2083 2084 6359
	414175	hypothetical protein DKFZp761D112	AI308876	Hs.103849	5.2	786 5394
	417405	ESTs	W28657	Hs.5307	5.2	1112 5649
	409172	ESTs	Z99399	Hs.122593	5.2	318 5031
	422627	transforming growth factor, beta-induce	BE336857	Hs.118787	5.2	1715 6097
25	414555	phospholipase A2, group IIA (platelets,	N98569	Hs.76422	5.2	830 5431
	426457	chimerin (chimaerin) 1	AW894667	Hs.380138	5.2	2229 6459
	400419	Target	AF084545		5.2	22 23 4626
	405681	C3000593*gi10120319jembI CAC08185.1			5.2	4793
	428981	ESTs, Weakly similar to ALU2_HUMAN ALU	BE313077	Hs.93135	5.2	2497 6660
30	453271	ESTs	AA903424	Hs.6786	5.2	4409 8232
	439920	neurotrimin	H05430	Hs.288433	5.2	3439 7421
	440652	ESTs	AI216751	Hs.143977	5.1	3478 7456
	435793	KIAA1313 protein	AB037734	Hs.4993	5.1	3152 3153 7162
	416084	deoxythymidylate kinase (thymidylate ki	L16991	Hs.79006	5.1	972 973 5540
35	437395	hypothetical protein DKFZp762M136	AL365408	Hs.351747	5.1	3258 3259 7254
	412564	cardiac ankyrin repeat protein	X83703	Hs.355934	5.1	606 607 5251
	415705	coilin	U06632	Hs.966	5.1	943 944 5516
	414683	hypothetical protein MGC12702	S78296	Hs.76888	5.1	846 847 5444
	411573	KIAA1077 protein	AB029000	Hs.70823	5.1	542 543 5199
40	447321	Homo sapiens cDNA FLJ14028 fis, clone H	AW271217	Hs.281434	5.1	3915 7827
	452683	progesterone membrane binding protein	AI089575	Hs.374574	5.1	4341 8175
	427876	ESTs	AI494291	Hs.369171	5.1	2381 6569
	437681	Homo sapiens, Similar to TEA domain fam	AI207958	Hs.166556	5.1	3280 7273
	417308	KIAA0101 gene product	H60720	Hs.81892	5.1	1094 5634
45	419235	neurotrimin	AW470411	Hs.288433	5.1	1320 5804
	443164	ESTs, Weakly similar to ALU1_HUMAN ALU	AI038503	Hs.55780	5.1	3606 7573
	427647	Homo sapiens cDNA FLJ20653 fis, clone K	W19744	Hs.180059	5.0	2354 6548
	409826	hypothetical protein FLJ23412	AW501112	Hs.353013	5.0	388 5082
	418532	neurotrophic tyrosine kinase, receptor,	F00797	Hs.374321	5.0	1252 5753
50	443883	serine (or cysteine) proteinase inhibit	AA114212	Hs.9930	5.0	3653 7614
	439627	hypothetical protein FLJ21841	BE621702	Hs.29076	5.0	3411 7394
	425256	collapsin response mediator protein 1	BE297611	Hs.155392	5.0	2074 6352
	428560	ESTs, Weakly similar to B47411 ADPribos	AI243209	Hs.98669	5.0	2453 6627
	430147	hair/enhancer-of-split related with YR	R60704	Hs.234434	5.0	2652 6773
55	427418	LAT1-3TM protein	AA402587	Hs.356667	5.0	2327 6527
	426413	gb:EST90805 Synovial sarcoma Homo sapie	AA377823		5.0	2219 6453
	410036	calsequestrin 2 (cardiac muscle)	R57171	Hs.57975	5.0	412 5100
	417068	hypothetical protein MGC3169	AA451910	Hs.85852	5.0	1069 5613
	416729	Ras-related associated with diabetes	U46165	Hs.1027	5.0	1026 1027 5581
60	433839	ESTs, Weakly similar to ALU1_HUMAN ALU	F35430	Hs.146070	5.0	3008 7043
	453874	collagen, type XIV, alpha 1 (undulin)	AW591783	Hs.36131	5.0	4456 8270
	425247	matrix metalloproteinase 11 (stromelysi	NM_005940	Hs.1 55324	5.0	2072 2073 6351
	413278	interferon-stimulated protein, 15 kDa	BE563085	Hs.833	4.9	695 5322
	416208	ESTs, Weakly similar to MUC2_HUMAN MUC1	AW291168	Hs.41295	4.9	981 5548
65	424893	Homo sapiens cDNA FLJ13303 fis, clone O	AW295112	Hs.153648	4.9	2020 6313
	457211	ESTs, Weakly similar to S51797 vasodila	AW085961	Hs.130093	4.9	4549 8344
	453341	adenylyl cyclase-associated protein 2	AI758912	Hs.296341	4.9	4414 8237
	433012	ATX1 (antioxidant protein 1, yeast) hom	NM_004045	Hs.2 79910	4.9	2925 2926 6978
	429524	KIAA1211 protein	AB033037	Hs.205293	4.9	2577 2578 6720
70	422599	non-metastatic cells 1, protein (NM23A)	BE387202	Hs.118638	4.9	1710 6092
	407824	Homo sapiens cDNA FLJ14388 fis, clone H	AA147884	Hs.9812	4.9	166 4910
	434398	serum-inducible kinase (SNK)	AA121098	Hs.3838	4.9	3052 7079
	458247	ESTs	AW580932	Hs.164170	4.9	4572 8368
	417089	Homo sapiens cDNA: FLJ21909 fis, clone	H52280	Hs.18612	4.9	1077 5619
75	447436	Homo sapiens cDNA: FLJ21449 fis, clone	AI932971	Hs.18593	4.9	3928 7837
	454024	hypothetical protein FLJ23403	AA993527	Hs.293907	4.9	4481 8290
	433447	neuronal pentraxin II	U29195	Hs.3281	4.8	2880 2981 7021
	434747	ESTs	AA837085	Hs.372254	4.8	3073 7097
	429707	matrix metalloproteinase 23B	W76631	Hs.211819	4.8	2606 6738
80	438964	ESTs	AA148982	Hs.29068	4.8	3371 7354
	435977	brain-specific membrane-anchored protei	AL138079	Hs.5012	4.8	3166 7174
	435367	for muscle specific ring finger 2	AI917684	Hs.85524	4.8	3119 7135
	439687	ESTs	W94546	Hs.124747	4.8	3417 7400
	426919	ELAV (embryonic lethal, abnormal visio	AL041228	Hs.166109	4.8	2284 6495
85	450676	ESTs	AI147155	Hs.279727	4.8	4180 8045
	419081	ESTs	AI798863	Hs.87191	4.8	1299 5788
	429139	ESTs	F09092	Hs.66087	4.8	2517 6675

	416433	ESTs	AI558904	Hs.84673	4.8	1004	5566
	419250	U5 snRNP-specific protein, 116 kD	AW770185	Hs.356066	4.8	1322	5806
	433122	ESTs	AB019391	Hs.58049	4.8	2941	6991
5	410687	lysyl oxidase-like 1	U24389	Hs.65436	4.8	485	486 5153
	432304	ESTs	AA932186	Hs.69297	4.8	2863	6927
	413132	protein kinase (cAMP-dependent, catalyt	NM_005823	Hs.7	5209	4.8	683 684 5314
	417376	LIM protein (similar to rat protein kin	AA253314	Hs.154103	4.7	1107	5645
	438085	ESTs	R52518	Hs.7957	4.7	3299	7292
10	428309	cellular retinoic acid-binding protein	M97815	Hs.183650	4.7	2427	2428 6608
	421778	actin related protein 2/3 complex, subu	AA428000	Hs.283072	4.7	1591	6003
	445363	tubulin-specific chaperone d	NM_005993	Hs.1	2570	4.7	3762 3763 7702
	429930	ESTs	AI580809	Hs.352364	4.7	2623	6751
	421913	osteoglycin (osteoinductive factor, mjm	AI934365	Hs.109439	4.7	1611	6020
15	419968	interleukin 6 (interferon, beta 2)	X04430	Hs.93913	4.7	1399	1400 5866
	422110	secreted protein, acidic, cysteine-rich	AI376736	Hs.121555	4.7	1648	6045
	402331	C19001390.gij399116[sp]P13688[BGP1_HUMA			4.7		4679
	413482	ESTs	AA129869	Hs.197143	4.7	727	5344
	425397	topoisomerase (DNA) II alpha (170kD)	J04088	Hs.156346	4.7	2099	2100 6369
20	412926	macrophage myristoylated alanine-rich C	AI879076	Hs.75061	4.7	655	5290
	430643	MEGF10 protein	AW970055	Hs.287425	4.7	2717	6817
	445669	ESTs	AI570830	Hs.174870	4.7	3789	7721
	423648	hypothetical protein FLJ20449	AK000456	Hs.130546	4.7	1833	1834 6184
	414961	myosin-binding protein H	U27266	Hs.927	4.7	896	897 5479
	408491	ESTs	AI088063	Hs.7882	4.7	230	4961
25	421016	transcription factor 3 (E2A immunoglobu	AA504583	Hs.101047	4.6	1497	5937
	411411	ESTs, Weakly similar to KIAA1330 protel	AA345241	Hs.55950	4.6	537	5194
	451292	KIAA1295 protein	AB037716	Hs.26204	4.6	4221	4222 8079
	422737	collagen, type III, alpha 1 (Ehlers-Dan	M26939	Hs.119571	4.6	1730	1731 6108
30	410628	ESTs, Moderately similar to similar to	AI131408	Hs.68756	4.6	483	5151
	412560	CCR4-NOT transcription complex, subunit R24601	Hs.350495	4.6	602	5248	
	441389	endocytic receptor (macrophage mannose	AF134838	Hs.7835	4.6	3514	3515 7488
	440650	Human DNA sequence from PAC 75N13 on ch R44692	Hs.326801	4.6	3477	7455	
	453935	ESTs	AI633770	Hs.42572	4.6	4470	8281
35	407228	hemoglobin, beta	M25079	Hs.155376	4.6	124	125 4876
	441611	ESTs	AW590829	Hs.133463	4.6	3528	7500
	450358	coronin, actin-binding protein, 2B	AB010098	Hs.24907	4.6	4157	4158 8027
	456816	hypothetical protein FLJ10647	AK001509	Hs.144391	4.6	4531	4532 8334
	424687	matrix metalloproteinase 9 (gelatinase	J05070	Hs.151738	4.6	1986	1987 6289
40	422648	Melanoma associated gene	D86983	Hs.118893	4.6	1720	1721 6100
	453041	Homo sapiens cDNA FLJ11918 fis, clone H	AI680737	Hs.289068	4.6	4384	8211
	421848	collagen, type VI, alpha 1	X15880	Hs.108885	4.6	1602	1603 6013
	451195	mesenchyme homeo box 1	U10492	Hs.438	4.6	4218	4219 8077
	429505	a disintegrin and metalloproteinase dom	AW820035	Hs.278679	4.6	2576	6719
45	424162	ESTs, Weakly similar to ALU2_HUMAN ALU	AA336229	-	Hs.93135	4.5	1907 6235
	424800	MyoD family inhibitor	AL035588	Hs.153203	4.5	2002	2003 6300
	427809	lipoprotein lipase	M26380	Hs.180878	4.5	2373	6562
	446681	kendrin	AJ003624	Hs.15896	4.5	3869	7789
	443402	elastin (supraaortic aortic stenosis,	U77846	Hs.9295	4.5	3619	3620 7585
50	428862	SRY (sex determining region Y)-box 9 (c	NM_000346	Hs.2	316	4.5	2483 2484 6650
	420486	caveolin 3	AF036365	Hs.98303	4.5	1456	1457 5909
	409553	semaphorin Y	AF055020	Hs.54937	4.5	359	360 5060
	424870	ESTs	T15545	Hs.244624	4.5	2014	6308
	452036	sema domain, seven thrombospondin repea	NM_003966	Hs.27621	4.5	4273	4274 8119
55	422562	AE-binding protein 1	AI962060	Hs.118397	4.5	1700	6085
	422424	prostate differentiation factor	AI186431	Hs.296638	4.5	1681	6070
	438704	ESTs	AI435060	Hs.6705	4.5	3349	7334
	424634	cartilage intermediate layer protein, n	NM_003613	Hs.1	51407	4.5	1981 1982 6285
	437117	ESTs	AL049256	Hs.122593	4.5	3235	7234
60	457411	Iroquois-class homeobox protein IRX2	AW972881	Hs.276507	4.5	4552	8349
	423013	secreted modular calcium-binding protei	AW875443	Hs.22209	4.5	1769	6135
	441689	ESTs	AI123705	Hs.289068	4.5	3533	7505
	416391	mesoderm specific transcript (mouse) ho	AI878927	Hs.79284	4.5	999	5562
	419648	thyroid hormone responsive SPOT14 (rat)	T73661	Hs.91877	4.5	1366	5839
65	447205	ESTs, Moderately similar to T17372 plas	BE617015	Hs.11006	4.5	3900	7816
	451820	ESTs	AW058357	Hs.199248	4.5	4260	8107
	439755	B7 homolog 3	AW748482	Hs.77873	4.5	3430	7413
	418994	selectin E (endothelial adhesion molecu	AA296520	Hs.89546	4.5	1290	5781
	432503	ESTs	AA551196	Hs.188952	4.4	2878	6940
70	421814	thrombospondin 2	L12350	Hs.108623	4.4	1596	1597 6008
	424066	ESTs, Weakly similar to I38022 hypothet	Z99348	Hs.112461	4.4	1891	6223
	412563	ESTs, Weakly similar to I38022 hypothet	Z25372	Hs.350621	4.4	605	5250
	446619	secreted phosphoprotein 1 (osteopontin,	AU076643	Hs.313	4.4	3861	7782
	409182	ESTs	AA064970	Hs.376137	4.4	320	5033
75	453079	LIM protein (similar to rat protein kin	AW160480	Hs.154103	4.4	4387	8214
	417259	chondroitin sulfate proteoglycan 2 (ver	AW903838	Hs.81800	4.4	1092	5632
	424262	DKFZP564C103 protein	BE294493	Hs.144058	4.4	1924	6245
	413333	fibroblast growth factor 1 (acidic)	M74028	Hs.75297	4.4	703	5327
	408443	ESTs	N33937	Hs.10336	4.4	222	4956
80	422809	hypothetical protein FLJ10549	AK001379	Hs.121028	4.4	1741	1742 6115
	420895	gb:yy23b03.r1 Morton Fetal Cochlea Homo	H88685		4.4	1489	5932
	419682	paired-like homeodomain transcription f	H13139	Hs.92282	4.4	1368	5841
	433001	clone HQ0310 PRO0310p1	AF217513	Hs.279905	4.4	2923	2924 6977
	447357	ESTs	AI375922	Hs.132821	4.4	3917	7829
	414467	copline II	AW903820	Hs.85752	4.4	821	5424
85	413289	forkhead box L2	AA128061	Hs.289292	4.4	696	5323
	407239	leukocyte immunoglobulin-like receptor,	AA076350	Hs.67846	4.4	129	4879

	446962	muscle specific ring finger protein 1	AI351421	Hs.279709	4.4	3884 7801
	423922	muscle-specific beta 1 integrin binding	AK001663	Hs.135458	4.4	1871 1872 6210
	425262	GS3955 protein	D87119	Hs.155418	4.4	2076 2077 6354
5	417421	nuclear receptor subfamily 4, group A,	AL138201	Hs.82120	4.4	1118 5653
	418283	cathepsin K (pseudosarcosin)	S79895	Hs.83942	4.4	1210 1211 5724
	419407	hypothetical protein FLJ21276	AW410377	Hs.41502	4.3	1334 5817
	453221	ESTs	AW590263	Hs.232311	4.3	4404 8228
	426395	hypothetical protein FLJ23316	BE151985	Hs.355669	4.3	2217 6451
10	436411	gb:ba63c07.y1 NIH_MGC_12 Homo sapiens c	AW674352	Hs.293836	4.3	3185 7190
	423057	ESTs, Moderately similar to I38022 hypo	AW961597	Hs.130816	4.3	1773 6139
	441104	ESTs	AI382357	Hs.143903	4.3	3499 7474
	410762	HSKM-B protein	AF226053	Hs.66170	4.3	492 493 5157
	414715	amylase-1,6-glucosidase, 4-alpha-glucanot	AA587891	Hs.904	4.3	855 5450
	433209	KIAA1474 protein	AB040907	Hs.278436	4.3	2953 2954 6999
15	418036	latent transforming growth factor beta	Z37976	Hs.83337	4.3	1180 1181 5699
	440087	hypothetical protein FLJ22678	W28969	Hs.7718	4.3	3452 7433
	417160	proteolipid protein 1 (Pelizaeus-Merzba	N76497	Hs.355807	4.3	1086 5626
	420456	SH3-domain binding protein 1	Z83844	Hs.97658	4.3	3281 5906
20	428046	ESTs, Moderately similar to I38022 hypo	AW812795	Hs.337634	4.3	2393 6579
	451154	ESTs	AA015879	Hs.33536	4.3	4215 8074
	410929	ESTs	H47233	Hs.30643	4.3	504 5166
	423563	protein kinase (cAMP-dependent, catalyt	R34734	Hs.75209	4.3	1817 6171
	411929	ESTs	AA098880	Hs.69297	4.3	561 5213
	427826	myomegalin	AL043194	Hs.265848	4.3	2375 6564
25	430702	H factor 1 (complement)	U56979	Hs.250651	4.3	2724 2725 6823
	415885	KIAA0161 gene product	D79983	Hs.78894	4.3	953 954 5524
	437696	hypothetical protein dJ37E16.5	Z83844	Hs.5790	4.3	3281 7274
	453452	ESTs	AI080235	Hs.174497	4.3	4420 8242
30	421307	Homo sapiens mRNA; cDNA DKFZp434B0425 (BE539976	Hs.103305	4.3	1528 5963
	433043	lymphoid nuclear protein (LAF-4) mRNA	W57554	Hs.125019	4.3	2930 6982
	426054	ELAV (embryonic lethal, abnormal vision	U12431	Hs.166109	4.3	2164 2165 6413
	449342	hypothetical protein DKFZp434D1428	AA814517	Hs.321775	4.3	4082 7964
	403088	NM_003319*:Homo sapiens tñin (TTN), mR			4.3	4707
35	436315	hypothetical protein MGC4837	BE390513	Hs.27935	4.3	3182 7187
	407711	KIAA1808 protein	AI085846	Hs.25522	4.2	151 4896
	422414	ESTs	AW875237	Hs.132160	4.2	1680 6069
	432943	HSPC018 protein	AW575160	Hs.283677	4.2	2917 6971
	443105	chondroitin sulfate proteoglycan 4 (mel	X96753	Hs.9004	4.2	3600 3601 7568
40	450534	KIAA0470 gene product	AI570189	Hs.25132	4.2	4175 8040
	431632	Homo sapiens cDNA FLJ10130 fis, clone H	AK000992	Hs.333144	4.2	2804 6882
	452195	ESTs	AA994712	Hs.116878	4.2	4296 8138
	448386	KIAA1329 protein	AB037750	Hs.21061	4.2	3997 3998 7896
	409716	Homo sapiens mRNA; cDNA DKFZp586J1717 (AL117454	Hs.56027	4.2	383 5077
45	417796	ESTs	AA206141	Hs.367818	4.2	1159 5682
	410055	gene for serine/threonine protein kinas	AJ250839	Hs.58241	4.2	414 415 5102
	420582	Homo sapiens chromosome 19, cosmid R283	BE047878	Hs.99093	4.2	1464 5915
	417675	similar to murine leucine-rich repeat p	AI080607	Hs.3781	4.2	1144 5670
	424806	MSTP031 protein	AA382523	Hs.105689	4.2	2004 6301
50	438072	ESTs	AA992149	Hs.121899	4.2	3297 7290
	407330	gb:nn51b05.s1 NCI_CGAP_Kid6 Homo sapien	AA582607	Hs.156289	4.2	136 4884
	416857	FGENESH predicted TM containing protein	AA188775	Hs.292453	4.2	1042 5592
	439737	Homo sapiens mRNA full length insert cD	AI751438	Hs.41271	4.2	3427 7410
	423914	Human DNA sequence from clone RP3-466N1	BE379485	Hs.135259	4.2	1868 6208
55	425494	ESTs, Weakly similar to similar to anky	N55540	Hs.78026	4.2	2107 6374
	423171	hypothetical protein DKFZp761G1913	AW138498	Hs.245880	4.2	1778 6143
	451811	hypothetical protein MGC1136	AA663485	Hs.8719	4.2	4259 8106
	408449	dynamitin 1	NM_004408	Hs.1 66161	4.2	224 225 4958
	409882	heat shock 27kD protein family, member	AJ243191	Hs.56874	4.2	395 396 6087
60	443163	ESTs	AI082610	Hs.132079	4.2	3605 7572
	456508	ESTs, Weakly similar to AF208855 1 BM-0	AA502764	Hs.123469	4.2	4521 8325
	454090	gb:MR0-CT0064-100899-002-h09 CT0064	Hom AW062462		4.2	4490 8298
	432211	hypothetical protein FLJ10986	BE274530	Hs.273333	4.2	2852 6917
	431830	small inducible cytokine subfamily A (C	Y16645	Hs.271387	4.2	2827 2828 6900
65	445677	ras homolog gene family, member E	H96577	Hs.6838	4.2	3791 7723
	417114	ESTs	AA193472	Hs.20007	4.2	1080 5621
	400653	NM_001104*:Homo sapiens actinin, alpha			4.2	4637
	433323	ESTs	AA805132	Hs.159142	4.2	2970 7011
	420139	lipase, hormone-sensitive	NM_005357	Hs.9 5351	4.2	1419 1420 5881
70	447946	ESTs	AI566164	Hs.277445	4.2	3968 7870
	445263	KIAA1560 protein	H57646	Hs.42586	4.2	3755 7697
	407896	Zic family member 1 (odd-paired Drosoph	D76435	Hs.41154	4.2	176 177 4919
	428317	ESTs	AW022609	Hs.50745	4.2	2431 6610
	415668	Homo sapiens lysyl oxidase-like 4 (LOXL	AW957684	Hs.306814	4.2	936 5510
75	414774	plasminogen activator, urokinase	X02419	Hs.77274	4.2	869 870 5461
	431103	pleiotrophin (heparin binding growth fa	M57399	Hs.44	4.2	2748 2749 6840
	425712	ESTs, Moderately similar to ALU1_HUMAN	AA412548	Hs.21423	4.2	2130 6389
	408202	DKFZP586L151 protein	AA227710	Hs.43658	4.1	202 4942
	424119	ESTs	AI141999	Hs.113314	4.1	1899 6229
80	426369	Kreiser (mouse) maf-related leucine zi	AF134157	Hs.169487	4.1	2213 2214 6448
	453876	ESTs, Weakly similar to I38022 hypothet	AW021748	Hs.110406	4.1	4457 8271
	435406	calcium/calmodulin-dependent protein ki	F26698	Hs.4884	4.1	3124 7140
	429951	zinc finger protein 106	AL040521	Hs.15220	4.1	2624 6752
	408920	fibronectin leucine rich transmembrane	AL120071	Hs.48998	4.1	276 4999
85	444412	Homo sapiens clone HH409 unknown mRNA	AI147652	Hs.216381	4.1	3700 7655
	450336	Homo sapiens cDNA: FLJ23296 fis, clone	AA046814	Hs.288928	4.1	4155 8025
	414117	proteolipid protein 1 (Pelizaeus-Merzba	W88559	Hs.355807	4.1	777 5386

429317	Homo sapiens cDNA: FLJ21243 fis, clone	AA831552	Hs.268016	4.1	2544 6696	
416783	monocyte to macrophage differentiation-	AA206186	Hs.79889	4.1	1031 5584	
450842	ESTs	AA011358	Hs.103316	4.1	4200 8061	
451669	Homo sapiens, clone IMAGE:3603836, mRNA	AA349726	Hs.294151	4.1	4243 8095	
5	416728	casein kinase 1, epsilon	AB024597	Hs.79658	4.1	1024 1025 5580
452991	ESTs	AI393659	Hs.375560	4.1	4376 8204	
413004	Interleukin enhancer binding factor 2,	T35901	Hs.75117	4.1	667 5300	
448866	myogenic factor 3	BE297743	Hs.284203	4.1	4044 7932	
447628	ESTs	AI914617	Hs.161353	4.1	3943 7850	
10	452242	glycosyltransferase	R50956	Hs.159993	4.1	4305 8145
426996	Homo sapiens cDNA: FLJ21897 fis, clone	AW968934	Hs.173108	4.1	2295 6503	
407965	heat shock 27kD protein 3	W21483	Hs.41707	4.1	183 4925	
428303	regulator of G-protein signalling 16	AW974476	Hs.183601	4.1	2425 6606	
439450	ESTs	R51613	Hs.125304	4.1	3397 7380	
15	435937	ESTs	AA830893	Hs.119769	4.1	3164 7172
433972	cisplatin resistance-associated overexp	AI878910	Hs.278670	4.1	3021 7054	
428418	ESTs	AI368826	Hs.8768	4.1	2441 6619	
423550	ESTs	F37675	Hs.152129	4.1	1815 6169	
406627	ESTs	T64904	Hs.163780	4.1	30 4812	
20	436555	ESTs, Weakly similar to 2003319A ankyri	AI972007	Hs.304646	4.1	3200 7202
408696	NS1-associated protein 1	AW958157	Hs.355960	4.1	249 4979	
426433	thrombospondin 3	L38969	Hs.169875	4.1	2226 2227 6457	
408753	SH3 domain binding glutamic acid-rich p	AI337192	Hs.47438	4.1	254 4983	
409038	small inducible cytokine subfamily A (C	T97490	Hs.50002	4.1	298 5016	
25	416140	roundabout (axon guidance receptor, Dro	AI918035	Hs.301198	4.0	978 5545
422961	B-cell CLL/lymphoma 9	Y13620	Hs.122607	4.0	1763 1764 6131	
446508	hypothetical protein FLJ13441	H11701	Hs.232146	4.0	3844 7768	
430558	KIAA1067 protein	AB028990	Hs.325530	4.0	2710 2711 6813	
411127	hypothetical protein	AA668995	Hs.323463	4.0	516 5176	
30	446019	histone deacetylase 3	AI362520	Hs.302718	4.0	3810 7739
415580	ESTs, Weakly similar to ALU1_HUMAN ALU	F12306	Hs.369191	4.0	931 5505	
417994	cytotoxic T-lymphocyte-associated prote	AI791416	Hs.247824	4.0	1173 5694	
421937	hematological and neurological expresse	AI878857	Hs.109706	4.0	1617 6024	
446510	retinoic acid induced 14	H58306	Hs.15165	4.0	3847 7770	
35	426817	Homo sapiens mRNA; cDNA DKFZp564C0671 (AL122088	Hs.172627	4.0	2276 6488
421483	hypothetical protein MGC11333	NM_003388	Hs.1 04717	4.0	1545 1546 5973	
412473	ESTs	F23393	Hs.153060	4.0	594 5241	
424223	putative DNA/chromatin binding motif	AJ243706	Hs.143323	4.0	1915 1916 6240	
449030	Homo sapiens mRNA for FLJ00016 protein,	AI365582	Hs.57100	4.0	4059 7943	
40	426344	transcriptional activator of the c-fos	H41821	Hs.322469	4.0	2209 6445
432787	HSPC054 protein	NM_014152	Hs.2 78946	4.0	2905 2906 6962	
426304	Homo sapiens cDNA FLJ11477 fis, clone	H AA374532	Hs.124673	4.0	2198 6438	
419290	spinal cord-derived growth factor-B	AI128114	Hs.112885	4.0	1327 5810	
406850	collagen, type I, alpha 1	AI624300	Hs.172928	4.0	70 4837	
45	401284	Target Exon			4.0	4648
448121	hypothetical protein DKFZp564F013	ALD45714	Hs.128653	4.0	3979 7881	
448646	transcription factor 12 (HTF4, helix-to	AU077149	Hs.21704	4.0	4022 7914	
459578	EST			4.0	8391	
440594	ESTs	AW445167	Hs.126036	4.0	3475 7453	
50	419452	PTK7 protein tyrosine kinase 7	U33635	Hs.90572	4.0	1340 1341 5821
424511	ESTs, Moderately similar to ALU7_HUMAN	BE300512	Hs.193557	4.0	1967 6276	
443072	gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapie	AI937532	Hs.353026	4.0	3599 7567	
429713	thioredoxin, mitochondrial	N41898	Hs.211929	4.0	2608 6740	
55	446452	KIAA0740 gene product	AB018283	Hs.15099	3.9	3839 3840 7765
451678	DKFZP564D0764 protein	AA374181	Hs.26799	3.9	4244 8096	
419940	ESTs	AW611903	Hs.144585	3.9	1397 5864	
415024	ESTs	AI983981	Hs.296141	3.9	902 5483	
445470	ESTs	AI239871	Hs.154758	3.9	3772 7710	
60	418399	hypothetical protein FLJ12442	AF131781	Hs.84753	3.9	1232 1233 5738
413929	collagen, type IV, alpha 2	BE501689	Hs.75617	3.9	754 5368	
430030	lectin, galactoside-binding, soluble, 1	BE300094	Hs.227751	3.9	2641 6764	
452701	glutamine-fructose-6-phosphate transami	NM_005110	Hs.3 0332	3.9	4345 4346 8178	
426363	transforming growth factor, beta 3	M58524	Hs.2025	3.9	2210 2211 6446	
445900	Homo sapiens clone 24787 mRNA sequence	AF070526	Hs.125036	3.9	3803 7733	
65	435520	HNOEL-iso protein	AA297990	Hs.9315	3.9	3130 7146
411962	gb:zk85d12.r1 Soares_pregnant_uterus_Nb	AA099050		3.9	563 5215	
432098	cytochrome P450 retinoid metabolizing p	AF252297	Hs.91546	3.9	2839 2840 6908	
418647	gb:nc26a07.s1 NCI_CGAP_Pr1 Homo saplens	AA226198		3.8	1263 5761	
70	452277	KIAA1223 protein	ALD49013	Hs.28783	3.8	4308 8148
408562	roundabout (axon guidance receptor, Dro	AI436323	Hs.31141	3.8	240 4971	
452239	protein tyrosine phosphatase, receptor	AW379378	Hs.356289	3.8	4303 8143	
439424	hypothetical protein FLJ22833	AI478667	Hs.118183	3.8	3396 7379	
433430	ESTs	AI863735	Hs.369982	3.8	2977 7018	
75	439673	Homo sapiens cDNA: FLJ22290 fis, clone	T53169	Hs.9587	3.8	3416 7399
451691	ESTs	AI809278	Hs.208152	3.8	4248 8099	
417024	ESTs	AI467951	Hs.133326	3.8	1061 5606	
443617	papillary renal cell carcinoma (translo	AA496425	Hs.9629	3.8	3629 7592	
435553	KIAA0176 protein	D79998	Hs.4935	3.8	3134 3135 7149	
434868	collagen, type VI, alpha 2	R50032	Hs.159263	3.7	3085 7106	
80	441965	ESTs	AA972712	Hs.269737	3.7	3544 7516
422565	singed (Drosophila)-like (sea urchin fa	BE259035	Hs.118400	3.7	1701 6086	
429290	neurofilament, heavy polypeptide (200kD	AF203032	Hs.198760	3.7	2538 2539 6692	
416322	pyrroline-5-carboxylate reductase 1	BE019494	Hs.79217	3.7	989 5554	
432842	hypothetical protein MGC4485	AW674093	Hs.334822	3.7	2911 6966	
85	430818	gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapien	AI311928	Hs.348156	3.7	2728 6826
442578	hypothetical protein FLJ10781	AK001643	Hs.8395	3.7	3572 3573 7543	

422084	hypothetical protein	AK001266	Hs.111279	3.7	1637 1638 6038
426316	meningioma (disrupted in balanced trans	NM_002430	Hs.2 68515	3.7	2203 2204 6441
418745	sprouty (Drosophila) homolog 1 (antagon	AW882645	Hs.88044	3.7	1273 5768
412978	homeo box C6	AI431708	Hs.820	3.7	665 6298
425741	Homo sapiens clone 24628 mRNA sequence	AF052152	Hs.129997	3.7	2133 6391
414358	ESTs	AA476456	Hs.98969	3.6	807 5412
432179	EphB3	X75208	Hs.2913	3.6	2849 2850 6915
442831	ESTs	AI798959	Hs.131686	3.6	3586 7554
453327	tryptophanyl-tRNA synthetase	AW500180	Hs.356109	3.6	4412 8235
407454	gb:Homo sapiens mRNA for axonemal dynei	AJ132089		3.6	140 141 4887
427375	metallocarboxypeptidase CPX-1	AL035460	Hs.177538	3.6	2320 2321 6522
421920	gamma-aminobutyric acid (GABA) receptor	BE551245	Hs.1438	3.6	1614 6022
448111	interferon-induced protein with tetratr	AA053486	Hs.20315	3.6	3978 7880
410422	Homo sapiens, clone MGC:15203, mRNA, co	AL042014	Hs.63348	3.6	462 5136
418741	ESTs, Weakly similar to S41044 chromoso	H83265	Hs.8881	3.6	1272 5767
416406	lipoma HMGIC fusion partner-like 2	D86961	Hs.79299	3.5	1001 1002 5564
431176	ESTs	AI026984	Hs.293662	3.5	2755 6844
448412	ESTs, Moderately similar to ALU8_HUMAN	AJ219083	Hs.42532	3.5	4002 7899
417426	laminin, beta 1	NM_002291	Hs.8 2124	3.5	1119 1120 5654
447471	sprouty (Drosophila) homolog 2	AF039843	Hs.18676	3.5	3930 3931 7839
414612	protein inhibitor of activated STAT3	BE274552	Hs.76578	3.5	838 5438
430598	hypothetical protein FLJ10902	AK001764	Hs.247112	3.5	2712 2713 6814
407325	ESTs, Weakly similar to alternatively s	AA291180	Hs.328476	3.5	135 4883
443228	KIAA1710 protein	W24781	Hs.293798	3.4	3610 7577
406972	gb:Human H19 RNA gene, complete cds.	M32053		3.4	89 4848
439668	frizzled (Drosophila) homolog 8	AI091277	Hs.302634	3.4	3414 7397
458300	ribosomal protein L31	AW612538	Hs.304491	3.4	4573 8370
448309	N-deacetylase/N-sulfotransferase (hepar	AI282120	Hs.20894	3.4	3993 7892
410023	slit (Drosophila) homolog 3	AB017169	Hs.57929	3.4	410 411 5099
453905	LIM domain kinase 1	NM_002314	Hs.3 6566	3.4	4462 4463 8276
435189	ESTs	AW581418	Hs.196244	3.4	3113 7131
447809	ESTs, Highly similar to JC7266 3',5'-cy	AW207605	Hs.164230	3.4	3964 7866
429709	dicckopf (Xenopus laevis) homolog 2	BE047680	Hs.211869	3.3	2607 6739
424651	ESTs	AI493206	Hs.120785	3.3	1984 6287
422048	spondin 2, extracellular matrix protein	NM_012445	Hs.2 88126	3.3	1631 1632 6034
441499	ESTs	AW298235	Hs.101689	3.3	3522 7495
437036	ESTs	AI571514	Hs.133022	3.3	3232 7231
409430	splicing factor, arginine/serine-rich 6	R21945	Hs.346735	3.3	348 5052
407137	gb:ye53h05.s1 Soares fetal liver spleen	T97307		3.2	114 4866
409433	ESTs	AA074382	Hs.135255	3.2	349 5053
429640	angiopoietin 1	U83508	Hs.2463	3.2	2596 2597 6732
442828	FK506-binding protein 9 (63 kD)	BE263255	Hs.302749	3.2	3585 7553
450161	ESTs	H78516	Hs.201362	3.2	4137 8012
439456	hypothetical protein FLJ20980	AI752409	Hs.109314	3.2	3400 7383
440614	hypothetical protein FLJ12879	AA781530	Hs.127236	3.2	3476 7454
417043	collagen, type VI, alpha 3	NM_004369	Hs.8 0988	3.1	1064 1065 5609
426027	platelet-derived growth factor beta pol	NM_002608	Hs.1 976	3.1	2161 2162 6411
409197	chromosome 11 open reading frame 24	U54706	Hs.303025	3.1	322 5035
442487	hypothetical protein, estradiol-induced	AF191019	Hs.8361	3.1	3564 3565 7536
456856	Homo sapiens, Similar to DiGeorge syndr	AK001528	Hs.347285	3.0	4533 8335

TABLE 3B:

	Pkey:	Unique Eos probeset identifier number	
55	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Pkey	CAT Number	Accession
	418059	1164438_1	AA211586 F35799 F29720 AW937408 AW937387 AA211641
60	426413	372468_1	AW954494 AA377823 BG219617 BG195685 BG616269 AI022688
	420895	263604_1	AA557228 AI275977 H88644 AA281495 H88685
	454090	579894_1	AW062465 AW062462 BF333918 AW176554 AW062482 AW062481 AW062468 AW062467
	459578	996433_1	BE937231 BI712437 AW612538 BI712664 BI712740 BI712501
	411962	2307710_1	AA099050 AA099526 T47733
65	418647	243680_1	AA226513 AA383773 AA226198

TABLE 3C:

70

Pkey:
Ref:

Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand:
Nt_position:

Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons.

75

Pkey
405001
400499
400651
402621
403081
401566
406519
404977
405681
402331
403088

Ref
6015406
9796071
8117978
9930950
8954241
8469090
3962489
3738341
4544348
8050898
8954241

Strand
Minus
Minus
Minus
Plus
Plus
Minus
Plus
Minus
Minus
Minus
Plus

Nt_position
104646-104819
148495-148806
81488-81646
130806-131036
155749-156048,156142-156459
96277-96420,96979-97160
34617-34928
43081-43229
79420-79605
53610-53888
169894-170193,170504-170806

80

85

400653 8117978 Plus 109077-109307
401284 9800819 Minus 101307-101421

5 TABLE 4A

PKay: Unique Eos probeset identifier number
Gene name: Unigene gene title
Accession: Exemplar Accession number, Genbank accession number
UniGene: Unigene number
RATIO: 95th percentile of liposarcoma AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator
SEQ ID #: nucleic acid and protein sequences provided on CD for search purposes

PKay	Gene Name	Accession	UniGene	RATIO	SEQ ID #
413778	myosin, light polypeptide 2, regulatory	AA090235	Hs.75535	37.3	740 5356
407245	titin	X90568	Hs.172004	28.5	132 133 4881
426752	titin	X69490	Hs.172004	22.4	2266 2267 6482
425545	Homo sapiens, clone MGC:12401, mRNA, co	N98529	Hs.158295	21.0	2114 6379
412519	troponin T1, skeletal, slow	AA196241	Hs.73980	19.9	598 5244
400440	nebulin	X83957	Hs.83870	19.0	24 25 4627
426300	delta-like homolog (Drosophila)	U15979	Hs.169228	18.8	2196 2197 6437
407013	gb:Human nebulin mRNA, partial cds	U35637	Hs.83870	18.3	94 95 4851
453857	Ras-induced senescence 1 (RIS1)	AL080235	Hs.35861	18.1	4449 4450 8266
416931	adipose most abundant gene transcript 1	D45371	Hs.80485	17.9	1047 1048 5597
417070	titin	Z19077	Hs.172004	16.3	1070 5614
406704	myosin, heavy polypeptide 7, cardiac mu	M21665	Hs.929	14.6	55 56 4826
417435	carbonic anhydrase III, muscle specific	NM_005181	Hs.8 2129	14.3	1121 1122 5655
420139	lipase, hormone-sensitive	NM_005357	Hs.9 5351	14.1	1419 1420 5881
421296	perlipin	NM_002666	Hs.1 03253	14.0	1525 1526 5961
405001	interleukin enhancer binding factor 1			13.2	4767
428087	troponin C2, fast	AA100573	Hs.182421	13.0	2396 6582
413385	indoleamine-pyrrole 2,3 dioxygenase	M34455	Hs.840	12.9	710 711 5331
422060	ESTs, Moderately similar to ALU5_HUMAN	R20893	Hs.325823	12.7	1633 6035
422640	troponin C, slow	M37984	Hs.118845	12.5	1718 1719 6099
406964	FGFES predicted novel secreted protein	M21305		12.4	87 88 4847
419648	thyroid hormone responsive SPOT14 (rat)	T73661	Hs.91877	12.2	1366 5839
427809	lipoprotein lipase	M26380	Hs.180878	12.2	2373 6562
411393	B-factor, properdin (COMPLEMENT FACTOR	AW797437	Hs.69771	12.1	531 5189
458079	Homo sapiens similar to RIKEN cDNA 2810	AI796870	Hs.381220	12.0	4566 8363
418399	hypothetical protein FLJ12442	AF131781	Hs.84753	11.9	1232 1233 5738
431830	small inducible cytokine subfamily A (C	Y16645	Hs.271387	11.8	2827 2828 6900
429359	matrix metalloproteinase 14 (membrane-i	W00482	Hs.2399	11.8	2551 6702
410621	titin	AA194329	Hs.172004	11.7	481 5149
425292	37 kDa leucine-rich repeat (LRR) protei	NM_005824	Hs.1 55545	11.6	2083 2084 6359
453331	ESTs	AI240655	Hs.352537	11.6	4413 8236
417389	midkine (neurite growth-promoting facto	BE260964	Hs.82045	11.6	1109 5647
428182	ESTs, Weakly similar to GGC1_HUMAN	G AN BE386042	Hs.293317	11.4	2403 6588
419222	spermine synthase	AD001528	Hs.89718	11.2	1318 1319 5803
416373	ESTs, Weakly similar to S12658 cysteine	AA195845	Hs.73680	11.0	996 5559
444381	hypothetical protein BC014245	BE387335	Hs.283713	10.9	3697 7652
431089	ESTs, Weakly similar to unknown protein	BE041395	Hs.374629	10.9	2745 6838
410407	carbonic anhydrase IX	X66839	Hs.63287	10.9	460 461 5135
411296	growth suppressor 1	BE207307	Hs.10114	10.7	524 5183
427254	ESTs	AL121523	Hs.97774	10.6	2312 6516
446619	secreted phosphoprotein 1 (osteopontin,	AU076643	Hs.313	10.5	3861 7782
422069	titin-cap (telethonin)	AJ010063	Hs.343603	10.4	1635 1636 6037
418054	lysyl oxidase-like 2	NM_002318	Hs.8 3354	10.4	1184 1185 5702
418986	ESTs	AI123555	Hs.293821	10.4	1288 5779
416378	ankyrin repeat domain 2 (stretch respon	AW044467	Hs.73708	10.3	997 5560
413902	CD36 antigen (collagen type I receptor,	AU076743	Hs.75613	10.2	752 5366
411789	Adiccan	AF245505	Hs.72157	10.2	553 554 5207
414152	thrombospondin 4	NM_003248	Hs.7 5774	10.1	782 783 5391
418478	cyclin-dependent kinase inhibitor 2A (m	U38945	Hs.1174	10.1	1245 1246 5747
414219	ALL1-fused gene from chromosome 1q	W20010	Hs.75823	10.0	789 5397
429185	ESTs	AW203961	Hs.104977	9.8	2528 6682
403593	Target Exon			9.8	4725
407102	glycerol-3-phosphate dehydrogenase 1 (s	AA007629	Hs.348601	9.7	109 4861
418391	troponin I, skeletal, slow	NM_003281	Hs.8 4673	9.6	1228 1229 5736
428769	ESTs	AW207175	Hs.106771	9.5	2470 6640
407788	S100 calcium-binding protein A2	BE514982	Hs.38991	9.5	161 4905
449109	ESTs, Weakly similar to ALU7_HUMAN	ALU AW270992	Hs.120949	9.4	4064 7948
452620	ESTs	AA436504	Hs.119286	9.4	4338 8172
425367	protein tyrosine phosphatase, receptor	BE271188	Hs.155975	9.4	2095 6366
418390	titin immunoglobulin domain protein (my	AF133820	Hs.84665	9.4	1226 1227 5735
403088	NM_003319*:Homo sapiens titin (TTN), mR			9.3	4707
426509	pentaxin-related gene, rapidly induced	M31166	Hs.2050	9.2	2243 2244 6468
430476	tachykinin, precursor 1 (substance K, s	AA447465	Hs.2563	9.2	2701 6807
419833	Homo sapiens triptophanyl-tRNA syntheta	AA251131	Hs.220697	9.1	1388 5856
410687	lysyl oxidase-like 1	U24389	Hs.65436	9.0	485 486 5153
457869	Homo sapiens, alpha-1 (VI) collagen	AU077186	Hs.108885	8.9	4561 8359
410361	guanylate binding protein 1, interferon	BE391804	Hs.62661	8.9	456 5132
443514	ESTs	BE464288	Hs.25475	8.9	3624 7588
443071	complement component 1, q subcomponent	AL080021	Hs.8986	8.9	3598 7566
414386	haploglobin	X00442	Hs.75990	8.8	810 811 5415
450098	hypothetical protein FLJ21080	W27249	Hs.8109	8.7	4134 8009

409169	(clone PWHL2-24) myosin light chain 2	F00991	Hs.50889	8.7	316 5029
413011	biglycan	AW068115	Hs.821	8.6	669 5302
420197	ESTs, Weakly similar to A57291 cytokine	AW139647	Hs.88134	8.5	1429 5889
418678	cancer/testis antigen (NY-ESO-1)	NM_001327	Hs.8 7225	8.5	1269 1270 5765
450375	a disintegrin and metalloproteinase dom	AA009547	Hs.352537	8.5	4159 8028
408202	DKFZP586L151 protein	AA227710	Hs.43658	8.4	202 4942
411021	titin	F00055	Hs.172004	8.4	508 5169
413278	Interferon-stimulated protein, 15 kDa	BE563085	Hs.833	8.4	695 5322
423739	ESTs	AA398155	Hs.97600	8.4	1842 6190
438089	nuclear receptor subfamily 1, group I,	W05391	Hs.351546	8.4	3301 7294
426429	myosin-binding protein C, slow-type	X73114	Hs.169849	8.4	2224 2225 6456
424408	collagen, type V, alpha 1	A1754813	Hs.146428	8.3	1943 6260
423778	flavin containing monooxygenase 2	Y09267	Hs.132821	8.3	1846 1847 6193
407112	ESTs, Weakly similar to ALU7_HUMAN	AA070801	Hs.51615	8.3	111 4863
417370	tryptophanyl-RNA synthetase	T28651	Hs.374466	8.2	1105 5643
451099	Interleukin 13 receptor, alpha 2	R52795	Hs.25954	8.1	4212 8071
423024	ESTs, Moderately similar to ALU5_HUMAN	AA593731	Hs.325823	8.1	1770 6136
418026	fatty acid binding protein 4, adipocyte	BE379727	Hs.83213	8.0	1179 5698
434352	small muscle protein, X-linked	AF129505	Hs.86492	8.0	3047 3048 7075
447131	retinoic acid receptor responder (lazar	NM_004585	Hs.1 7466	8.0	3891 3892 7808
452838	preferentially expressed antigen in mel	U65011	Hs.30743	7.9	4357 4358 8188
427335	G antigen 7B	AA448542	Hs.278444	7.9	2317 6520
431211	gap junction protein, beta 2, 26kD (con	M86849	Hs.323733	7.8	2762 2763 6850
444006	type 1 transmembrane protein Fn14	BE395085	Hs.334762	7.8	3668 7627
400499	C10001858:g[6679124]ref[NP_032759.1]			7.8	4628
448498	ESTs	AA418276	Hs.375003	7.8	4007 7904
447205	ESTs, Moderately similar to T17372 plas	BE617015	Hs.11006	7.7	3900 7816
412326	small inducible cytokine A3 (homologous	R07566	Hs.73817	7.7	582 5231
427639	Homo sapiens, clone MGC:18257, mRNA, co	AW444530	Hs.350860	7.7	2353 6547
430413	small inducible cytokine A5 (RANTES)	AW842182	Hs.241392	7.7	2693 6801
414821	Fc fragment of IgG, high affinity Ia, r	M63835	Hs.77424	7.6	876 877 5465
409096	sarcomeric muscle protein	AA194412	Hs.50550	7.6	302 5019
418728	ESTs	AW970937	Hs.293843	7.6	1271 5766
442573	branched chain aminotransferase 1, cyto	H93366	Hs.7567	7.5	3570 7541
442089	membrane-bound transcription factor pro	AW664144	Hs.297007	7.5	3548 7520
437330	Homo sapiens mRNA; cDNA DKFZp761J1112 (AL353944	Hs.50115	7.5	3253 7250
420137	CD3D antigen, delta polypeptide (TIT3 c	AA306478	Hs.95327	7.5	1418 5880
428289	complement component 2	M26301	Hs.2253	7.5	2421 2422 6603
435523	membrane-spanning 4-domains, subfamily	T62849	Hs.11090	7.5	3131 7147
400288	Integrin, alpha 5 (fibronectin receptor	X06256	Hs.149609	7.4	1 2 4614
438746	Human melanoma-associated antigen p97 (A1885815	Hs.184727	7.3	3353 7337
426310	neuropeptide Y receptor Y1	NM_000909	Hs.1 69266	7.3	2199 2200 6439
429973	ESTs	A1423317	Hs.164680	7.3	2628 6756
425088	hypothetical protein FLJ12015	AA663372	Hs.169395	7.3	2049 6334
444090	natural killer cell group 7 sequence	S69115	Hs.10305	7.3	3675 3676 7634
422633	enolase 3, (beta, muscle)	X56832	Hs.118804	7.3	1716 1717 6098
449722	cyclin B1	BE280074	Hs.23960	7.2	4112 7990
432606	granzyme K (serine protease, granzyme 3	NM_002104	Hs.3066	7.2	2891 2892 6951
438091	nuclear receptor subfamily 1, group I,	AW373062	Hs.351546	7.2	3302 7295
419490	granzyme A (granzyme 1, cytotoxic T-lym	NM_006144	Hs.9 0708	7.2	1343 1344 5823
418156	nuclear receptor subfamily 1, group I,	W17056	Hs.83623	7.1	1198 5715
424687	matrix metalloproteinase 9 (gelatinase	J05070	Hs.151738	7.1	1986 1987 6289
417308	KIAA0101 gene product	H60720	Hs.81892	7.0	1094 5634
423961	perlestin (OSF-2os)	D13666	Hs.136348	7.0	1878 1879 6215
410021	X-prolyl aminopeptidase (aminopeptidase	AL023653	Hs.57922	7.0	409 5098
401403	Target Exon			7.0	4651
406673	major histocompatibility complex, class	M34996	Hs.198253	7.0	90 91 4821
434449	hypothetical protein FLJ22041 similar t	AW953484	Hs.3849	7.0	3057 7083
421508	absent in melanoma 2	NM_004833	Hs.1 05115	7.0	1551 1552 5977
418460	CD8 antigen, alpha polypeptide (p32)	M26315	Hs.85258	7.0	1243 1244 5746
430678	ESTs	A1458174	Hs.192855	7.0	2718 6818
445937	UDP-Gal:betaGlcNAc beta 1,4- galactosyl	A1452943	Hs.321231	7.0	3807 7737
420202	putative lymphocyte G0/G1 switch gene	AL036557	Hs.95910	6.9	1430 5890
456063	retinol-binding protein 4, interstitial	NM_006744	Hs.7 6461	6.9	4511 4512 8317
429500	hexabrachion (tenascin C, cytotoxic)	X78565	Hs.289114	6.8	2574 2575 6718
415989	ESTs	A1267700	Hs.351201	6.8	962 5530
425234	ESTs, Weakly similar to I38022 hypothet	AW152225	Hs.165909	6.8	2070 6349
452701	glutamine-fructose-6-phosphate transami	NM_005110	Hs.3 0332	6.8	4345 4346 8178
424825	procollagen-lysine, 2-oxoglutarate 5-di	AF207069	Hs.153357	6.8	2005 2006 6302
440709	ESTs	AW797724	Hs.130350	6.8	3484 7460
424503	integrin, alpha 5 (fibronectin receptor	NM_002205	Hs.1 49609	6.8	1965 1966 6275
449523	chemokine (C-C motif) receptor 5	NM_000579	Hs.5 4443	6.8	4094 4095 7976
412584	DNA segment on chromosome 12 (unique)	2 X54870	Hs.74085	6.7	612 613 5255
414812	monokine induced by gamma interferon	X72755	Hs.77367	6.7	874 875 5464
424086	lysyl oxidase	A1351010	Hs.102267	6.7	1896 6227
410274	hypoxia-inducible protein 2	AA381807	Hs.336402	6.7	444 5122
403081	NM_003319:Homo sapiens titin (TTN), mR			6.7	4704
437220	GS1999full	AL117542	Hs.334305	6.7	3247 7244
442553	hypothetical protein MGC4825	H87867	Hs.40065	6.7	3568 7539
451934	ESTs	A1540842	Hs.61082	6.7	4262 8109
418062	thioredoxin peroxidase (antioxidant enz	AW630656	Hs.83383	6.7	1187 5704
422627	transforming growth factor, beta-induce	BE336857	Hs.118787	6.7	1715 6097
420981	peroxisome proliferative activated rece	L40904	Hs.100724	6.7	1495 1496 5936
432522	phosphatidylinositol glycan, class A (p	D11466	Hs.51	6.6	2880 2881 6942
439285	hypothetical protein FLJ20093	AL133916	Hs.47860	6.6	3389 7372
444329	hypothetical protein FLJ12921	W73753	Hs.209637	6.6	3693 7648

	442173	KIAA0144 gene product	N76101	Hs.8127	6.6	3552 7524
	407366	gb:Homo sapiens cip33 mRNA, partial seq	AF026942	Hs.17518	6.6	137 4885
	427337	Fc fragment of IgG, low affinity IIb,	Z46223	Hs.176663	6.6	2318 2319 6521
	424420	prostaglandin E synthase	BE614743	Hs.146688	6.5	1949 6264
5	419741	ubiquitin carrier protein E2-C	NM_007019	Hs.9 3002	6.5	1379 1380 5850
	439092	gb:cc44f08.s1 NCI_CGAP_GCB1 Homo sapien	AAB30149		6.5	3376 7359
	422530	bone marrow stromal cell antigen 2	AW972300	Hs.118110	6.5	1696 6082
	439237	ESTs, Weakly similar to A47582 B-cell g	AW408158	Hs.318893	6.5	3384 7367
	445263	KIAA1560 protein	H57646	Hs.42586	6.4	3755 7697
10	450447	hypothetical protein P15-2	AF212223	Hs.25010	6.4	4168 4169 8036
	428976	ras homolog gene family, member I	AL037824	Hs.194695	6.4	2495 6658
	406625	stearoyl-CoA desaturase (delta-9-desatu	Y13647	Hs.119597	6.4	28 29 4811
	446523	sarcophilin	NM_003063	Hs.3 34629	6.4	3852 3853 7774
	401566	NM_005159:Homo sapiens actin, alpha, ca			6.4	4654
15	447770	frizzled (Drosophila) homolog 4	AB032417	Hs.19545	6.4	3961 3962 7864
	429294	Homo sapiens cDNA: FLJ22463 fis, clone	AA095971	Hs.198793	6.4	2540 6693
	447733	MAD2 (mitotic arrest deficient, yeast,	AF157482	Hs.19400	6.4	3955 3956 7860
	437206	ESTs, Weakly similar to I38344 titin, c	AW975934	Hs.172004	6.4	3245 7242
	425397	topoisomerase (DNA) II alpha (170kD)	J04088	Hs.156346	6.4	2099 2100 6369
20	406922	gb:stearoyl-CoA desaturase (human, adip	S70284	Hs.119597	6.3	79 80 4843
	406837	immunoglobulin kappa constant	R70292	Hs.156110	6.3	69 4836
	409142	SMC4 (structural maintenance of chromos	AL136877	Hs.50758	6.3	312 313 5027
	410270	tumor endothelial marker 1 precursor	AF279142	Hs.195727	6.3	442 443 5121
	450787	aquaporin 7	AB006190	Hs.25475	6.3	4194 4195 8057
25	407061	gb:H.sapiens PTX3 gene promotor region.	X97748		6.3	102 4856
	429626	holocytochrome c synthase (cytochrome c	U36787	Hs.211571	6.3	2593 2594 6730
	439424	hypothetical protein FLJ22833	AI478667	Hs.118183	6.3	3396 7379
	418113	SRY (sex determining region Y)-box 4	AI272141	Hs.83484	6.3	1194 5711
	418607	KIAA1402 protein	AL137426	Hs.86392	6.2	1260 5759
30	414053	transgelin 2	BE391635	Hs.75725	6.2	774 5383
	426991	Homo sapiens cDNA FLJ10674 fis, clone	N AK001536	Hs.214410	6.2	2294 6502
	439755	B7 homolog 3	AW748482	Hs.77873	6.2	3430 7413
	447519	ESTs	U46258	Hs.339665	6.2	3936 7844
35	430699	ESTs, Weakly similar to RET2_HUMAN RET	AW969847	Hs.292718	6.2	2723 6822
	426798	ESTs	AA385052	Hs.130260	6.2	2275 6487
	419913	ESTs	AW270040	Hs.34455	6.2	1395 5862
	414002	FBJ murine osteosarcoma viral oncogene	NM_006732	Hs.75678	6.2	763 764 5375
	424688	myosin, light polypeptide 3, alkali; ve	AA216287	Hs.1815	6.2	1988 6290
	452862	ADAMT2 (a disintegrin-like and metal	AW378065	Hs.8687	6.1	4360 8190
40	423575	intron of perostin (OSF-2os)	C18863	Hs.163443	6.1	1820 6173
	424078	paternally expressed 3	AB006625	Hs.139033	6.1	1893 1894 6225
	423858	Homo sapiens mRNA; cDNA DKFZp434B0650	(AL137326	Hs.133483	6.1	1858 6201
	416349	myomesin (M-protein) 2 (165kD)	X69089	Hs.79227	6.1	991 992 5556
	413436	sphingosine kinase 1	AF238083	Hs.68061	6.1	721 722 5339
45	448698	ESTs	AA279913	Hs.31922	6.1	4107 7987
	411358	KIAA1691 protein	R47479	Hs.94761	6.1	527 5186
	436496	glia maturation factor, gamma	AA281959	Hs.5210	6.1	3195 7199
	443426	chromosome 20 open reading frame 1	AF098158	Hs.9329	6.1	3621 3622 7586
	431204	cytochrome c oxidase subunit VIa polype	F28841	Hs.250760	6.1	2760 6848
50	421512	myomegalin	AB007923	Hs.265848	6.1	1554 1555 5979
	432239	matrix metalloproteinase 13 (collagenas	X81334	Hs.2936	6.1	2856 2857 6921
	419846	Williams-Beuren syndrome chromosome reg	NM_015977	Hs.285681	6.1	1389 5857
	429490	ESTs, Weakly similar to ALU7_HUMAN ALU	AI971131	Hs.23889	6.1	2571 6715
	426312	interferon-induced protein with tetratr	AF026939	Hs.181874	6.1	2201 2202 6440
55	410223	calsequestrin 1 (fast-twitch, skeletal	S73775	Hs.60708	6.1	433 434 5115
	430681	ESTs	AW969675	Hs.291232	6.0	2719 6819
	426691	PCTAIRE protein kinase 1	NM_006201	Hs.1 71834	6.0	2262 2263 6480
	416047	DNA segment, numerous copies, expressed	BE439894	Hs.78991	6.0	965 5533
60	406664	glycerol-3-phosphate dehydrogenase 1 (s	L34041	Hs.348601	6.0	83 84 4819
	452363	Homo sapiens, Similar to complement com	AI582743	Hs.94953	6.0	4322 8159
	403087	NM_003319:Homo sapiens titin (TTN), mR			6.0	4706
	417079	interleukin 1 receptor antagonist	U65590	Hs.81134	6.0	1073 1074 5616
	451533	serum deprivation response (phosphatidy	NM_004657	Hs.2 6530	6.0	4239 4240 8092
	419138	ryanodine receptor 1 (skeletal)	U48508	Hs.89631	6.0	1309 1310 5796
65	413773	ESTs	AA131780	Hs.269925	6.0	739 5355
	427596	extracellular glycoprotein EMILIN-2 pre	AA449506	Hs.270143	6.0	2350 6544
	427019	hypothetical protein FLJ10970	AA001732	Hs.173233	6.0	2296 6504
	438885	ESTs	AI886558	Hs.184987	6.0	3363 7346
	450300	ESTs, Highly similar to ITH4_HUMAN INTE	AL041440	Hs.58210	5.9	4154 8024
70	413670	hypothetical protein, expressed in oste	AB000115	Hs.75470	5.9	735 736 5352
	414315	gb:HSB65D052 STRATAGENE Human skeletal	Z24878		5.9	803 5409
	423903	interleukin 11	M57765	Hs.1721	5.9	1865 1866 6206
	422100	ADP-ribosylation factor-like 7	AI096988	Hs.111554	5.9	1644 6042
	449579	ESTs, Weakly similar to T46425 hypothet	AW207260	Hs.134014	5.9	4097 7978
75	421566	early growth response 2 (Krox-20 (Droso	NM_000399	Hs.1 395	5.9	1563 1564 5984
	412577	CD163 antigen	Z22968	Hs.74076	5.9	608 609 5252
	402507	Target Exon			5.8	4683
	411102	triadin	AA401295	Hs.23926	5.8	515 5175
	412955	procollagen-lysine, 2-oxoglutarate 5-di	L06419	Hs.75093	5.8	659 660 5294
80	406836	immunoglobulin kappa constant	AW514501	Hs.156110	5.8	68 4835
	449717	cerebral cell adhesion molecule	AB040935	Hs.23954	5.8	4110 4111 7989
	431205	tropomodulin 4 (muscle)	AA194560	Hs.250763	5.8	2761 6849
	409103	XAGE-1 protein	AF251237	Hs.112208	5.8	304 305 5021
	409731	thymosin, beta, identified in neuroblas	AA125985	Hs.56145	5.8	386 5080
85	412471	endothelial cell growth factor 1 (plate	M63193	Hs.73946	5.8	591 592 5239
	427792	tumor necrosis factor receptor superfam	M63928	Hs.180841	5.8	2371 2372 6561

	419301	tenomodulin protein	AA236166	Hs.132957	5.8	1328	5811
	424440	ESTs	AA340743	Hs.133208	5.8	1951	6266
	431806	tumor necrosis factor (ligand) superfam	AF186114	Hs.270737	5.8	2824	2825 6898
5	409028	Z-band alternatively spliced PDZ-motif	AB014513	Hs.49998	5.8	296	297 5015
	415702	gb:HSPD18414 HM3 Homo sapiens cDNA clon F28877	Hs.73680	5.8	942	5515	
	406925	glycerol-3-phosphate dehydrogenase 1 (s L34041	Hs.348601	5.8	83	84 4845	
	408882	heat shock 27kD protein family, member	AJ243191	Hs.56874	5.7	395	396 5087
	412129	tropoin T3, skeletal, fast	M21984	Hs.73454	5.7	571	572 5222
10	443595	PPAR(gamma) angiotensin related proteI	AF169312	Hs.9613	5.7	3626	3627 7590
	418299	integrin, beta 2 (antigen CD18 (p95), I	AA279530	Hs.83968	5.7	1212	5725
	434474	holocytochrome c synthase (cytochrome c	AL042936	Hs.211571	5.7	3058	7084
	416783	monocyte to macrophage differentiation-	AA206186	Hs.79889	5.7	1031	5584
	423057	ESTs, Moderately similar to I38022 hypo	AW961597	Hs.130816	5.7	1773	6139
15	447165	Homo sapiens, Similar to RIKEN cDNA 170	AL042400	Hs.75668	5.7	3895	7811
	415192	aldo-keto reductase family 1, member C3	D17793	Hs.78183	5.7	917	918 5494
	425003	apurinic/apyrimidinic endonuclease(APEX	AF119046	Hs.154149	5.7	2038	2039 6326
	436326	aldo-keto reductase family 1, member B1	BE085236	Hs.42636	5.7	3183	7188
	443623	complement component 1, q subcomponent,	AA345519	Hs.9641	5.7	3631	7594
20	422667	ESTs	H25642	Hs.132821	5.7	1723	6102
	436608	down syndrome critical region protein D	AA628980	Hs.192371	5.7	3205	7207
	430838	hypothetical protein FLJ12015	N46664	Hs.169395	5.7	2733	6829
	410011	PPTAIRE protein kinase 1	AB020641	Hs.57856	5.6	406	407 5096
	409253	CD5 antigen-like (scavenger receptor cy	H91200	Hs.52002	5.6	332	5041
25	456534	phospholipase C, beta 3, neighbor pseud	X91195	Hs.100623	5.6	4522	8326
	414531	allograft inflammatory factor 1	T69387	Hs.76364	5.6	829	5430
	437442	ESTs, Moderately similar to similar to	T85104	Hs.222779	5.6	3263	7258
	419745	slug (chicken homolog), zinc finger pro	AF042001	Hs.93005	5.6	1381	1382 5851
	431671	polymerase (DNA directed), alpha	NM_016937	Hs.2.67289	5.6	2807	2808 6884
30	447232	interleukin 10 receptor, alpha	AW499834	Hs.327	5.6	3905	7820
	438707	amino acid system N transporter 2; porc	L08239	Hs.5326	5.6	3350	3351 7335
	436856	ESTs	AJ469355	Hs.127310	5.6	3220	7221
	451681	ESTs, Weakly similar to AA64_HUMAN 64	K228564	Hs.25950	5.6	4245	8097
	444666	long-chain fatty acid coenzyme A ligase	BE293347	Hs.11638	5.6	3712	7664
35	453454	PRP4/STK4WD splicing factor	AW052006	Hs.374973	5.6	4421	8243
	417678	2',5'-oligoadenylate synthetase 1 (40-4	X06560	Hs.82396	5.6	1145	1146 5671
	456508	ESTs, Weakly similar to AF208855 1 BM-0	AA502764	Hs.123469	5.6	4521	8325
	450785	Homo sapiens, alpha-1 (VI) collagen	AA852713	Hs.108885	5.6	4193	8056
	422526	ESTs	AA311763	Hs.131056	5.6	1695	6081
40	409041	Hypothetical protein, XP_051860 (KIAA11	AB033025	Hs.50081	5.6	299	300 5017
	411127	hypothetical protein	AA668995	Hs.323463	5.6	516	5176
	430044	ESTs	AA464510	Hs.152812	5.5	2642	6765
	408122	hypothetical protein FLJ10718	AJ432652	Hs.42824	5.5	193	4935
	421779	wingless-type MMTV integration site fam	AJ879159	Hs.108219	5.5	1592	6004
45	422726	faciogenital dysplasia (Aarskog-Scott s	U11690	Hs.1572	5.5	1727	1728 6106
	427378	melanoma antigen, family D, 1	BE515037	Hs.177556	5.5	2322	6523
	414561	Homo sapiens amino acid transport syste	AJ064813	Hs.195155	5.5	831	5432
	422173	phorbol-in-like protein MDS019 (CEM15)	BE385828	Hs.250619	5.5	1656	6052
	421369	U2 small nuclear ribonucleoprotein auxi	NM_005089	Hs.1.71909	5.5	1533	1534 5966
50	412170	very low density lipoprotein receptor	D16532	Hs.73729	5.5	575	576 5225
	406722	Homo sapiens SNC73 protein (SNC73) mRNA	H27498	Hs.293441	5.5	64	4831
	409361	sine oculis homeobox (Drosophila) homol	NM_005982	Hs.5.4416	5.5	344	345 5049
	403071	NM_003319:Homo sapiens titin (TTN), mR			5.5		4702
	420005	ESTs	AW271106	Hs.133294	5.5	1407	5871
55	448988	gamma-aminobutyric acid (GABA) A recept	Y09763	Hs.22785	5.5	4055	4056 7940
	418059	gb:zn56d05.s1 Stratagene muscle 937209	AA211586		5.5	1186	5703
	444783	anillin (Drosophila Scraps homolog), ac	AK001468	Hs.62180	5.5	3722	3723 7672
	422106	Fc fragment of IgG binding protein	D84239	Hs.111732	5.5	1646	1647 6044
	433570	ESTs, Weakly similar to S55916 ribosoma	AI580053	Hs.109007	5.5	2988	7027
60	426304	Homo sapiens cDNA FLJ11477 fis, clone H	AA374532	Hs.124673	5.5	2198	6438
	406387	Target Exon			5.5		4805
	429142	ESTs	AA835639	Hs.104972	5.5	2518	6676
	453905	LIM domain kinase 1	NM_002314	Hs.3.6566	5.5	4462	4463 8276
	403362	NM_001815:Homo sapiens actin, gamma 2,			5.5		4715
65	427557	plasminogen activator, urokinase recept	NM_002659	Hs.1.79657	5.4	2343	2344 6539
	430478	apolipoprotein L, 3	NM_014349	Hs.2.41535	5.4	2702	2703 6808
	438915	Williams-Beuren syndrome chromosome reg	AA280174	Hs.355711	5.4	3365	7348
	418203	CDC28 protein kinase 2	X54942	Hs.83758	5.4	1202	1203 5719
	452046	KIAA0802 protein	AB018345	Hs.27657	5.4	4275	4276 8120
70	418532	neurotrophic tyrosine kinase, receptor,	F00797	Hs.374321	5.4	1252	5753
	414555	phospholipase A2, group IIA (platelets,	N98569	Hs.76422	5.4	830	5431
	417336	disabled (Drosophila) homolog 2 (mitoge	R70429	Hs.81988	5.4	1097	5637
	427923	FGENESH predicted 11 TM protein	AW274357	Hs.301406	5.4	2385	6572
	428450	KIAA0175 gene product	NM_014791	Hs.1.84339	5.4	2443	2444 6621
75	420168	serine carboxypeptidase vitellogenic-II	AF217508	Hs.95594	5.4	1424	1425 5885
	429134	ESTs	AA446953	Hs.99004	5.4	2514	6673
	431620	2'-5'-oligoadenylate synthetase 2 (69-7	AA126109	Hs.264981	5.3	2802	6880
	430233	Homo sapiens mRNA; cDNA DKFZp564N1063	(AW367902	Hs.236443	5.3	2664	6781
	456181	ras inhibitor	L36463	Hs.1030	5.3	4516	4517 8321
80	422567	glypican 6	AF111178	Hs.118407	5.3	1702	1703 6087
	406703	myosin, heavy polypeptide 3, skeletal m	X13100	Hs.173084	5.3	53	54 4825
	443907	TYRO protein tyrosine kinase binding pr	AU076484	Hs.9983	5.3	3656	7617
	427239	ubiquitin carrier protein	BE270447	Hs.356512	5.3	2311	6515
	448569	signal transducer and activator of tran	BE382657	Hs.21486	5.3	4014	7909
85	458916	ESTs	N58327	Hs.302755	5.3	4583	8380
	421848	collagen, type VI, alpha 1	X15880	Hs.108885	5.3	1602	1603 6013
	406868	immunoglobulin heavy constant gamma 3	(AA505445	Hs.300697	5.3	72	4839

	446500	sushi-repeat-containing protein, X chro	U78093	Hs.15154	5.3	3842 3843 7767
	406663	immunoglobulin heavy constant mu	U24683		5.3	39 40 4818
	422048	spondin 2, extracellular matrix protein	NM_012445	Hs.2 88126	5.3	1631 1632 6034
5	435750	KIAA1089 protein	AB029012	Hs.4990	5.3	3149 3150 7160
	414459	CCAAT/enhancer binding protein (C/EBP), Y11525		Hs.76171	5.3	818 819 5422
	443672	butyrobetaine (gamma), 2-oxoglutarate d	AA323362	Hs.9667	5.3	3634 7597
	409512	melanoma differentiation associated pro	AW979187	Hs.293591	5.3	354 5057
	433138	semaphorin sem2	AB029496	Hs.59729	5.3	2944 2945 6994
10	435854	putative ankyrin-repeat containing prot	AJ278120	Hs.4996	5.2	3157 3158 7166
	422491	neuronatin	AA338548	Hs.117546	5.2	1691 6077
	445084	hypothetical protein FLJ14761	H38914	Hs.250848	5.2	3742 7687
	433365	ESTs	AF026944	Hs.293797	5.2	2973 7014
	417900	CDC20 (cell division cycle 20, S. cerev	BE250127	Hs.82906	5.2	1165 5688
15	421064	tumor necrosis factor, alpha-induced pr	AI245432	Hs.101382	5.2	1503 5942
	416406	lipoma HMGIC fusion partner-like 2	D86961	Hs.79299	5.2	1001 1002 5564
	433135	dolichyl-phosphate mannosyltransferase	AA443873	Hs.110477	5.2	2943 6993
	401961	NM_021626:Homo sapiens serine carboxype			5.2	4669
	433001	clone HQ0310 PROQ310p1	AF217513	Hs.279905	5.2	2923 2924 6977
	424090	XAP associated factor-1	X99699	Hs.139262	5.2	1897 1898 6228
20	436252	Homo sapiens cDNA FLJ11562 fis, clone H	AI539519	Hs.142827	5.2	3179 7184
	443898	Sec61 gamma	AW804296	Hs.9950	5.2	3655 7616
	445584	PTD012 protein	AF217518	Hs.8360	5.2	3786 3787 7719
	421778	actin related protein 2/3 complex, subu	AA428000	Hs.283072	5.2	1591 6003
25	422481	DNAX-activation protein 10	AL050163	Hs.117339	5.2	1687 1688 6075
	442619	ESTs, Weakly similar to AF164793 1 prot	AA447492	Hs.20183	5.2	3575 7545
	419405	ESTs	AI377043	Hs.42189	5.2	1333 5816
	445107	ESTs, Weakly similar to I38022 hypothet	AI208121	Hs.147313	5.2	3744 7689
	434096	pleiomorphic adenoma gene-like 1	AW662958	Hs.75825	5.2	3029 7062
30	416982	creatine kinase, mitochondrial 2 (sarco	J05401	Hs.80691	5.2	1055 1056 5602
	439926	ESTs	AW014875	Hs.137007	5.2	3440 7422
	435680	Homo sapiens galectin-related inhibitor	H50946	Hs.284183	5.2	3145 7157
	421155	lysyl oxidase	H87879	Hs.102267	5.2	1512 5950
	457211	ESTs, Weakly similar to S51797 vasodila	AW972565	Hs.32399	5.2	4543 8344
	412473	ESTs	F23393	Hs.153060	5.2	594 5241
35	438086	nuclear receptor subfamily 1, group I,	AA336519	Hs.83623	5.2	3300 7293
	431103	pleiotrophin (heparin binding growth fa	M57399	Hs.44	5.2	2748 2749 6840
	413350	t-complex-associated-testis-expressed 1	U02556	Hs.75307	5.2	704 705 5328
	450506	fibroblast activation protein, alpha	NM_004460	Hs.4 18	5.2	4170 4171 8037
40	449118	Bel1 (S. cerevisiae) homolog	R67477	Hs.23103	5.2	4065 7949
	418072	Human DNA sequence from clone RP3-353C1	F35210	Hs.86507	5.2	1190 5707
	428227	small inducible cytokine subfamily B (C	AA321649	Hs.2248	5.1	2410 6593
	434868	collagen, type VI, alpha 2	R50032	Hs.159263	5.1	3085 7106
	424982	phosphorylase, glycogen; muscle (McArd	U94777	Hs.351580	5.1	2036 2037 6325
45	443883	serine (or cysteine) proteinase inhibit	AA114212	Hs.9930	5.1	3653 7614
	427527	immunoglobulin heavy constant mu	AI809057	Hs.153261	5.1	2340 6536
	414695	proteasome (prosome, macropain) subunit	BE439915	Hs.76913	5.1	850 5446
	441783	Homo sapiens clone Z5012 mRNA sequence	BE313412	Hs.7961	5.1	3537 7509
	436748	collagen, type VI, alpha 2	BE159107	Hs.159263	5.1	3212 7213
50	444186	ESTs	AI127666	Hs.146447	5.1	3685 7642
	452056	Homo sapiens, clone IMAGE:4054156, mRNA	AW955065	Hs.101150	5.1	4280 8123
	429997	apolipoprotein B mRNA editing enzyme, c	NM_006789	Hs.2 27457	5.1	2636 2637 6761
	433048	ESTs, Weakly similar to ALU8_HUMAN ALU	R91007	Hs.194116	5.1	2932 6984
	410889	twist (Drosophila) homolog (acrocephalo	X91662	Hs.66744	5.1	501 502 5164
55	414020	small inducible cytokine A4 (homologous	NM_002984	Hs.75703	5.1	767 768 5378
	431241	ESTs	AA496799	Hs.36958	5.1	2765 6852
	421458	carbohydrate (keratan sulfate Gal-6) su	NM_003654	Hs.1 04576	5.1	1543 1544 5972
	416586	secreted modular calcium-binding protei	D44643	Hs.14144	5.1	1016 5574
	412006	ESTs	AW451618	Hs.380683	5.1	555 5217
60	418452	C-type (calcium dependant, carbohydrate	BE379749	Hs.85201	5.1	1241 5744
	430252	testes development-related NYD-SP20	AI638774	Hs.105328	5.1	2668 6784
	415672	ESTs	N53097	Hs.193579	5.1	937 5511
	429415	procollagen C-endopeptidase enhancer	NM_002593	Hs.2 02097	5.1	2557 2558 6706
	443780	activating transcription factor 5	NM_012068	Hs.9 754	5.1	3643 3644 7606
65	418322	cyclin-dependent kinase inhibitor 3 (CD	AA284166	Hs.84113	5.0	1214 5727
	416433	ESTs	AI658904	Hs.84673	5.0	1004 5566
	448694	E3 ubiquitin ligase SMURF2	AA478756	Hs.194477	5.0	4027 7919
	407172	gb:ya92c05.s1 Stratagene placenta (9372	T54095	Hs.379019	5.0	117 4869
	433446	ESTs	AW469546	Hs.122116	5.0	2979 7020
70	446157	Homo sapiens cDNA: FLJ22562 fis, clone	BE270828	Hs.131740	5.0	3821 7749
	447343	ESTs, Highly similar to S02392 alpha-2-	AA256641	Hs.236894	5.0	3916 7828
	427051	Homo sapiens cDNA FLJ10500 fis, clone N	BE178110	Hs.173374	5.0	2297 6505
	440087	hypothetical protein FLJ22678	W28969	Hs.7718	5.0	3452 7433
	425825	lymphocyte antigen 6 complex, locus H	AI929508	Hs.159590	5.0	2147 6399
75	425843	death associated protein 3	BE313280	Hs.159627	5.0	2149 6401
	426968	amphiphysin (Stiff-Mann syndrome with b	U07616	Hs.173034	5.0	2290 2291 6499
	441020	ESTs	W79283	Hs.35962	5.0	3495 7471
	411894	GLI-Kruppel family member GLI3 (Greig c	M57609	Hs.72916	5.0	559 560 5212
	436222	Homo sapiens cDNA FLJ11489 fis, clone H	AI208737	Hs.122810	5.0	3177 7182
80	416431	titin	AW384459	Hs.172004	5.0	1003 5565
	445417	a disintegrin-like and metalloprotease	AK001058	Hs.12680	5.0	3766 7705
	424291	ephrin-B1	AL120051	Hs.144700	5.0	1931 6249
	413186	solute carrier family 16 (monocarboxyli	AU077141	Hs.75231	5.0	685 5315
	410600	ESTs, Moderately similar to S65657 alph	AW575742	Hs.351676	5.0	479 5147
85	425514	integrin, alpha 10	AF112345	Hs.158237	5.0	2108 2109 6375
	431385	membrane-spanning 4-domains, subfamily	BE178536	Hs.11090	5.0	2779 6863
	432485	CDW52 antigen (CAMPATH-1 antigen)	N90866	Hs.276770	5.0	2877 6939

5	438158	ESTs	A1796556	Hs.187884	5.0	3305 7298
	425398	hypothetical protein similar to tenasci	AL049689	Hs.156369	5.0	2101 2102 6370
	406621	immunoglobulin lambda locus	X57809	Hs.181125	5.0	26 27 4810
	421483	hypothetical protein MGC11333	NM_003388	Hs.1 04717	5.0	1545 1546 5973
	450701	hypothetical protein XP_098151 (leucine)	H39960	Hs.288467	5.0	4183 8048
	441188	ESTs	AW292830	Hs.255609	5.0	3503 7478
	408989	KIAA0746 protein	AW361666	Hs.49500	5.0	290 5010
	439867	ESTs	AA847510	Hs.161292	5.0	3435 7418
10	410867	fibrillin 1 (Marfan syndrome)	X63556	Hs.750	5.0	498 499 5162
	403086	NM_003319*:Homo sapiens titin (TTN), mR			5.0	4705
	419726	bone morphogenetic protein 1	U50330	Hs.1274	4.9	1376 1377 5848
	448807	ESTs	A1571940	Hs.7549	4.9	4041 7930
	425708	hypothetical protein FLJ22530	AK001342	Hs.14570	4.9	2128 2129 6388
15	452438	JM4 protein	BE514230	Hs.29595	4.9	4331 8165
	409649	hypothetical protein FLJ20442	AA159216	Hs.55505	4.9	373 5070
	430009	ESTs	AA894564	Hs.22242	4.9	2638 6762
	417640	protein C receptor, endothelial (EPCR)	D30857	Hs.82353	4.9	1143 5669
	452106	ESTs	A1141031	Hs.21342	4.9	4289 8131
20	415701	gamma-glutamyl hydrolase (conjugase, fo	NM_003878	Hs.78619	4.9	940 941 5514
	428242	leukemia inhibitory factor (cholinergic	H55709	Hs.2250	4.9	2411 6594
	424623	ESTs	AW963062	Hs.270737	4.9	1977 6282
	422609	sialidase 1 (lysosomal sialidase)	Z46023	Hs.118721	4.9	1711 6093
	444476	isocitrate dehydrogenase 1 (NADP), solu	AF020038	Hs.11223	4.9	3701 3702 7656
25	417511	chordin-like	AL049176	Hs.82223	4.9	1125 1126 5657
	429044	ESTs	AJ261490	Hs.145527	4.9	2506 6667
	441362	RAD51 (S. cerevisiae) homolog (E coli R	BE614410	Hs.23044	4.9	3512 7486
	438203	ESTs	BE540090	Hs.7345	4.9	3308 7300
	416737	LIM domain protein	AF154335	Hs.79691	4.9	1028 1029 5582
30	449318	Homo sapiens, Similar to RIKEN cDNA 573	AW236021	Hs.78531	4.9	4080 7962
	450390	Human DNA sequence from clone RP11-234G	N93227	Hs.348805	4.9	4163 8031
	410701	RNA binding motif protein 8A	AF198620	Hs.10283	4.9	487 488 5154
	422867	cartilage oligomeric matrix protein (ps	L32137	Hs.1584	4.9	1751 1752 6122
	439981	ESTs, Weakly similar to T14742 hypothet	AI348408	Hs.124675	4.9	3443 7425
	427399	KIAA0914 gene product	NM_014883	Hs.1 77664	4.9	2323 2324 6524
35	421395	pyruvate dehydrogenase (lipoamide) alph	D90084	Hs.1023	4.9	1538 1539 5969
	438441	ESTs	AW664960	Hs.205319	4.9	3322 7312
	416404	ESTs	AA180138	Hs.107924	4.9	1000 5563
	447297	protease, cysteine, 1 (legumain)	BE617970	Hs.18069	4.9	3914 7826
40	427209	KIAA1566 protein	H06509	Hs.92423	4.9	2309 6513
	406646	major histocompatibility complex, class	M33600	Hs.375570	4.8	36 37 4816
	415076	guanylate cyclase 1, soluble, beta 3	NM_000857	Hs.7 7890	4.8	906 907 5486
	421143	immunoglobulin superfamily containing I	AB024536	Hs.102171	4.8	1510 1511 5949
	423750	prefoldin 2	AF165883	Hs.298229	4.8	1843 1844 6191
45	423732	solute carrier family 16 (monocarboxyli	AF058056	Hs.132183	4.8	1840 1841 6189
	408482	adenosine A2b receptor	NM_000676	Hs.4 5743	4.8	226 227 4959
	439688	hypothetical protein FLJ12921	AW445181	Hs.209637	4.8	3418 7401
	431070	transcription factor 19 (SC1)	AW408164	Hs.249184	4.8	2744 6837
	426935	collagen, type I, alpha 1	NM_000088	Hs.1 72928	4.8	2288 2289 6498
50	417011	ESTs, Weakly similar to 2109260A B cell	F08212	Hs.234898	4.8	1060 5605
	413945	CD14 antigen	NM_000591	Hs.7 5627	4.8	758 759 5371
	418205	troponin I, skeletal, fast	L21715	Hs.83760	4.8	1204 1205 5720
	432211	hypothetical protein FLJ10986	BE274530	Hs.273333	4.8	2852 6917
	440086	v-ral simian leukemia viral oncogene ho	NM_005402	Hs.6 906	4.8	3450 3451 7432
55	408901	hypothetical protein FLJ10468	AK001330	Hs.48855	4.8	272 273 4997
	443021	Ig superfamily protein	AA368546	Hs.8904	4.8	3593 7561
	431801	Homo sapiens cDNA FLJ10302 fis, clone N	AJ907522	Hs.270555	4.8	2823 6897
	414600	transducin (beta)-like 1	NM_005647	Hs.7 6536	4.8	835 836 5436
	408380	diubiquitin	AF123050	Hs.44532	4.8	217 218 4952
60	402621	Target Exon			4.8	4684
	424755	KIAA1268 protein	AB033094	Hs.152925	4.8	1995 1996 6295
	409485	ficolin (collagen/fibrinogen domain-con	S80990	Hs.252136	4.8	351 352 5055
	421362	hypothetical protein FLJ20043	AK000050	Hs.103853	4.8	1531 1532 5965
	445537	EGF-like-domain, multiple 6	AJ245671	Hs.12844	4.8	3780 3781 7716
65	433819	ESTs	AW511097	Hs.110069	4.8	3007 7042
	425280	phosphoenolpyruvate carboxykinase 1 (so	U31519	Hs.1872	4.8	2080 2081 6357
	427498	methyl-CpG binding domain protein 3	NM_003926	Hs.1 78728	4.8	2336 2337 6534
	444931	general transcription factor IIIA	AV652066	Hs.75113	4.8	3735 7681
	450000	hypothetical protein FLJ21709	AJ952797	Hs.10888	4.8	4126 8003
70	425776	parathyroid hormone receptor 2	U25128	Hs.159499	4.8	2138 2139 6394
	412755	ESTs, Weakly similar to P4HA_HUMAN PRO	BE144306	Hs.179891	4.8	637 5274
	445043	ESTs	AW014413	Hs.196066	4.8	3741 7686
	407824	Homo sapiens cDNA FLJ14388 fis, clone H	AA147884	Hs.9812	4.8	166 4910
	418918	CD2 antigen (p50), sheep red blood cell	X07871	Hs.89476	4.8	1282 1283 5775
75	435080	hypothetical protein FLJ14428	AJ831760	Hs.155111	4.8	3103 7122
	423225	Thy-1 cell surface antigen	AA852604	Hs.125359	4.8	1786 6148
	453985	ESTs	N44545	Hs.251865	4.8	4477 8287
	417849	nidogen 2	AW291587	Hs.82733	4.8	1161 5684
	430441	desmoplakin (DPI, DPII)	BE398091	Hs.374850	4.8	2699 6805
80	417621	interferon-induced, hepatitis C-associat	AV654694	Hs.82316	4.8	1140 5666
	431183	KDEL (Lys-Asp-Glu-Leu) endoplasmic reti	NM_006855	Hs.250696	4.8	2756 2757 6845
	402408	NM_030920*:Homo sapiens hypothetical pr			4.8	4681
	408024	ESTs	AW905599	Hs.171501	4.8	186 4928
	414313	coatomer protein complex, subunit alpha	NM_004371	Hs.7 5887	4.7	801 802 5408
	420059	RAB23, member RAS oncogene family	AF161486	Hs.94769	4.7	1412 1413 5875
85	406636	gb:Homo sapiens (clone WR4.12VL) anti-I	L12064		4.7	32 33 4814
	445434	hypothetical protein FLJ20917	BE391690	Hs.9265	4.7	3769 7707

	411962	gbzk85d12.r1 Soares_pregnant_uterus_Nb	AA099050	Hs.42146	4.7	563 5215
	417166	Paired box protein Pax-3	AA431323	Hs.42146	4.7	1088 5628
	441187	hypothetical protein FLJ22174	AW195237	Hs.7734	4.7	3502 7477
5	432878	Pirin	BE386490	Hs.279663	4.7	2914 6969
	435554	early B-cell factor	AF208502	Hs.32425	4.7	3136 3137 7150
	456804	caveolin 2	AI421645	Hs.139851	4.7	4529 8332
	446035	Sam68-like phosphotyrosine protein, T-S	NM_006558	Hs.1 3565	4.7	3813 3814 7742
	435099	flap structure-specific endonuclease 1	AC004770	Hs.4756	4.7	3104 3105 7123
10	407903	bHLH factor Hes4	AI287341	Hs.154029	4.7	178 4920
	407204	ESTs, Weakly similar to ALU1_HUMAN	ALU_R41933	Hs.140237	4.7	121 4873
	452613	ESTs	AA461599	Hs.23459	4.7	4337 8171
	431347	Insulin-like growth factor 2 (somatomed	AI133461	Hs.251664	4.7	2774 6859
	447660	ESTs	AW160386	Hs.163667	4.7	3946 7853
15	433036	ESTs	AA574091	Hs.105984	4.7	2929 6981
	453828	ESTs	AW970960	Hs.293821	4.7	4444 8262
	417767	acyloxyacyl hydrolase (neutrophil)	BE242241	Hs.82542	4.7	1155 5678
	454024	hypothetical protein FLJ23403	AA993527	Hs.293907	4.7	4481 8290
	422809	hypothetical protein FLJ10549	AK001379	Hs.121028	4.7	1741 1742 6115
20	458208	ESTs, Weakly similar to T4S4_HUMAN	TRAN AI380016	Hs.352394	4.7	4570 8367
	416391	mesoderm specific transcript (mouse) ho	AI878927	Hs.79284	4.7	999 5562
	448030	membrane-spanning 4-domains, subfamily	N30714	Hs.325960	4.7	3971 7873
	414166	N-myc downstream regulated	AW888941	Hs.75789	4.7	784 5392
	422477	ankyrin repeat domain 2 (stretch respon	AA345800	Hs.73708	4.7	1686 6074
25	417376	LIM protein (similar to rat protein kin	AA253314	Hs.154103	4.7	1107 5645
	405259	C12000526:g[7512168]pir T30886 integ			4.7	4774
	431706	adenylyl cyclase-associated protein 2	AI816086	Hs.296341	4.7	2811 6887
	437802	ESTs	AI475995	Hs.122910	4.7	3288 7281
	412749	signal sequence receptor, beta (translo	AA378417	Hs.74564	4.7	635 5272
30	435370	ESTs	AI964074	Hs.225838	4.7	3120 7136
	404977	Insulin-like growth factor 2 (somatomed			4.7	4766
	433264	cysteine dioxygenase, type I	D85782	Hs.3229	4.7	2965 2966 7007
	400528	NM_020975*:Homo sapiens ret proto-oncog			4.7	4631
	406707	myosin, heavy polypeptide 2, skeletal m	S73840	Hs.931	4.6	61 62 4829
35	428405	cholinergic receptor, nicotinic, alpha	Y00762	Hs.2266	4.6	2436 2437 6615
	422424	prostate differentiation factor	AI186431	Hs.296638	4.6	1681 6070
	426413	gb:EST90805 Synovial sarcoma Homo sapie	AA377823		4.6	2219 6453
	414694	HSPC002 protein	NM_015362	Hs.7 6907	4.6	848 849 5445
	412490	Homo sapiens cDNA: FLJ22528 fis, clone	AW803564	Hs.288850	4.6	595 5242
40	415812	TATA box binding protein (TBP)-associat	AA077268	Hs.78865	4.6	949 5521
	429930	ESTs	AI580809	Hs.352364	4.6	2623 6751
	407252	ESTs	AA659037	Hs.163780	4.6	134 4882
	426272	ESTs	AW450671	Hs.88012	4.6	2191 6434
	406627	ESTs	T64904	Hs.163780	4.6	30 4812
45	454029	homeo box A5	W05150	Hs.37034	4.6	4482 8291
	414004	ESTs, Moderately similar to Z115357A	TY AA737033	Hs.7155	4.6	765 5376
	429380	secretory carrier membrane protein 3	AF023268	Hs.200600	4.6	2554 2555 6704
	428291	interferon stimulated gene (20kD)	AA534009	Hs.183487	4.6	2423 6604
	402855	NM_001839*:Homo sapiens calponin 3, aci			4.6	4694
50	418140	microfibrillar-associated protein 2	BE613836	Hs.83551	4.6	1196 5713
	400297	hypothetical protein DKFZp564O1278	AI127076	Hs.288381	4.6	7 4618
	414416	hypothetical protein MGC2721	AW409985	Hs.76084	4.6	813 5417
	424876	Homo sapiens clone IMAGE:297403, mRNA s	AI056991	Hs.269873	4.6	2016 6310
	419260	U5 snRNP-specific protein, 116 kD	AW770185	Hs.356066	4.6	1322 5806
55	458207	U2 small nuclear ribonucleoprotein auxi	T28472	Hs.7655	4.6	4569 8366
	445930	Homo sapiens clone 24747 mRNA sequence	AF055009	Hs.13456	4.6	3804 7734
	411027	leukocyte immunoglobulin-like receptor,	AF072099	Hs.67846	4.6	509 510 5170
	414809	transferrin receptor (p90, CD71)	AI434699	Hs.77356	4.6	873 5463
	419407	hypothetical protein FLJ21276	AW410377	Hs.41502	4.6	1334 5817
60	431231	ESTs	AA653552	Hs.116532	4.6	2764 6851
	438451	ESTs	AI081972	Hs.220261	4.6	3323 7313
	417750	synovial sarcoma, translocated to X chr	AI267720	Hs.260523	4.6	1154 5677
	407930	Homo sapiens cDNA FLJ12807 fis, clone	N AA045847	Hs.188361	4.6	182 4924
	410738	titin	AA197128	Hs.172004	4.6	491 5156
65	422765	baculoviral IAP repeat-containing 5 (su	AW409701	Hs.1578	4.6	1734 6110
	436802	ESTs	N34486	Hs.132183	4.6	3216 7217
	437669	ESTs, Weakly similar to match to ESTs A	AI358105	Hs.123164	4.6	3278 7271
	416658	fibrillin 2 (congenital contractual ar	U03272	Hs.79432	4.6	1020 1021 5577
	432290	Homo sapiens cDNA FLJ10237 fis, clone	H AK001099	Hs.274273	4.6	2862 6926
	453767	extracellular matrix protein 2, female	AB011792	Hs.35094	4.6	4439 4440 8258
70	424651	ESTs	AI493206	Hs.120785	4.6	1984 6287
	421016	transcription factor 3 (E2A immunoglobu	AA504583	Hs.101047	4.5	1497 5937
	435460	ESTs	AA682439	Hs.118380	4.5	3126 7142
	449353	ESTs	AA001220	Hs.242947	4.5	4084 7966
75	413441	Src-like-adaptor	AI929374	Hs.75367	4.5	723 5340
	425568	ESTs	AW963118	Hs.161784	4.5	2115 6380
	433614	cytochrome c oxidase subunit IV isoform	W07475	Hs.277101	4.5	2993 7031
	427600	proteasome (prosome, macropain) activat	AW630918	Hs.179774	4.5	2351 6545
	444638	ESTs	AI445775	Hs.143806	4.5	3709 7661
80	417352	gb:zp95h09.r1 Stralagene muscle 937209	AA195919	Hs.86045	4.5	1099 5639
	413943	Homo sapiens cDNA FLJ12981 fis, clone	N AW294416	Hs.144687	4.5	757 5370
	439332	Homo sapiens mRNA; cDNA DKFZp547M072 (f	AW842747	Hs.378821	4.5	3393 7376
	452052	midline 1 (Opit/BBB syndrome)	NM_000381	Hs.2 7695	4.5	4277 4278 8121
	410817	protein disulfide isomerase related pro	AI262789	Hs.93659	4.5	497 5161
	444842	bromodomain adjacent to zinc finger dom	AF084479	Hs.194688	4.5	3729 3730 7676
85	400419	Target	AF084545		4.5	22 23 4626
	417920	adenosine monophosphate deaminase 2 (ls	S47833	Hs.82927	4.5	1167 1168 5690

408964	beta-site APP-cleaving enzyme	AF201468	Hs.49349	4.5	284 285 5006
439453	thyroid hormone receptor interactor 13	BE264974	Hs.6566	4.5	3399 7382
408212	hypothetical protein	AA297567	Hs.43728	4.5	206 4945
443142	protein phosphatase 2 (formerly 2A), re	AI696513	Hs.108705	4.5	3604 7571
452063	ESTs, Weakly similar to TWIST_HUMAN	TWIS R53185	Hs.32366	4.5	4281 8124
439815	hypothetical protein FLJ20420	AA206079	Hs.6693	4.5	3433 7416
403074	NM_003319: Homo sapiens titin (TTN), mR			4.5	4703
447898	6.2 kd protein	AW969638	Hs.380920	4.5	3966 7868
431757	Homo sapiens chromosome 21q22.1 anonymo	AA196930	Hs.268526	4.5	2817 6892
426822	ESTs	W78950	Hs.220823	4.5	2277 6489
424001	paternally expressed 10	W67883	Hs.137476	4.5	1882 6217
414178	ESTs, Weakly similar to I38022 hypothet	AW957372	Hs.46791	4.5	788 5396
414862	single-stranded DNA-binding protein	BE621310	Hs.923	4.5	882 5468
443960	hypothetical protein FLJ21986	AI093577	Hs.255416	4.5	3663 7623
427458	ESTs, Weakly similar to LKHU proteoglyc	BE208364	Hs.29283	4.5	2332 6530
418867	msh (Drosophila) homeo box homolog 2	D31771	Hs.89404	4.5	1277 1278 5772
415656	ESTs	W84346	Hs.84673	4.5	933 5507
447484	hypothetical protein FLJ14697	AA464839	Hs.292566	4.5	3933 7841
435373	ESTs	AW665538	Hs.117689	4.5	3121 7137
424834	Homo sapiens cDNA FLJ10570 fis, clone N	AK001432	Hs.153408	4.5	2009 6304
439731	hypothetical protein FLJ14084	AI953135	Hs.45140	4.5	3425 7408
453859	myogenic factor 6 (herculin)	NM_002469	Hs.3 5937	4.5	4451 4452 8267
431104	ESTs	AW970859	Hs.313503	4.5	2750 6841
452698	chemokine (C-C motif) receptor 1	NM_001295	Hs.301921	4.5	4343 4344 8177
414883	CDC28 protein kinase 1	AA926960	Hs.348669	4.5	885 5471
409197	chromosome 11 open reading frame 24	N54706	Hs.303025	4.5	322 5035
412974	emopamil-binding protein (sterol isomer	R18978	Hs.75105	4.5	664 5297
430770	ESTs	AA765694	Hs.123296	4.5	2727 6825
444681	chromosome 6 open reading frame 9	AJ243937	Hs.288316	4.4	3715 3716 7667
447463	Mitochondrial Acyl-CoA Thioesterase	AW378685	Hs.18625	4.4	3929 7838
428281	ATPase, H transporting, lysosomal (vacu	AA194554	Hs.183434	4.4	2419 6601
408866	ESTs	AW292096	Hs.255036	4.4	270 4995
449175	homolog of yeast SPB1	AJ005892	Hs.23170	4.4	4068 4069 7952
444669	ESTs	F18939	Hs.153827	4.4	3713 7665
431093	eomesoderm (Xenopus laevis) homolog	AB031038	Hs.301704	4.4	2746 2747 6839
412448	tumor necrosis factor receptor superfam	L12964	Hs.73895	4.4	587 588 5236
444385	CGI-111 protein	BE278964	Hs.11085	4.4	3698 7653
423595	ESTs	R82826	Hs.220702	4.4	1823 6176
457567	gb:QV1-DT0069-010200-057-c12 DT0069	Hom AW939074		4.4	4557 8355
407896	Zic family member 1 (odd-paired Drosoph	D76435	Hs.41154	4.4	176 177 4919
451938	down-regulator of transcription 1, TBP-	AI354355	Hs.16697	4.4	4263 8110
432680	interferon, alpha-inducible protein 27	T47364	Hs.278613	4.4	2895 6954
428795	ESTs, Highly similar to A39769 N-acetyl	R45503	Hs.97469	4.4	2475 6643
407907	procollagen-lysine, 2-oxoglutarate 5-di	AI752235	Hs.41270	4.4	179 4921
440184	dedicator of cyto-kinesis 3	AB002297	Hs.7022	4.4	3459 3460 7439
452664	hypothetical protein FLJ23221	AA398859	Hs.18397	4.4	4339 8173
445893	ESTs, Weakly similar to TRHY_HUMAN	TRIC AI610702	Hs.202613	4.4	3802 7732
412430	fumarylacetoacetate hydrolase (fumaryl	AW675064	Hs.73875	4.4	584 5233
452203	transporter 1, ATP-binding cassette, su	X57522	Hs.352018	4.4	4298 4299 8140
441224	calumenin	AJ076964	Hs.7753	4.4	3504 7479
436519	myozenin	AJ278124	Hs.238756	4.4	3196 3197 7200
439265	Homo sapiens cDNA: FLJ23197 fis, clone	AL134430	Hs.6906	4.4	3388 7371
428048	gb:z41b1.1.s1 Soares_fetal_heart_NbHH19	AA705745		4.4	2394 6580
414653	procollagen-proline, 2-oxoglutarate 4-d	M24486	Hs.76768	4.4	841 842 5441
408787	Rho guanine exchange factor (GEF) 11	NM_014784	Hs.4 7822	4.4	258 259 4987
406672	major histocompatibility complex, class	M26041	Hs.198253	4.4	43 44 4820
403291	Target Exon			4.4	4713
422624	KDEL (Lys-Asp-Glu-Leu) endoplasmic reti	BE616678	Hs.380986	4.4	1714 6096
459531	hypothetical protein FLJ11500 similar t	AI200996	Hs.148533	4.4	4594 8390
412014	ESTs, Weakly similar to A46010 X-linked	AI620650	Hs.43761	4.4	566 5218
451186	ESTs, Weakly similar to leucine-rich gl	AW023469	Hs.65256	4.4	4217 8076
439302	ESTs	AW467516	Hs.208109	4.4	3390 7373
407103	hypothetical protein MGC13170	AA424881	Hs.256301	4.4	110 4862
429052	ESTs	AA443938	Hs.368387	4.4	2509 6669
407754	Homo sapiens cDNA FLJ14105 fis, clone M	AA527348	Hs.288967	4.4	158 4902
408365	hypothetical protein FLJ20514	AK000521	Hs.44423	4.4	214 215 4950
410079	glycogenin 2	U94362	Hs.380757	4.4	418 419 5104
421893	vascular cell adhesion molecule 1	NM_001078	Hs.1 09225	4.4	1608 1609 6018
407241	gb:Human omega light chain protein 14.1	M34516		4.4	130 131 4880
414283	ESTs	AW960011	Hs.154993	4.3	797 5404
453817	ESTs	AW755253	Hs.379636	4.3	4442 8260
444969	ESTs	AI203334	Hs.171862	4.3	3736 7682
423600	ESTs	AI633559	Hs.310359	4.3	1824 6177
415169	ATPase, vacuolar, 14 kD	W42913	Hs.78089	4.3	915 5492
407756	ubiquitin specific protease 18	AA116021	Hs.38260	4.3	159 4903
456115	titin	F01082	Hs.172004	4.3	4515 8320
422241	protein tyrosine phosphatase, receptor	Y00062	Hs.170121	4.3	1663 1664 6058
443639	proteasome (prosome, macropain) subunit	BE269042	Hs.9661	4.3	3632 7595
448258	hypothetical protein FLJ20396	BE386983	Hs.343214	4.3	3990 7889
424218	cystatin F (leukocystatin)	AF031824	Hs.143212	4.3	1913 1914 6239
426283	kynureninase (L-kynurenine hydrolase)	NM_003937	Hs.1 69139	4.3	2192 2193 6435
438568	major histocompatibility complex, class	R98865	Hs.11135	4.3	3336 7324
411000	ESTs, Weakly similar to S38383 SEB4B pr	N40449	Hs.201619	4.3	505 5167
429351	hypothetical protein FLJ10628	AK001490	Hs.200016	4.3	2549 2550 6701
448019	ESTs, Moderately similar to I38022 hypo	AW947164	Hs.195641	4.3	3970 7872
410006	eukaryotic translation initiation facto	AW732308	Hs.57783	4.3	405 5095

412359	gb:QV3-LT0048-140200-083-e05 LT0048 Hom	AW837985	Hs.56729	4.3	583 5232
427871	Homo sapiens, clone IMAGE:3507281, mRNA	AW992405	Hs.352406	4.3	2380 6568
433757	ESTs	A1949974	Hs.152670	4.3	3002 7038
429455	CD209 antigen	A1472111	Hs.278694	4.3	2563 6710
442426	hypothetical protein MGC5370	A1373062	Hs.332938	4.3	3562 7534
415512	paralemmin	Y16270	Hs.78482	4.3	929 930 5504
428618	Target CAT	AA885360	Hs.351796	4.3	2456 6629
402685	Target Exon			4.3	4687
424192	P311 protein	U30521	Hs.142827	4.3	1911 1912 6238
417911	chaperonin containing TCP1, subunit 6A	AA333387	Hs.82916	4.3	1166 5689
428125	leucine aminopeptidase	AA393071	Hs.182579	4.3	2400 6585
446742	putative G-protein coupled receptor	AA232119	Hs.16085	4.3	3870 7790
453862	Homo sapiens mRNA; cDNA DKFZp434B1231 (AL137493	Hs.35945	4.3	4453 4454 8268
409267	transducin (beta)-like 2	NM_012453	Hs.5 2515	4.3	337 338 5044
411149	ESTs	N68715	Hs.269128	4.3	517 5177
449194	ESTs	R43799	Hs.23783	4.3	4070 7953
436827	guanine nucleotide binding protein (G p	H72187	Hs.356668	4.3	3218 7219
447178	ESTs	AW594641	Hs.192417	4.3	3896 7812
422801	nuclear receptor co-repressor 2	AF125672	Hs.287994	4.3	1739 1740 6114
426156	natriuretic peptide receptor A/guanylat	BE244537	Hs.167382	4.3	2183 6427
436895	carbonic anhydrase XII	AF037335	Hs.5338	4.3	3224 3225 7224
413328	guanylate cyclase 1, soluble, alpha 3	Y15723	Hs.75295	4.3	701 702 6326
426108	programmed cell death 5	AA622037	Hs.166468	4.3	2173 6420
432503	ESTs	AA551196	Hs.188952	4.3	2878 6940
428342	Homo sapiens cDNA FLJ13458 fis, clone P	A1739168	Hs.349283	4.3	2432 6611
408864	excision repair cross-complementing rod	AA521132	Hs.48576	4.3	269 4994
407868	proline-rich Gla (G-carboxyglutamic aci	NM_000950	Hs.4 0637	4.3	172 173 4916
420261	fibroblast growth factor receptor 1 (fm	AW206093	Hs.748	4.3	1440 5897
426858	ubiquitously-expressed transcript	NM_004182	Hs.1 72791	4.3	2280 2281 6492
412520	H2A histone family, member O	AA442324	Hs.795	4.3	599 5245
429228	ESTs	A1553633	Hs.356828	4.3	2533 6687
444670	hypothetical protein MGC5370	H58373	Hs.332938	4.3	3714 7666
421873	chromosome 14 open reading frame 2	A1132988	Hs.109052	4.3	1605 6015
436962	DKFZP564I052 protein	AW377314	Hs.5364	4.3	3229 7228
452291	CDC7 (cell division cycle 7, S. cerevis	AF015592	Hs.28853	4.3	4310 4311 8150
425071	deiodinase, iodothyronine, type II	NM_013989	Hs.1 54424	4.3	2043 2044 6330
419050	adenosine monophosphate deaminase 1 (ls	NM_000036	Hs.89570	4.3	1293 1294 5784
414285	ESTs	AA312914	Hs.71719	4.3	798 5405
452277	KIAA1223 protein	AL049013	Hs.28783	4.3	4308 8148
418457	Deleted in split-hand/split-foot 1 regi	N95406	Hs.333495	4.3	1242 5745
430683	Homo sapiens PAC clone RP4-697H17 from	AC004862		4.3	2720 6820
442376	Homo sapiens cDNA FLJ12228 fis, clone M	W95588	Hs.129982	4.3	3557 7529
412805	Homo sapiens, Similar to bromodomain-co	AW954569	Hs.278675	4.2	647 5283
421225	MCT-1 protein	AA463798	Hs.102696	4.2	1517 5954
417045	Homo sapiens ORF1	F01180	Hs.332030	4.2	1066 5610
412856	basigin (OK blood group)	BE386745	Hs.74631	4.2	652 5287
400517	lengsin			4.2	4630
414031	hypothetical protein MGC10848	W22615	Hs.207443	4.2	770 5380
452960	protein tyrosine phosphatase, receptor	AK001335	Hs.31137	4.2	4373 8201
418741	ESTs, Weakly similar to S41044 chromoso	H83265	Hs.8881	4.2	1272 5767
410512	hypothetical protein MGC3180	AA085603	Hs.250570	4.2	468 5140
414260	KIAA0218 gene product	NM_014760	Hs.75863	4.2	793 794 5401
448888	caspase recruitment domain protein 6	AW196663	Hs.200242	4.2	4049 7935
438596	ESTs	AA829427	Hs.243081	4.2	3337 7325
424321	lymphocyte-specific protein tyrosine ki	W74048	Hs.1765	4.2	1933 6251
444172	ESTs, Moderately similar to I38022 hypo	BE147740	Hs.279789	4.2	3684 7641
409703	2'-5'-oligoadenylate synthetase 3 (100	NM_006187	Hs.5 6009	4.2	381 382 5076
442432	hypothetical protein FLJ23468	BE093589	Hs.38178	4.2	3563 7535
409556	phosphorylase kinase, alpha 2 (liver)	D38616	Hs.54941	4.2	361 362 5061
400991	Target Exon			4.2	4641
411252	MD-2 protein	AB018549	Hs.69328	4.2	521 522 5181
452260	RAB9, member RAS oncogene family	AA453208	Hs.330994	4.2	4307 8147
420311	Human DNA sequence from clone RP4-530I1	AW445044	Hs.38207	4.2	1444 5901
435101	ESTs	A1743156	Hs.131064	4.2	3106 7124
406519	C10001858:gil6679124[ref NP_032759.1] n			4.2	4808
414522	Immunoglobulin J chain	AW518944	Hs.76325	4.2	827 5428
432692	ESTs	AW974944	Hs.285814	4.2	2899 6957
446291	Interferon, gamma-inducible protein 30	BE397753	Hs.14623	4.2	3833 7760
414747	centromere protein F (350/400kD, mitosi	U30872	Hs.77204	4.2	861 862 5455
424494	phosphatidylinositol-4-phosphate 5-kin	U78575	Hs.149255	4.2	1961 1962 6273
453000	retinoblastoma-binding protein 7	AW411340	Hs.31314	4.2	4378 8206
448771	SNARE protein	BE315511	Hs.296244	4.2	4034 7925
415938	A kinase (PRKA) anchor protein 1	BE383507	Hs.78921	4.2	959 5528
450423	sialoadhesin	AA486735	Hs.31869	4.2	4167 8035
414915	myxovirus (influenza) resistance 1, hom	NM_002462	Hs.7 6391	4.2	888 889 5473
416804	spondyloepiphyseal dysplasia, late	NM_014563	Hs.1 74038	4.2	1033 1034 5586
441283	ESTs	AA927670	Hs.131704	4.2	3506 7481
435232	cyclin-dependent kinase inhibitor 2C (p	NM_001262	Hs.4 854	4.2	3114 3115 7132
450923	ESTs	AW043951	Hs.38449	4.2	4203 8063
458806	Homo sapiens PNAS-13 mRNA, complete cds	BE514753	Hs.292057	4.2	4580 8377
424880	retinitis pigmentosa GTPase regulator	NM_000328	Hs.1 53614	4.2	2018 2019 6312
413384	exostoses (multiple) 2	NM_000401	Hs.7 5334	4.2	708 709 5330
427274	colony stimulating factor 1 receptor, f	NM_005211	Hs.1 74142	4.2	2313 2314 6517
439039	ESTs	A1656707	Hs.48713	4.2	3373 7356
429803	RAB31, member RAS oncogene family	W81489	Hs.223025	4.2	2612 6743
417675	similar to murine leucine-rich repeat p	A1808607	Hs.3781	4.2	1144 5670

	416330	galactosidase, beta 1	AU077101	Hs.79222	4.2	990 5555
	451806	RNA 3'-terminal phosphate cyclase	NM_003729	Hs.27076	4.2	4257 4258 8105
	452401	tumor necrosis factor, alpha-induced pr	NM_007115	Hs.2 9352	4.2	4325 4326 8161
5	443462	ESTs	AI064690	Hs.171176	4.2	3623 7587
	414907	polo (Drosophila)-like kinase	X90725	Hs.77597	4.2	886 887 5472
	412642	hepatocyte growth factor (hepatopoietin A	BE244598	Hs.809	4.2	622 5261
	431882	engrafted homolog 1	NM_001426	Hs.2 71977	4.2	2832 2833 6903
	413833	centromere protein E (312kD)	Z15005	Hs.75573	4.2	748 749 5363
10	413048	mannose receptor, C type 1	M93221	Hs.75182	4.2	672 673 5305
	434883	hypothetical protein MGC12959	AW381538	Hs.19807	4.2	3088 7108
	414878	ADP-ribosylation factor 5	AA341040	Hs.77541	4.2	884 5470
	452240	ESTs	AI591147	Hs.61232	4.2	4304 8144
	416322	pyrroline-5-carboxylate reductase 1	BE019494	Hs.79217	4.2	989 5554
15	413004	interleukin enhancer binding factor 2,	T35901	Hs.75117	4.2	667 5300
	432435	ESTs	BE218886	Hs.282070	4.2	2874 6936
	421485	hypothetical protein FLJ10134	AA243499	Hs.104800	4.2	1547 5974
	418197	gb:zn58g02r1 Stratagene muscle 937209	AA214253	Hs.50794	4.1	1200 5717
	420238	ESTs, Weakly similar to 2109260A B cell	AA256783	Hs.12549	4.1	1436 5894
20	437275	ESTs, Weakly similar to A47582 B-cell g	AW976035	Hs.292396	4.1	3251 7248
	441406	phosphoprotein regulated by mitogenic p	Z45957	Hs.7837	4.1	3518 7491
	445272	hematopoietic cell-specific Lyn substra	BE268912	Hs.14601	4.1	3832 7759
	433230	ESTs	AW136134	Hs.220277	4.1	2960 7004
	430522	KIAA0471 gene product	N75750	Hs.242271	4.1	2706 6810
25	427954	metaxin 1	J03060	Hs.247551	4.1	2387 6574
	434974	eukaryotic translation initiation facto	AA778711	Hs.362973	4.1	3094 7113
	439223	UL16 binding protein 2	AW238299	Hs.250618	4.1	3383 7366
	448111	interferon-induced protein with tetratr	AA053486	Hs.20315	4.1	3978 7880
	452012	kinesin family member 4A	AA307703	Hs.279766	4.1	4269 8116
30	429623	G protein-coupled receptor kinase 5	NM_005308	Hs.2 11569	4.1	2591 2592 6729
	433839	ESTs, Weakly similar to ALU1_HUMAN ALU	F35430	Hs.146070	4.1	3008 7043
	451514	beta-1,3-glucuronyltransferase 3 (glucu	NM_012200	Hs.2 6492	4.1	4237 4238 8091
	425797	platelet activating receptor homolog	AF002986	Hs.159545	4.1	2142 2143 6396
	427747	serine/threonine kinase 12	AW411425	Hs.180655	4.1	2365 6557
35	438866	tissue inhibitor of metalloproteinase 2	U44385	Hs.6441	4.1	3360 3361 7344
	409461	N-myc (and STAT) interactor	AA382169	Hs.54483	4.1	350 5054
	444371	forkhead box M1	BE540274	Hs.239	4.1	3696 7651
	419081	ESTs	AI798863	Hs.87191	4.1	1299 5788
	409154	interferon-induced protein 35	U72882	Hs.50842	4.1	314 315 5028
40	438662	cleavage and polyadenylation specific f	AA223599	Hs.6351	4.1	3345 7330
	424800	MyoD family inhibitor	AL035588	Hs.153203	4.1	2002 2003 6300
	435408	ESTs, Weakly similar to T29299 hypothet	H07897	Hs.4302	4.1	3125 7141
	418526	solute carrier family 16 (monocarboxyli	BE019020	Hs.85838	4.1	1251 5752
	402474	NM_004079:Homo sapiens cathepsin S (CTS			4.1	4682
45	429599	ESTs	AA806106	Hs.123664	4.1	2583 6724
	438708	Homo sapiens phenylethylamine binding p	BE279778	Hs.30619	4.1	3352 7336
	435575	triggering receptor expressed on myeloi	AF213457	Hs.44234	4.1	3139 3140 7152
	426363	transforming growth factor, beta 3	M58524	Hs.2025	4.1	2210 2211 6446
	410036	caldesmon 2 (cardiac muscle)	R57171	Hs.57975	4.1	412 5100
50	407874	Homo sapiens cDNA FLJ14059 fis, clone H	AI766311	Hs.289047	4.1	175 4918
	430255	Homo sapiens mRNA for KIAA1551 protein,	AK000703	Hs.323822	4.1	2669 2670 6785
	451149	RNA binding motif protein 8B	AL047586	Hs.10283	4.1	4214 8073
	425289	Interferon, gamma-inducible protein 16	AW139342	Hs.155530	4.1	2082 6358
	424665	caveolin 2	AW368576	Hs.139851	4.1	1985 6288
55	434815	core 1 UDP-galactose:N-acetylgalactosami	AF155582	Hs.46744	4.1	3076 3077 7100
	431448	hypothetical protein DKFZp564O1278	AL137517	Hs.306201	4.1	2785 2786 6869
	453149	DKFZP434G145 protein	BE614781	Hs.31931	4.1	4395 8221
	434203	hypothetical protein PRO1855	BE262677	Hs.283558	4.1	3033 7066
	432169	phosphoribosyl pyrophosphate synthetase	Y00971	Hs.2910	4.1	2847 2848 6914
60	418400	KIAA0246 protein	BE243026	Hs.301989	4.1	1234 5739
	418990	proteasome (prosome, macropain) subunit	BE410285	Hs.89545	4.1	1289 5780
	452281	Homo sapiens cDNA FLJ11041 fis, clone P	T93500	Hs.28792	4.1	4309 8149
	448503	DNA segment on chromosome X and Y (uniq	L03426	Hs.21595	4.1	4017 4018 7911
	432842	hypothetical protein MGC4485	AW674093	Hs.334822	4.1	2911 6966
65	431124	doublesex and mab-3 related transcript	AF284221	Hs.59506	4.1	2753 2754 6843
	449609	guanine nucleotide binding protein (G p	BE246434	Hs.289026	4.1	4099 7980
	422085	zinc finger protein 294	AB018257	Hs.288773	4.1	1639 1640 6039
	422532	protective protein for beta-galactosida	AL008726	Hs.118126	4.1	1697 1698 6083
	424792	origin recognition complex, subunit 5 (U92538	Hs.153138	4.1	2000 2001 6299
	446948	peroxisomal long-chain acyl-coA thioest	BE409053	Hs.299629	4.1	3883 7800
70	408331	dual specificity phosphatase 12	NM_007240	Hs.4 4229	4.1	211 212 4948
	417601	KIAA0215 gene product	NM_014735	Hs.8 2292	4.1	1136 1137 5664
	449129	ESTs	AI631602	Hs.258949	4.1	4066 7950
	420890	6-phosphogluconolactonase	AA434058	Hs.100071	4.1	1488 5931
75	431735	thymosin, beta 4, X chromosome	AW977724	Hs.356629	4.1	2815 6890
	452093	Homo sapiens mRNA; cDNA DKFZp586M0723 (AA447453	Hs.27860	4.1	4286 8129
	435937	ESTs	AA830893	Hs.119769	4.1	3164 7172
	450755	ESTs	AA010984	Hs.159464	4.1	4190 8054
	407214	CGI-39 protein; cell death-regulatory p	AA412048	Hs.279574	4.1	122 4874
80	444367	hypothetical protein FLJ22390	H54892	Hs.10974	4.1	3695 7650
	443351	Homo sapiens cDNA FLJ13471 fis, clone P	AW016783	Hs.30799	4.1	3617 7583
	434001	angiotensinogen	AW950905	Hs.3697	4.1	3022 7055
	446231	interferon consensus sequence binding p	NM_002163	Hs.1 4453	4.1	3827 3828 7755
	446618	COP9 subunit 6 (MOV34 homolog, 34 kD)	AL110307	Hs.15591	4.1	3860 7781
	433800	lung type-I cell membrane-associated gl	AI034361	Hs.135150	4.1	3004 7040
85	421379	small inducible cytokine subfamily B (C	Y15221	Hs.103982	4.1	1535 1536 5967
	419652	hypothetical protein	AL157485	Hs.91973	4.1	1367 5840

420911	O-linked N-acetylglucosamine (GlcNAc) t	U77413	Hs.100293	4.1	1491 1492 5934
447188	ESTs	D61523	Hs.283435	4.1	3898 7814
407239	leukocyte immunoglobulin-like receptor,	AA076350	Hs.67846	4.1	129 4879
412582	proteasome (prosome, macropain) subunit	BE270631	Hs.74077	4.1	611 5254
444143	ESTs, Moderately similar to A56194 thro	AW747996	Hs.160999	4.1	3679 7637
444914	WD repeat domain 13	AA046947	Hs.12142	4.0	3734 7680
446936	ESTs	H10207	Hs.47314	4.0	3880 7798
449030	Homo sapiens mRNA for FLJ00016 protein,	AI365582	Hs.57100	4.0	4059 7943
424806	MSTP031 protein	AA382523	Hs.105689	4.0	2004 6301
423550	ESTs	F37675	Hs.152129	4.0	1815 6169
437741	putative transmembrane protein; homolog	BE561610	Hs.5809	4.0	3283 7276
430713	eukaryotic translation elongation facto	AA351647	Hs.2642	4.0	2726 6824
439551	ESTs	W72062	Hs.11112	4.0	3406 7389
409208	Integrin, alpha X (antigen CD11C (p150)	Y00093	Hs.172631	4.0	326 327 5038
431468	nuclear prelamin A recognition factor	AW248431	Hs.256526	4.0	2790 6872
433364	ESTs, Moderately similar to I54374 gene	AI075407	Hs.296083	4.0	2972 7013
435520	HNOEL-iso protein	AA297990	Hs.9315	4.0	3130 7146
427897	apelin; peptide ligand for APJ receptor	NM_017413	Hs.3 03084	4.0	2382 2383 6570
419431	actin related protein 2/3 complex, subu	AW805152	Hs.90370	4.0	1337 5819
443727	ESTs	Z25389	Hs.18459	4.0	3640 7603
420842	hypothetical protein MGC10986	AI083668	Hs.50601	4.0	1485 5929
451118	ESTs	AI862096	Hs.60640	4.0	4213 8072
426530	complement component 4A	U24578	Hs.278625	4.0	2249 2250 6472
451811	hypothetical protein MGC1136	AA663485	Hs.8719	4.0	4259 8106
456629	histone deacetylase 3	AW891965	Hs.367942	4.0	4526 8329
417374	ESTs	D44865	Hs.86045	4.0	1106 5644
422675	eukaryotic translation Initiation facto	BE018517	Hs.381005	4.0	1725 6104
400295	AI905687:IL-BT095-190199-019 BT095 Homo	W72838	Hs.348419	4.0	6 4617
447560	phospholipase A2, group IVC (cytosolic,	'AF065214	Hs.18858	4.0	3937 3938 7845
414831	protein kinase, cAMP-dependent, regulat	M31158	Hs.77439	4.0	878 879 5466
448413	ESTs	AI745379	Hs.42911	4.0	4003 7900
406782	gb:zw20f11.s1 Soares ovary tumor NbHOT	AA430373		4.0	65 4832
424006	CD84 antigen (leukocyte antigen)	AF054815	Hs.137548	4.0	1885 1886 6219
427668	hypothetical protein FLJ14904	AA298760	Hs.180191	4.0	2357 6551
423201	growth hormone receptor	NM_000163	Hs.1 25180	4.0	1782 1783 6146
413995	syntaxin 1A (brain)	BE048146	Hs.75671	4.0	761 5373
429614	hypothetical protein MGC4248	AJ371172	Hs.211539	4.0	2588 6727
433545	ESTs	AA868510	Hs.112496	4.0	2986 7025
426482	gb:EST92649 Skin tumor I Homo sapiens c	AA379768		4.0	2237 6464
422451	ESTs, Weakly similar to S65657 alpha-1C	AA310753	Hs.72988	4.0	1684 6072
408106	Homo sapiens cDNA FLJ12417 fis, clone M	AW152449	Hs.226469	4.0	191 4933
417636	ESTs	R08916	Hs.191212	4.0	1142 5668
436555	ESTs, Weakly similar to 2003319A ankyri	AI972007	Hs.304646	4.0	3200 7202
447164	viplrin; similar to inflammatory respo	AF026941	Hs.17518	4.0	3894 7810
453046	ESTs, Highly similar to CA58_HUMAN CARB	AA284040	Hs.31535	3.9	4385 8212
438482	ESTs	AA909229	Hs.371970	3.8	3327 7317
437390	ESTs	AI125859	Hs.112607	3.7	3257 7253
421170	ESTs	BE217797	Hs.126052	3.7	1513 5951
445492	ESTs	AI240582	Hs.214678	3.6	3775 7712
459362	gb:EST386176 MAGE resequences, MAGM Hom	AW974073		3.6	4592 8388
405004	interleukin enhancer binding factor 1			3.6	4768
446028	Homo sapiens cDNA FLJ13136 fis, clone N	R44714	Hs.106795	3.6	3812 7741
435039	ESTs	AW043921	Hs.130526	3.6	3099 7118
458474	ESTs	AW207346	Hs.143202	3.5	4575 8372
457976	ESTs	AI222422	Hs.121846	3.4	4564 8361
421060	ESTs	AA810953	Hs.89104	3.4	1502 5941
420147	ESTs	AI918692	Hs.88109	3.2	1421 5882
437571	ESTs	AA760894	Hs.125350	3.1	3271 7265
459034	ESTs	BE550133	Hs.277254	3.0	4589 8385
408660	ESTs, Moderately similar to PC4259 ferr	AA525775	Hs.89040	3.0	247 4977
436202	ESTs	AA706315	Hs.374191	2.6	3176 7181

TABLE 4B:

65	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
70	Pkey	CAT Number Accession
	439092	919640_1 AW978407 AA830149 M85983 AW503637 BF352096
	414315	203914_2 AA494098 Z24878 F13654 AA494040
	418059	1164438_1 AA211586 F35799 F29720 AW937408 AW937387 AA211641
	406636	0_0 L12064 L12083 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080
	411962	2307710_1 AA099050 AA099526 T47733
75	426413	372468_1 AW954494 AA377823 BG219617 BG195685 BG616269 AI022688
	457567	1028609_1 AW970057 AW939073 AW940012 AW939074 AW939938 AW939205 AW939076 AA574383 BE160476 AA573577 AW750479
	428048	140288_1 AA420433 AA420850 AA705745
	430683	32178_-1 NA
	406782	0_0 AA430373 AA968771
80	426482	1296615_1 AA379768 AA379769 AA379568
	459362	1238130_1 AW974073 T56957

TABLE 4C:

85	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA

sequence of human chromosome 22* Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

5	Pkey	Ref	Strand	NL_position
	405001	6015406	Minus	104646-104819
	403593	6862650	Minus	62554-62712,69449-69602
	403088	8954241	Plus	169894-170193,170504-170806
10	400499	9796071	Minus	148495-148806
	401403	7710966	Plus	146180-146294
	403081	8954241	Plus	155749-156048,156142-156459
	401566	8469090	Minus	96277-96420,96979-97160
	403087	8954241	Plus	169511-169795
	402507	9797889	Plus	118979-119086
15	403071	8954241	Plus	136688-137096
	406387	9256180	Plus	116229-116371,117512-117651
	403362	8571772	Plus	64099-64260
	401961	4581193	Minus	124054-124209
	403086	8954241	Plus	169170-169412
20	402621	9930950	Plus	130806-131036
	402408	9796239	Minus	110326-110491
	405259	7329310	Plus	137102-137224,137698-137821
	404977	3738341	Minus	43081-43229
	400528	6981824	Plus	472381-472528,474170-474277,475328-47554
25	402855	9662953	Minus	59763-59909
	403074	8954241	Plus	143375-143561
	403291	7230870	Plus	95177-95435
	402685	8318556	Plus	58962-59294
30	400517	9796686	Minus	49996-50346
	400991	8096825	Plus	159197-159320
	406519	3962489	Plus	34617-34928
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	405004	6015406	Minus	186054-186365

TABLE 5A

40	Pkey:	Unique Eos probeset identifier number				
	Gene name:	Unigene gene title				
	Accession:	Exemplar Accession number, Genbank accession number				
	UniGene:	Unigene number				
	RATIO:	95th percentile of synovial sarcoma AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator				
45	SEQ ID #:	nucleic acid and protein sequences provided on CD for search purposes				
	Pkey	Gene Name	Accession	UniGene	RATIO	SEQ ID #
	420208	silver (mouse homolog) like	BE276055	Hs.95972	25.1	1431 5891
	451497	Wnt inhibitory factor-1	H83294	Hs.284122	17.5	4235 8089
50	452838	preferentially expressed antigen in mel	U65011	Hs.30743	16.5	4357 4358 8188
	441134	cellular retinoic acid-binding protein	W29092	Hs.346950	16.3	3500 7475
	445160	sine oculis homeobox (Drosophila) homol	AI299144	Hs.101937	16.1	3748 7692
	422424	prostate differentiation factor	AI186431	Hs.296638	14.8	1681 6070
	419628	ESTs	H67546	Hs.49768	14.8	1364 5837
	424687	matrix metalloproteinase 9 (gelatinase	J05070	Hs.151738	14.1	1986 1987 6289
55	436485	immunoglobulin kappa constant	X59135	Hs.156110	12.9	3193 3194 7198
	452223	hypothetical protein MGC2827	AA425467	Hs.8035	12.6	4302 8142
	417153	collagen, type II, alpha 1 (primary ost	X57010	Hs.81343	12.5	1084 1085 5625
	413916	apolipoprotein C-II	N49813	Hs.75615	12.3	753 5367
	413063	chitinase 3-like 1 (cartilage glycoprot	AL035737	Hs.75184	12.3	676 5308
60	418678	cancer/testis antigen (NY-ESO-1)	NM_001327	Hs.8 7225	12.2	1269 1270 5765
	442117	ESTs; hypothetical protein for IMAGE:44	AW664964	Hs.128899	12.1	3551 7523
	426600	VEGF nerve growth factor inducible	NM_003378	Hs.1 71014	11.9	2255 2256 6475
	419556	chitinase 1 (chitotriosidase)	U29615	Hs.91093	11.9	1351 1352 5829
	414812	monokine induced by gamma interferon	X72755	Hs.77367	11.6	874 875 5464
65	447377	transcription factor AP-2 alpha	X77343	Hs.334334	11.0	3920 3921 7831
	430377	dopachrome tautomerase (dopachrome del	NM_001922	Hs.301865	10.3	2682 2683 6795
	446921	small inducible cytokine subfamily A (C	AB012113	Hs.16530	10.3	3878 3879 7797
	431958	cadherin 3, type 1, P-cadherin (placent	X63629	Hs.2877	10.2	2834 2835 6904
	404854	Target Exon			10.1	4762
70	426555	tyrosinase (oculocutaneous albinism IA)	NM_000372	Hs.2 053	10.0	2251 2252 6473
	428398	ESTs	AI249368	Hs.98558	10.0	2435 6614
	429083	BCL2-related protein A1	Y09397	Hs.227817	9.9	2510 2511 6670
	450149	Zic family member 2 (odd-paired Drosoph	AW969781	Hs.132863	9.8	4136 8011
75	453837	baculoviral IAP repeat-containing 7 (li	AL138387	Hs.256126	9.7	4448 8265
	406663	immunoglobulin heavy constant mu	U24683		9.7	39 40 4818
	422311	cytokine receptor-like factor 1	AF073515	Hs.114948	9.6	1669 1670 6062
	450390	Human DNA sequence from clone RP11-234G	N93227	Hs.348805	9.5	4163 8031
	426300	delta-like homolog (Drosophila)	U15979	Hs.169228	9.4	2196 2197 6437
	428289	complement component 2	M26301	Hs.2253	9.3	2421 2422 6603
80	458079	Homo sapiens similar to RIKEN cDNA 2810	AI796870	Hs.381220	9.2	4566 8363
	433447	neuronal pentraxin II	U29195	Hs.3281	9.1	2980 2981 7021
	431830	small inducible cytokine subfamily A (C	Y16645	Hs.271387	9.0	2827 2828 6900
	408380	diubiquitin	AF123050	Hs.44532	9.0	217 218 4952
	403349	ephrin-B3			9.0	4714
85	412719	ESTs	AW016610	Hs.816	8.9	633 5270
	432874	melanoma inhibitory activity	W94322	Hs.279651	8.9	2913 6968

427527	immunoglobulin heavy constant mu	AJ809057	Hs.153261	8.9	2340 6536
427634	hypothetical protein MGC10820	AJ399745	Hs.18449	8.8	2352 6546
451668	cartilage acidic protein 1	Z43948	Hs.326444	8.8	4242 8094
412104	Homo sapiens, Similar to RIKEN cDNA 221 AW205197	AW205197	Hs.240951	8.8	569 5220
418054	lysyl oxidase-like 2	NM_002318	Hs.8 3354	8.8	1184 1185 5702
424001	paternally expressed 10	W57883	Hs.137476	8.7	1882 6217
430822	glyceraldehyde-3-phosphate dehydrogenase	AJ005371	Hs.248017	8.7	2729 2730 6827
419833	Homo sapiens tryptophanyl-tRNA synthetase	AA251131	Hs.220697	8.7	1388 5856
447499	protocadherin beta 16	AW262580	Hs.147674	8.6	3934 7842
418506	Unknown protein for MGC:29643 (formerly AA084248)	AA084248	Hs.372651	8.6	1247 5748
434449	hypothetical protein FLJ22041 similar 1	AW953484	Hs.3849	8.5	3057 7083
417308	KIAA0101 gene product	H60720	Hs.81892	8.4	1094 5634
447210	phosphatidylserine-specific phospholipase	AF035269	Hs.17752	8.4	3902 3903 7818
416640	neuron-specific protein	BE262478	Hs.13406	8.4	1019 5576
407233	carcinoembryonic antigen-related cell adhesion molecule 1	X16354	Hs.50964	8.3	126 127 4877
417389	midkine (neurite growth-promoting factor)	BE260964	Hs.82045	8.3	1109 5647
408915	hepatocellular carcinoma novel gene-3 protein	NM_016651	Hs.4 8950	8.2	274 275 4998
409361	sine oculis homeobox (Drosophila) homolog	NM_005982	Hs.5 4416	8.2	344 345 5049
437898	ESTs	W81260	Hs.43410	8.0	3293 7286
406837	immunoglobulin kappa constant	R70292	Hs.156110	7.9	69 4836
418857	msh (Drosophila) homeobox homolog 2	D31771	Hs.89404	7.9	1277 1278 5772
406672	major histocompatibility complex, class II	M26041	Hs.198253	7.9	43 44 4820
441633	normal mucosa of esophagus specific 1	AW958544	Hs.112242	7.8	3529 7501
428227	small inducible cytokine subfamily B (C)	AA321649	Hs.2248	7.7	2410 6593
424170	hypothetical protein MGC2827	AA337449	Hs.8035	7.7	1908 6236
421563	granulysin	NM_006433	Hs.1 05806	7.7	1561 1562 5983
421592	bagpipe homeobox (Drosophila) homolog 1	AF009801	Hs.105941	7.7	1569 1570 5988
438915	Williams-Beuren syndrome chromosome region	AA280174	Hs.355711	7.6	3365 7348
424800	MyoD family inhibitor	AL035588	Hs.153203	7.6	2002 2003 6300
409103	XAGE-1 protein	AF251237	Hs.112208	7.6	304 305 5021
402992	Target Exon			7.6	4700
406684	carcinoembryonic antigen-related cell adhesion molecule 1	X16354	Hs.50964	7.6	126 127 4822
418064	S100 calcium-binding protein, beta (neu)	BE387287	Hs.83384	7.6	1188 5705
442711	hypothetical protein	AF151073	Hs.8645	7.5	3579 3580 7549
410361	guanylate binding protein 1, interferon	BE391804	Hs.62661	7.5	456 5132
440042	ESTs	AJ073387	Hs.133898	7.4	3448 7430
418140	microfibrillar-associated protein 2	BE613836	Hs.83551	7.4	1196 5713
411027	leukocyte immunoglobulin-like receptor	AF072099	Hs.67846	7.3	509 510 5170
446519	secreted phosphoprotein 1 (osteopontin)	AU076643	Hs.313	7.3	3861 7782
434175	ESTs	AW979081	Hs.165469	7.3	3032 7065
431779	apolipoprotein C-I	AW971178	Hs.268571	7.3	2820 6894
452203	transporter 1, ATP-binding cassette, subfamily	X57522	Hs.352018	7.3	4298 4299 8140
419741	ubiquitin carrier protein E2-C	NM_007019	Hs.9 3002	7.3	1379 1380 5850
406698	major histocompatibility complex, class II	X83068	Hs.73931	7.2	51 52 4824
417355	endothelin receptor type B	D13168	Hs.82002	7.2	1100 1101 5640
448357	RAB38, member RAS oncogene family	N20169	Hs.108923	7.2	3994 7893
417437	interferon regulatory factor 4	U52682	Hs.82132	7.2	1123 1124 5656
427558	growth differentiation factor 10	D49493	Hs.2171	7.2	2345 2346 6540
420267	ESTs	N37030	Hs.173337	7.2	1441 5898
432247	ESTs	AA531287	Hs.105805	7.2	2859 6923
432800	AIM-1 protein	BE391046	Hs.278962	7.1	2909 6964
452852	ADAMTS2 (a disintegrin-like and metalloprotease with thrombospondin type 1 motifs)	AW378065	Hs.8687	7.1	4360 8190
414312	ESTs	AA155694	Hs.191060	7.0	800 5407
421815	membrane protein CH1	AW592146	Hs.108636	7.0	1598 6009
448140	BCM-like membrane protein precursor	AF146761	Hs.20450	7.0	3980 3981 7882
409327	collagen, type IX, alpha 3	L41162	Hs.53563	7.0	341 342 5047
427961	ESTs	AW293165	Hs.143134	6.9	2388 6575
415989	ESTs	AI267700	Hs.351201	6.9	962 5530
415052	mesenchyme homeobox 2 (growth arrest-5 related)	NM_005924	Hs.77858	6.9	904 905 5485
443184	ESTs	AI638728	Hs.135159	6.8	3607 7574
414299	ESTs	AA142989	Hs.71730	6.8	799 5406
424326	ADAM-like disintegrin protease, decysin	NM_014479	Hs.1 45296	6.7	1934 1935 6252
409007	Homo sapiens mRNA; cDNA DKFp434G0827 (AL122107)	Hs.49599	6.7	292 5012	
410889	twist (Drosophila) homolog (acrocephalo)	X91662	Hs.66744	6.7	501 502 5164
447674	cyclin-dependent kinase 2	BE270640	Hs.19192	6.6	3947 7854
406367	NM_022357:Homo sapiens putative metalloproteinase			6.6	4804
438568	major histocompatibility complex, class II	R98865	Hs.11135	6.6	3336 7324
421458	carbohydrate (keratan sulfate Gal-6) su	NM_003654	Hs.1 04576	6.6	1543 1544 5972
414821	Fc fragment of IgG, high affinity Ia, r	M63835	Hs.77424	6.6	876 877 5465
407792	putative secreted ligand homologous to	AI077715	Hs.39384	6.6	162 4906
420602	regulator of G-protein signalling 20	AF060877	Hs.99236	6.5	1469 1470 5918
404378	C7000450:g[17768636]dbj BAA95483.1 (A)			6.5	4746
426991	Homo sapiens cDNA FLJ10674 fis, clone NAK001536	Hs.214410	6.5	2294 6502	
449669	Homo sapiens cDNA FLJ14337 fis, clone P AW295142	Hs.180187	6.5	4123 8001	
418203	CDC28 protein kinase 2	X54942	Hs.83758	6.5	1202 1203 5719
432098	cytochrome P450 retinoid metabolizing p	AF252297	Hs.91546	6.5	2839 2840 6908
429986	sine oculis homeobox (Drosophila) homolog	AF092047	Hs.227277	6.5	2632 2633 6759
453883	cofactor required for Sp1 transcription	AI638516	Hs.347524	6.5	4459 8273
401797	Target Exon			6.5	4663
445337	fibronectin leucine rich transmembrane	NM_013280	Hs.1 2523	6.5	3760 3761 7701
408212	hypothetical protein	AA297567	Hs.43728	6.5	206 4945
406868	immunoglobulin heavy constant gamma 3 (A)	AA505445	Hs.300697	6.5	72 4839
421379	small inducible cytokine subfamily B (C)	Y15221	Hs.103982	6.4	1535 1536 5967
417370	tryptophanyl-tRNA synthetase	T28651	Hs.374466	6.4	1105 5643
417166	Paired box protein Pax-3	AA431323	Hs.42146	6.4	1088 5628
403404	Target Exon			6.4	4718

433001	clone HQ0310 PRO0310p1	AF217513	Hs.279905	6.4	2923 2924 6977
412140	RAB6 interacting, kinesin-like (rabkine	AA219691	Hs.73625	6.4	573 5223
423673	matrix metalloproteinase 12 (macrophage	BE003054	Hs.1695	6.3	1837 6186
421241	transketolase-like 1	X91817	Hs.102866	6.3	1519 1520 5956
447217	neuropilin 2	BE465754	Hs.17778	6.3	3904 7819
425397	topoisomerase (DNA) II alpha (170kD)	J04088	Hs.156346	6.3	2099 2100 6369
436557	ESTs, Weakly similar to A47582 B-cell g	W15573	Hs.271272	6.3	3201 7203
449294	ESTs	AI651786	Hs.195045	6.3	4079 7961
448961	ESTs	AI610643	Hs.187285	6.3	4052 7937
423739	ESTs	AA398155	Hs.97600	6.3	1842 6190
416208	ESTs, Weakly similar to MUC2_HUMAN	MUC1 AW291168	Hs.41295	6.3	981 5548
431290	cadherin-like 22	AF035300	Hs.264157	6.2	2771 2772 6857
433075	sortilin 1	NM_002959	Hs.3.51872	6.2	2936 2937 6987
406621	immunoglobulin lambda locus	X57809	Hs.181125	6.1	26 27 4810
438549	trinucleotide repeat containing 3	BE386801	Hs.21858	6.1	3331 7320
448390	hypothetical protein	AL035414	Hs.21068	6.1	3999 7897
428865	BarH-like homeobox 1	BE544095	Hs.164960	6.1	2485 6651
424408	collagen, type V, alpha 1	AI754813	Hs.146428	6.1	1943 6260
413385	indoleamine-pyrrole 2,3 dioxygenase	M34455	Hs.840	6.1	710 711 5331
404815	ENSP00000251989:DJ100N22.1 (NOVEL EGF-			6.0	4761
400295	AI905687:IL-BT095-190199-019 BT095 Homo	W72838	Hs.348419	6.0	6 4617
442432	hypothetical protein FLJ23468	BE093589	Hs.38178	6.0	3563 7535
443426	chromosome 20 open reading frame 1	AF098158	Hs.9329	6.0	3621 3622 7586
436481	HSPC150 protein similar to ubiquitin-co	AA379597	Hs.5199	6.0	3192 7197
422846	neutrophil cytosolic factor 1 (47kD, ch	BE513934	Hs.1583	6.0	1749 6120
436396	wingless-type MMTV integration site fam	AI683487	Hs.152213	6.0	3184 7189
444381	hypothetical protein BC014245	BE387335	Hs.283713	5.9	3697 7652
404030	NM_015669:Homo sapiens protocadherin b			5.9	4735
434916	Homo sapiens, Similar to RIKEN cDNA 111	AF161383	Hs.284207	5.9	3091 3092 7111
402888	Target Exon			5.9	4698
453271	ESTs	AA903424	Hs.6786	5.9	4409 8232
409637	Homo sapiens mRNA; cDNA DKFZp434K0621 (AA323948	Hs.55407	5.8	372 5069
403857	Target Exon			5.8	4730
422910	Human DNA sequence from PAC 257A7 on ch	AI269508	Hs.191979	5.8	1758 6127
441544	ESTs	AW300043	Hs.127137	5.8	3523 7496
415323	neutrophil cytosolic factor 2 (65kD, ch	BE269352	Hs.949	5.8	923 5499
409415	Homo sapiens cDNA: FLJ21028 fis, clone	AA579258	Hs.6083	5.8	347 5051
433068	sialyltransferase	NM_006456	Hs.2 88215	5.8	2934 2935 6986
430643	MEGF10 protein	AW970065	Hs.287425	5.8	2717 6817
407826	calpain 3, (p94)	AA128423	Hs.40300	5.8	167 4911
441859	interleukin-4 induced gene-1 protein (F	AW194364	Hs.380444	5.8	3540 7512
447414	neuroblastoma (nerve tissue) protein	D82343	Hs.74376	5.8	3924 3925 7834
457869	Homo sapiens, alpha-1 (VI) collagen	AU077186	Hs.108885	5.8	4561 8359
451766	ephritin-B3	NM_001406	Hs.2 6988	5.8	4255 4256 8104
448719	trinucleotide repeat containing 3	AA033627	Hs.21858	5.8	4028 7920
413794	myosin X	AF234532	Hs.61638	5.7	741 742 5357
452620	ESTs	AA436504	Hs.119286	5.7	4338 8172
411252	MD-2 protein	AB018549	Hs.69328	5.7	521 522 5181
427528	minichromosome maintenance deficient (S	AU077143	Hs.179565	5.7	2341 6537
423013	secreted modular calcium-binding protei	AW875443	Hs.22209	5.7	1769 6135
446291	interferon, gamma-inducible protein 30	BE397753	Hs.14623	5.7	3833 7760
425234	ESTs, Weakly similar to I38022 hypothet	AW152225	Hs.165909	5.6	2070 6349
420028	carbohydrate (N-acetylglucosamine-6-O)	AB014680	Hs.8786	5.6	1408 1409 5872
405542	Target Exon			5.6	4789
453173	KIAA0442 protein	AB007902	Hs.32168	5.6	4397 4398 8223
437044	differentially expressed in Fanconi's a	AL035864	Hs.69517	5.6	3233 7232
428484	solute carrier family 7 (cationic amino	AF104032	Hs.184601	5.6	2449 2450 6624
440650	Human DNA sequence from PAC 75N13 on ch	R44692	Hs.326801	5.6	3477 7455
449722	cyclin B1	BE280074	Hs.23960	5.6	4112 7990
435124	ESTs	AA725362	Hs.75514	5.6	3107 7125
429359	matrix metalloproteinase 14 (membrane-l	W00482	Hs.2399	5.6	2551 6702
421633	sorting nexin 10	AF121860	Hs.108260	5.6	1572 1573 5990
426514	bone morphogenetic protein 7 (osteogeni	BE616633	Hs.170195	5.6	2246 6470
436608	down syndrome critical region protein D	AA628980	Hs.192371	5.6	3205 7207
418110	hypothetical protein FLJ22202	R43523	Hs.217754	5.6	1193 5710
427923	FGENESH predicted 11 TM protein	AW274357	Hs.301406	5.6	2385 6572
429903	cyclin-dependent kinase 5, regulatory s	AL134197	Hs.93597	5.6	2616 6746
451763	hypothetical protein FLJ14220	AW294647	Hs.233634	5.6	4254 8103
408209	ets variant gene 5 (ets-related molecu	NM_004454	Hs.4 3697	5.6	204 205 4944
443378	proteasome (prosome, macropain) subunit	AW392550	Hs.381081	5.6	3618 7584
452194	olfactory receptor, family 2, subfamily	AI694413	Hs.373599	5.6	4295 8137
452363	Homo sapiens, Similar to complement com	AI582743	Hs.94953	5.6	4322 8159
438746	Human melanoma-associated antigen p97 (AI885815	Hs.184727	5.5	3353 7337
429170	dual specificity phosphatase 4	NM_001394	Hs.2 359	5.5	2524 2525 6680
419236	Homo sapiens cDNA FLJ11481 fis, clone H	AA330447	Hs.135159	5.5	1321 5805
452319	transducin-like enhancer of split 1, ho	M99435	Hs.28935	5.5	4313 4314 8152
406782	gb:zw20f11.s1 Soares ovary tumor NbHOT	AA430373		5.5	65 4832
430439	DKFZP434B061 protein	AL133561	Hs.380155	5.5	2695 2696 6803
453392	SRY (sex determining region Y)-box 11	U23752	Hs.32964	5.5	4416 4417 8239
420842	hypothetical protein MGC10986	AI083668	Hs.50601	5.5	1485 5929
413367	solute carrier family 16 (monocarboxyli	NM_006517	Hs.7 5317	5.5	706 707 5329
448985	carbonic anhydrase XI	AA324885	Hs.22777	5.5	4054 7939
412939	eukaryotic translation elongation facto	AW411491	Hs.75069	5.5	657 5292
400229	NM_021724:Homo sapiens nuclear recepto		Hs.276916	5.5	4602
452281	Homo sapiens cDNA FLJ11041 fis, clone P	T93500	Hs.28792	5.5	4309 8149
412471	endothelial cell growth factor 1 (plate	M63193	Hs.73946	5.5	591 592 5239

	406836	immunoglobulin kappa constant	AW514501	Hs.156110	5.5	68 4835
	404240	NM_018950:Homo sapiens major histocompa			5.4	4742
	428949	hypothetical protein DKFZp434J0617	AA442153	Hs.104744	5.4	2490 6655
	407846	Cbp/p300-Interacting transactivator, wi	AA426202	Hs.40403	5.4	169 4913
5	458208	ESTs, Weakly similar to T4S4_HUMAN TRAN	AI380016	Hs.352394	5.4	4570 8367
	423639	KIAA1405 protein	AB037826	Hs.130411	5.4	1831 1832 6183
	405451	Homo sapiens glutamyl-peptide cyclotr			5.4	4783
	400263	Eos Control		Hs.75309	5.4	4613
10	417007	chloride channel 7	AF224741	Hs.80768	5.4	1058 1059 5604
	403402	Target Exon			5.3	4717
	418956	KIAA0788 protein	AA234831	Hs.348493	5.3	1287 5778
	452698	chemokine (C-C motif) receptor 1	NM_001295	Hs.3 01921	5.3	4343 4344 8177
	424481	proteolipid protein 1 (Pelizaeus-Merzba	R19453	Hs.1787	5.3	1960 6272
15	450056	ESTs, Weakly similar to S71512 hypothet	BE047394	Hs.502	5.3	4129 8005
	416406	lipoma HMGIC fusion partner-like 2	D86961	Hs.79299	5.3	1001 1002 5564
	446142	ESTs	AI754693	Hs.145968	5.3	3820 7748
	402474	NM_004079:Homo sapiens calthepsin S (CTS			5.3	4682
	411089	cell division cycle 2-like 1 (PITSLRE p	AA456454	Hs.214291	5.3	513 5173
20	406636	gb:Homo sapiens (clone WR4.12VL) anti-t		L12064	5.3	32 33 4814
	419749	sparc/osteonectin, cwcv and kazal-like	X73608	Hs.93029	5.2	1383 1384 5852
	409430	splicing factor, arginine/serine-rich 5	R21945	Hs.346735	5.2	348 5052
	416975	granzyme B (granzyme 2, cytotoxic T-lym	NM_004131	Hs.1 051	5.2	1052 1053 5600
	436771	ESTs	AW975687	Hs.292979	5.2	3214 7215
25	413936	serine (or cysteine) proteinase inhibit	AF113676	Hs.297681	5.2	755 756 5369
	418883	acid phosphatase 5, tartrate resistant	BE387036	Hs.1211	5.2	1281 5774
	456974	apolipoprotein E	M12529	Hs.169401	5.2	4536 4537 8338
	410011	PFTAIRE protein kinase 1	AB020641	Hs.57856	5.2	406 407 5096
	448075	ESTs, Weakly similar to alpha-1 type 2	AW583284	Hs.286747	5.2	3975 7877
30	443907	TYRO protein tyrosine kinase binding pr	AU076484	Hs.9963	5.2	3656 7617
	443021	Ig superfamily protein	AA368546	Hs.8904	5.2	3593 7561
	407239	leukocyte immunoglobulin-like receptor,	AA076350	Hs.67846	5.1	129 4879
	425262	GS3955 protein	D87119	Hs.155418	5.1	2076 2077 6354
	422836	AKAP-binding sperm protein ropporin	AL037365	Hs.194093	5.1	1748 6119
35	417728	KIAA1573 protein	AW138437	Hs.24790	5.1	1151 5675
	432485	CDW52 antigen (CAMPATH-1 antigen)	U90866	Hs.276770	5.1	2877 6939
	424825	procollagen-lysine, 2-oxoglutarate 5-di	AF207069	Hs.153357	5.1	2005 2006 6302
	443071	complement component 1, q subcomponent,	AL080021	Hs.8986	5.1	3598 7566
	432693	ESTs	AW449630	Hs.293790	5.1	2900 6958
40	414034	early development regulator 1 (homolog	U89277	Hs.305985	5.1	771 772 5381
	409197	chromosome 11 open reading frame 24	N54706	Hs.303025	5.1	322 5035
	446659	ESTs	AI335361	Hs.226376	5.1	3865 7786
	419870	phosphoprotein associated with GEMs	AW403911	Hs.266175	5.1	1390 5858
	433671	19A24 protein	AW138797	Hs.132906	5.1	3000 7036
45	428862	SRY (sex determining region Y)-box9 (c	NM_000346	Hs.2 316	5.1	2483 2484 6650
	424378	neural cell adhesion molecule 1	W28020	Hs.167988	5.1	1940 6257
	448569	signal transducer and activator of tran	BE382657	Hs.21486	5.1	4014 7909
	415752	putative transmembrane protein	BE314524	Hs.78776	5.1	945 5517
	420568	protocadherin alpha 10	F09247	Hs.247735	5.1	1462 5913
50	407597	Homo sapiens brother of CDO (BOC) mRNA,	AA043925	Hs.339352	5.0	143 4889
	409893	minichromosome maintenance deficient (S	AW247090	Hs.57101	5.0	397 5088
	426418	collagen, type IV, alpha 5 (Alport synd	M90464	Hs.169825	5.0	2220 2221 6454
	438937	ESTs	AW952654	Hs.73964	5.0	3367 7350
	417796	ESTs	AA206141	Hs.367818	5.0	1159 5682
55	400235	NM_005336:Homo sapiens high density lip		Hs.177516	5.0	4604
	436748	collagen, type VI, alpha 2	BE159107	Hs.159263	5.0	3212 7213
	403668	Target Exon			5.0	4727
	437330	Homo sapiens mRNA; cDNA DKFZp761J1112 (AL353944	Hs.50115	5.0	3253 7250
	434431	ESTs	AW131454	Hs.168571	5.0	3056 7082
60	453344	ESTs	BE349075	Hs.44571	5.0	4415 8238
	453139	Human DNA sequence from clone RP11-234G	AA330620	Hs.348805	5.0	4394 8220
	431590	sema domain, transmembrane domain (TM),	AB037789	Hs.263395	5.0	2800 2801 6879
	448595	KIAA0644 gene product	AB014544	Hs.21572	5.0	4015 4016 7910
	418299	integrin, beta 2 (antigen CD18 (p95), I	AA279530	Hs.83968	5.0	1212 5725
65	411296	growth suppressor 1	BE207307	Hs.10114	4.9	524 5183
	438564	major histocompatibility complex, class	AA381553	Hs.198253	4.9	3335 7323
	440274	scrapie responsive protein 1	R24595	Hs.7122	4.9	3464 7443
	435461	ESTs	AI075846	Hs.133996	4.9	3127 7143
	424870	ESTs	T15545	Hs.244624	4.9	2014 6308
70	421707	lectomedin-2	NM_014921	Hs.1 07054	4.9	1581 1582 5995
	436291	protein regulator of cytokinesis 1	BE568452	Hs.344037	4.9	3180 7185
	444090	natural killer cell group 7 sequence	S69115	Hs.10306	4.9	3675 3676 7634
	424340	ESTs	AA339036	Hs.7033	4.9	1937 6254
	412659	olfactomedin related ER localized prote	AW753865	Hs.74376	4.9	627 5265
75	414024	gb:zm79g08.r1 Stratagene neuroepitheliu	AA134712	Hs.22410	4.9	769 5379
	408161	hypothetical protein MGC3032	AW952912	Hs.300383	4.9	195 4937
	452445	Homo sapiens mRNA from chromosome 5q21-	AB002438	Hs.263395	4.9	4332 8166
	430265	stromal cell-derived factor 1	L36033	Hs.237356	4.9	2671 2672 6786
	443254	ESTs	AW450180	Hs.65788	4.9	3612 7579
80	446630	Homo sapiens mRNA; cDNA DKFZp434E033 (f	AW384793	Hs.23960	4.8	3863 7784
	409698	short stature homeobox 2	AF022654	Hs.55967	4.8	378 379 5074
	414219	ALL1-fused gene from chromosome 1q	W20010	Hs.75823	4.8	789 5397
	435977	brain-specific membrane-anchored protei	AL138079	Hs.5012	4.8	3166 7174
	414020	small inducible cytokine A4 (homologous	NM_002984	Hs.7 5703	4.8	767 768 5378
	427400	hypothetical protein FLJ11939	AW245084	Hs.94229	4.8	2325 6525
85	427019	hypothetical protein FLJ10970	AA001732	Hs.173233	4.8	2296 6504
	439570	ESTs, Weakly similar to ALU1_HUMAN ALU	T79925	Hs.269165	4.8	3407 7390

	439979	hypothetical protein FLJ10430	AW600291	Hs.6823	4.8	3442 7424
	412507	EphA4	L36645	Hs.73964	4.8	596 597 5243
	414142	hemiscutin (fibulin 6)	AW368397	Hs.334485	4.8	781 5390
	453857	Ras-induced senescence 1 (RIS1)	AL080235	Hs.35861	4.8	4449 4450 8266
5	442910	ESTs, Weakly similar to T19326 hypothet	AI365130	Hs.11307	4.8	3589 7557
	403405	Target Exon			4.8	4719
	407241	gb:Human omega light chain protein 14.1	M34516		4.8	130 131 4880
	410342	Fc fragment of IgE, high affinity I, re	R31350	Hs.743	4.8	453 5129
10	435080	hypothetical protein FLJ14428	AI831760	Hs.155111	4.8	3103 7122
	453237	ESTs	AI969448	Hs.34578	4.8	4405 822
	424717	wingless-type MMTV integration site fam	H03754	Hs.152213	4.8	1989 6291
	413278	Interferon-stimulated protein, 15 kDa	BE563085	Hs.833	4.8	695 5322
	404977	Insulin-like growth factor 2 (somatomed			4.8	4766
15	409208	integrin, alpha X (antigen CD11C (p150)	Y00093	Hs.172631	4.8	326 327 5038
	437862	Homo sapiens mRNA; cDNA DKFZp586C0224 (AW978107	Hs.5884	4.8	3291 7284	
	439737	Homo sapiens mRNA full length Insert cD	AI751438	Hs.41271	4.8	3427 7410
	447343	ESTs, Highly similar to S02392 alpha-2-	AA256641	Hs.236894	4.8	3916 7828
	422799	neuraxophilin 4	AI933199	Hs.120911	4.8	1738 6113
20	416350	phospholipase A2, group IID	AF188625	Hs.189507	4.8	993 994 5557
	429150	smoothened (Drosophila) homolog	AF120103	Hs.197366	4.8	2519 2520 6677
	454390	KIAA0906 protein	AB020713	Hs.56966	4.8	4497 4498 8304
	416135	ESTs	AW473656	Hs.227277	4.7	976 5543
	432878	Pirin	BE386490	Hs.279663	4.7	2914 6969
25	423232	leucine-rich neuronal protein	BE244625	Hs.125742	4.7	1787 6149
	453914	fructose-1,6-bisphosphatase 1	NM_000507	Hs.5 74	4.7	4465 4466 8278
	421779	wingless-type MMTV integration site fam	AI879159	Hs.108219	4.7	1592 6004
	418558	Fas (TNFRSF6)-associated via death doma	AW082266	Hs.86131	4.7	1255 5755
	418322	cyclin-dependent kinase inhibitor 3 (CD	AA284166	Hs.84113	4.7	1214 5727
30	446051	ephrin-A3	BE048061	Hs.37054	4.7	3816 7744
	422616	selenophosphate synthetase 2	BE300330	Hs.118725	4.7	1713 6095
	448886	hypothetical protein FLJ10357	AL137291	Hs.22451	4.7	4047 4048 7934
	425934	Homo sapiens clone 25187 and 25188 mRNA	AF131842	Hs.163642	4.7	2155 2156 6407
	452683	progesterone membrane binding protein	AI089575	Hs.374574	4.7	4341 8175
35	429612	pituitary tumor-transforming 1	AF062649	Hs.252587	4.7	2586 2587 6726
	437723	ESTs	AI672731	Hs.13256	4.7	3282 7275
	453083	contactin associated protein 1	U87223	Hs.31622	4.7	4388 4389 8215
	418323	major histocompatibility complex, class	NM_002118	Hs.1 162	4.7	1215 1216 5728
	419113	ESTs	AI446586	Hs.21835	4.7	1305 5793
40	416801	sal (Drosophila)-like 2	X98834	Hs.79971	4.7	1032 5585
	426076	gb:EST374787 MAGE resequences, MAGG Hom	AW962714		4.7	2171 6418
	412773	similar to vaccinia virus HindIII K4L O	H15785	Hs.74573	4.7	639 5276
	455813	gb:QV2-HT0083-071299-018-a11 HT0083 Hom	BE141577		4.7	4509 8315
	427658	nogo receptor	H61387	Hs.30868	4.7	2355 6549
45	427337	Fc fragment of IgG, low affinity IIb,	Z46223	Hs.176663	4.7	2318 2319 6521
	412609	ocular albinism 1 (Nettleship-Falls)	Z48804	Hs.74124	4.7	615 616 5257
	449523	chemokine (C-C motif) receptor 5	NM_000579	Hs.5 4443	4.7	4094 4095 7976
	456508	ESTs, Weakly similar to AF208855 1 BM-0	AA502764	Hs.123469	4.7	4521 8325
50	415019	nuclear factor of activated T-cells, cy	AI674651	Hs.77810	4.7	901 5482
	428839	Homo sapiens cDNA FLJ14814 fis, clone N	AI767756	Hs.82302	4.6	2480 6648
	432383	Homo sapiens cDNA FLJ20137 fis, clone C	AK000144	Hs.274449	4.6	2868 6931
	437879	hypothetical protein FLJ10305	BE262082	Hs.5894	4.6	3292 7285
	434276	leucine zipper, putative tumor suppress	AF123659	Hs.93605	4.6	3039 3040 7070
	444410	ESTs, Moderately similar to S65657 alph	BE387360	Hs.33719	4.6	3699 7654
55	426470	ESTs	AA528794	Hs.128644	4.6	2232 6461
	422481	DNAX-activation protein 10	AL050163	Hs.117339	4.6	1687 1688 6075
	411789	Adlican	AF245505	Hs.72157	4.6	553 554 5207
	408561	hypothetical protein MGC13016	AI308037	Hs.84120	4.6	239 4970
	426150	BarH-like homeobox 2	NM_003658	Hs.1 67218	4.6	2180 2181 6425
60	450447	hypothetical protein P15-2	AF212223	Hs.25010	4.6	4168 4169 8036
	414747	centromere protein F (350/400kD, mitosi	U30872	Hs.77204	4.6	861 862 5455
	400262	Eos Control		Hs.75309	4.6	4612
	422175	ESTs, Highly similar to T00391 hypothet	N79885	Hs.6382	4.6	1657 6053
65	422397	MYEOV Myeloma overexpressed gene (in a	AJ223366	Hs.116051	4.6	1678 1679 6068
	423897	DKFZP434N178 protein	AB033062	Hs.134970	4.6	1863 1864 6205
	440952	ESTs	AI291804	Hs.118101	4.6	3490 7466
	449129	ESTs	AI631602	Hs.258949	4.6	4066 7950
	458098	metallothionein 1E (functional)	BE550224	Hs.351851	4.6	4567 8364
	414359	cadherin 11, type 2, OB-cadherin (osteo	M62194	Hs.75929	4.6	808 5413
70	439589	ESTs	AF086409	Hs.379390	4.5	3409 7392
	439219	ESTs	N33883	Hs.41322	4.5	3382 7365
	457211	ESTs, Weakly similar to S51797 vasodila	AW972565	Hs.32399	4.5	4543 8344
	410290	hypothetical protein DKFZp564A176	AA402307	Hs.322844	4.5	449 5126
	447208	hypothetical protein MGC5627	BE315291	Hs.237971	4.5	3901 7817
75	414175	hypothetical protein DKFZp761D112	AI308876	Hs.103849	4.5	786 5394
	429918	ESTs	AW873986	Hs.119383	4.5	2619 6748
	414875	major histocompatibility complex, class	H42679	Hs.77522	4.5	883 5469
	404277	NM_019111*:Homo sapiens major histocomp			4.5	4744
	424125	inhibin, beta B (activin AB beta polype	M31669	Hs.1735	4.5	1900 1901 6230
80	400543	C10001466.gil7299451[gb]AAF54640.1[(AE			4.5	4632
	424247	lysozyme (renal amyloidosis)	X14008	Hs.234734	4.5	1922 1923 6244
	407049	NM_021724*:Homo sapiens nuclear recepto	X72632		4.5	99 100 4854
	405104	Target Exon			4.5	4771
	452242	glycosyltransferase	R50956	Hs.159993	4.5	4305 8145
85	433867	hippocalcin-like 1	AK000596	Hs.3618	4.5	3011 7046
	422363	replication factor C (activator 1) 3 (3	T55979	Hs.115474	4.5	1673 6065
	448386	KIAA1329 protein	AB037750	Hs.21061	4.5	3997 3998 7896

	452466	hypothetical protein DKFZp564B052	N84635	Hs.29664	4.5	4334 8168
	404721	NM_005596*:Homo sapiens nuclear factor-			4.5	4759
	417079	interleukin 1 receptor antagonist	U65590	Hs.81134	4.5	1073 1074 5616
5	401357	tumor protein D52-like 1			4.5	4650
	426935	collagen, type I, alpha 1	NM_000088	Hs. 172928	4.5	2288 2289 6498
	415701	gamma-glutamyl hydrolase (conjugase, fo	NM_003878	Hs.78619	4.5	940 941 5514
	437681	Homo sapiens, Similar to TEA domain fam	AI207958	Hs.166556	4.5	3280 7273
	449444	solute carrier family 16 (monocarboxyl	AW818436	Hs.351306	4.5	4088 7970
10	451678	DKFZP564D0764 protein	AA374181	Hs.26799	4.5	4244 8096
	406648	major histocompatibility complex, class	AA563730	Hs.277477	4.5	38 4817
	450785	Homo sapiens, alpha-1 (VI) collagen	AA852713	Hs.108885	4.5	4193 8056
	402994	NM_002463*:Homo sapiens myxovirus (infl			4.5	4701
	446962	muscle specific ring finger protein 1	AJ351421	Hs.279709	4.5	3884 7801
15	416847	enhancer of filamentation 1 (cas-like d	L43821	Hs.80261	4.5	1039 1040 5590
	435013	NM_020142:Homo sapiens NADH:ubiquinone	H91923	Hs.110024	4.5	3096 7115
	405770	NM_002362:Homo sapiens melanoma antigen			4.4	4796
	400397	transcription factor 7-like 2 (T-cell s	AJ270770		4.4	18 19 4624
	420591	neurotrophin 3	X53655	Hs.99171	4.4	1465 1466 5916
20	422007	ESTs	AJ739435	Hs.39168	4.4	1624 6029
	429962	glutathione S-transferase pi	M69113	Hs.226795	4.4	2626 6754
	438666	tissue inhibitor of metalloproteinase 2	U44385	Hs.6441	4.4	3360 3361 7344
	439453	thyroid hormone receptor interactor 13	BE264974	Hs.6566	4.4	3399 7382
	408784	ESTs	AW971350	Hs.63386	4.4	257 4986
25	444863	serine (or cysteine) proteinase inhibit	AW384082	Hs.104879	4.4	3731 7677
	400228	NM_021724*:Homo sapiens nuclear recepto		Hs.276916	4.4	4601
	439318	G protein-coupled receptor 56	AW837046	Hs.6527	4.4	3391 7374
	422034	Ets2 repressor factor	AC006486	Hs.333069	4.4	1627 1628 6032
	419081	ESTs	AJ798863	Hs.87191	4.4	1299 5788
30	414883	CDC28 protein kinase 1	AA926960	Hs.348669	4.4	885 5471
	450224	collagen, type IV, alpha 6	D21337	Hs.408	4.4	4145 4146 8017
	425308	receptor tyrosine kinase-like orphan re	M97639	Hs.155585	4.4	2087 2088 6362
	443801	Intron of: trichorhinophalangeal syndr	AW206942	Hs.253594	4.4	3646 7608
	408787	Rho guanine exchange factor (GEF) 11	NM_014784	Hs.4 7822	4.4	258 259 4987
35	424735	short-chain alcohol dehydrogenase famil	U31875	Hs.272499	4.4	1993 1994 6294
	438596	ESTs	AA829427	Hs.243081	4.4	3337 7325
	435663	ESTs	AI023707	Hs.134273	4.4	3143 7155
	418990	proteasome (prosome, macropain) subunit	BE410285	Hs.89545	4.4	1289 5780
	411365	GM2 ganglioside activator protein	M76477	Hs.289082	4.4	528 529 5187
40	426413	gb:EST90805 Synovial sarcoma Homo sapie	AA377823		4.4	2219 6453
	400205	NM_006265*:Homo sapiens RAD21 (S. pombe		Hs.81848	4.4	4598
	435176	ESTs	AA744875	Hs.189413	4.4	3111 7129
	448499	p53-regulated DDA3	BE613280	Hs.77550	4.4	4008 7905
	443639	proteasome (prosome, macropain) subunit	BE269042	Hs.9661	4.4	3632 7595
45	418522	Homo sapiens cDNA: FLJ21950 fis, clone	AA605038	Hs.7149	4.4	1250 5751
	421143	immunoglobulin superfamily containing I	AB024536	Hs.102171	4.4	1510 1511 5949
	430413	small inducible cytokine A5 (RANTES)	AW842182	Hs.241392	4.4	2693 6801
	418216	AF15q14 protein	AA662240	Hs.283099	4.4	1206 5721
	446751	Human DNA sequence from clone RP11-16L2	AA766998	Hs.378780	4.4	3871 7791
50	442328	ESTs, Weakly similar to ALU4_HUMAN ALU	AI952430	Hs.150614	4.4	3556 7528
	406973	major histocompatibility complex, class	M34996	Hs.198253	4.3	90 91 4849
	418526	solute carrier family 16 (monocarboxyl	BE019020	Hs.85838	4.3	1251 5752
	426890	ESTs	AA393167	Hs.41294	4.3	2283 6494
	417142	ESTs	AI082507	Hs.85905	4.3	1083 5624
55	429716	collagen, type XIII, alpha 1	R25685	Hs.211933	4.3	2609 6741
	427378	melanoma antigen, family D, 1	BE515037	Hs.177556	4.3	2322 6523
	431639	phosphoprotein associated with GEMs	AK000680	Hs.266175	4.3	2805 2806 6883
	447198	ESTs	D61523	Hs.283435	4.3	3898 7814
	448258	hypothetical protein FLJ20396	BE386983	Hs.343214	4.3	3990 7889
60	407047	gb:H.sapiens SOD-2 gene for manganese s	X65965		4.3	98 4853
	439246	membrane-associated tyrosine- and threo	AI498072	Hs.351474	4.3	3386 7369
	439709	hypothetical protein FLJ20128	AW401433	Hs.6649	4.3	3422 7405
	404920	Target Exon			4.3	4765
	405372	NM_006841:Homo sapiens transporter prot			4.3	4778
65	412577	CD163 antigen	Z22968	Hs.74076	4.3	608 609 5252
	426283	kynureninase (L-kynurenine hydrolase)	NM_003937	Hs.1 69139	4.3	2192 2193 6435
	444371	forkhead box M1	BE540274	Hs.239	4.3	3696 7651
	426759	ESTs	AI590401	Hs.21213	4.3	2268 6483
	436045	DKFZP564O0423 protein	AB037723	Hs.5028	4.3	3169 3170 7176
70	433658	immunoglobulin kappa constant	L03678	Hs.156110	4.3	2996 2997 7034
	402876	NM_022181*:Homo sapiens livin inhibitor			4.3	4697
	409062	Homo sapiens mRNA; cDNA DKFZp564B182 (f	AL157488	Hs.50150	4.3	301 5018
	406642	gb:Homo sapiens mRNA for immunoglobulin	AJ245210		4.3	34 35 4815
	423989	OLF-1/EBF associated zinc finger gene	AF221712	Hs.137168	4.3	1880 1881 6216
75	442547	ESTs, Weakly similar to ALU1_HUMAN ALU	AA306997	Hs.217484	4.3	3566 7537
	422530	bone marrow stromal cell antigen 2	AW972300	Hs.118110	4.3	1696 6082
	400802	Target Exon			4.3	4638
	439627	hypothetical protein FLJ21841	BE621702	Hs.29076	4.3	3411 7394
	418618	GTP cyclohydrolase 1 (dopa-responsive d	U66097	Hs.86724	4.3	1261 1262 5760
80	444119	ESTs, Weakly similar to T26686 hypothet	R41231	Hs.184261	4.3	3677 7635
	453910	Kruppel-like zinc finger protein GLIS2	AL133794	Hs.16313	4.3	4464 8277
	447737	DKFZP564L0862 protein	AK000643	Hs.19404	4.3	3957 3958 7861
	414945	lymphocyte antigen 6 complex, locus E	BE076358	Hs.77667	4.3	894 5477
	437233	Homo sapiens brother of CDO (BOC) mRNA,	D81448	Hs.339352	4.3	3249 7246
	403130	NM_005400*:Homo sapiens protein kinase			4.3	4708
85	428291	interferon stimulated gene (20kD)	AA534009	Hs.183487	4.3	2423 6604
	418283	cathepsin K (pseudosclerosis)	S79895	Hs.83942	4.3	1210 1211 5724

	449611	ESTs	AI970394	Hs.197075	4.3	4100 7981
	412014	ESTs, Weakly similar to A46010 X-linked	AI620650	Hs.43761	4.3	566 5218
	439540	ESTs	AW979189	Hs.283367	4.3	3405 7388
5	408096	dihydrofolate reductase	BE250162	Hs.83765	4.3	189 4931
	419073	Homo sapiens cDNA FLJ12797 fis, clone	N AW372170	Hs.183918	4.2	1296 5786
	419745	slug (chicken homolog), zinc finger pro	AF042001	Hs.93005	4.2	1381 1382 5851
	406634	GDP dissociation inhibitor 1	AA386235	Hs.74576	4.2	31 4813
	454429	hypothetical protein PP3501	BE273437	Hs.301406	4.2	4500 8306
10	407818	jumonji (mouse) homolog	AL021938	Hs.40154	4.2	165 4909
	400261	Eos Control		Hs.1802	4.2	4611
	453597	myo-inositol 1-phosphate synthase A1	BE281130	Hs.381118	4.2	4429 8249
	430622	Homo sapiens, Similar to DNA segment, C	BE616971	Hs.247478	4.2	2714 6815
	453204	ESTs	R10799	Hs.191990	4.2	4403 8227
15	412926	macrophage myristoylated alanine-rich C	AI879076	Hs.75061	4.2	655 5290
	432388	v-ski avian sarcoma viral oncogene homo	X15218	Hs.2969	4.2	2869 2870 6932
	455169	gb:QV0-CT0387-170200-121-h07 CT0387	Hom AW860908		4.2	4505 8311
	424842	signal transducing adaptor molecule (SH	AA034127	Hs.153487	4.2	2013 6307
	438451	ESTs	AI081972	Hs.220261	4.2	3323 7313
20	421774	Homo sapiens mRNA; cDNA DKFZp586C1619 (AL050374	Hs.108169	4.2	1589 6001
	418918	CD2 antigen (p50), sheep red blood cell	X07871	Hs.89476	4.2	1282 1283 5775
	452301	ESTs	BE041144	Hs.127699	4.2	4312 8151
	453779	28kD interferon responsive protein	N35187	Hs.43388	4.2	4441 8259
	427239	ubiquitin carrier protein	BE270447	Hs.356512	4.2	2311 6515
25	443572	cleavage and polyadenylation specific f	AA025610	Hs.9605	4.2	3625 7589
	413048	mannose receptor, C type 1	M93221	Hs.75182	4.2	672 673 5305
	423767	F-box only protein 2	H18283	Hs.132753	4.2	1845 6192
	420162	cyclin-dependent kinase 4	BE378432	Hs.95577	4.2	1422 5883
	421506	thymidine kinase 1, soluble	BE302796	Hs.105097	4.2	1650 5976
30	418312	Rai guanine nucleotide exchange factor	AW972468	Hs.170307	4.2	1213 5726
	403508	Target Exon			4.2	4723
	432729	hypothetical protein FLJ20285	AK000292	Hs.130732	4.2	2902 2903 6960
	414085	aldehyde dehydrogenase 1 family, member	AA114016	Hs.75746	4.2	775 5384
	418113	SRY (sex determining region Y)-box 4	AI272141	Hs.83484	4.2	1194 5711
35	452106	ESTs	AI141031	Hs.21342	4.2	4289 8131
	429922	H1 histone family, member 0	Z97630	Hs.226117	4.2	2621 2622 6750
	457400	cathepsin Z	AF032906	Hs.252549	4.2	4547 4548 8347
	420255	membrane metallo-endopeptidase (neutral	NM_007289	Hs.1298	4.2	1438 1439 5896
	417080	small nuclear ribonucleoprotein polypep	BE392846	Hs.1063	4.2	1075 5617
40	445472	Homo sapiens mRNA for KIAA0293 gene, pa	AB006631	Hs.12784	4.2	3773 3774 7711
	453060	hypothetical protein MGC15754	AW294092	Hs.21594	4.2	4386 8213
	414586	lymphocyte cytosolic protein 1 (L-plast	AA306160	Hs.381099	4.2	833 5434
	434669	core histone macroH2A2.2	AF151534	Hs.92023	4.1	3068 3069 7093
	434149	hypothetical protein MGC5469	Z43829	Hs.244624	4.1	3030 7063
45	445333	hypothetical protein FLJ12538 similar t	BE537641	Hs.44278	4.1	3759 7700
	401176	Target Exon			4.1	4646
	416926	HT018 protein	H03109	Hs.263395	4.1	1046 5596
	408196	SRY (sex determining region Y)-box 22	AL034548	Hs.43627	4.1	199 200 4940
	430422	ESTs	AI078115	Hs.54680	4.1	2694 6802
50	411020	macrophage receptor with collagenous st	NM_006770	Hs.6 7726	4.1	506 507 5168
	452436	ESTs, Moderately similar to A46010 X-li	BE077546	Hs.31447	4.1	4330 8164
	443264	ESTs, Moderately similar to A47582 B-ce	BE221477	Hs.132137	4.1	3615 7581
	417866	collagen, type XI, alpha 1	AW067903	Hs.82772	4.1	1162 5685
	431863	spindlin	AA188185	Hs.289043	4.1	2829 6901
55	422032	polymerase (RNA) III (DNA directed) pol	AA476966	Hs.110857	4.1	1625 6030
	440028	ESTs, Weakly similar to T17227 hypothel	AW473675	Hs.367649	4.1	3446 7428
	407756	ubiquitin specific protease 18	AA116021	Hs.38260	4.1	159 4903
	452833	KIAA0124 protein	BE559681	Hs.30736	4.1	4355 8186
	429345	hypothetical protein	R11141	Hs.199695	4.1	2548 6700
60	423447	ESTs	D31043	Hs.282596	4.1	1807 6163
	426501	ESTs	AW043782	Hs.293616	4.1	2242 6467
	429415	procollagen C-endopeptidase enhancer	NM_002593	Hs.2 02097	4.1	2557 2558 6706
	446531	ESTs	AW301023	Hs.150854	4.1	3854 7775
	439668	frizzled (Drosophila) homolog 8	AI091277	Hs.302634	4.1	3414 7397
65	440087	hypothetical protein FLJ22678	W28969	Hs.7718	4.1	3452 7433
	425170	transcription factor CP2	AU077315	Hs.154970	4.1	2061 6342
	414522	Immunoglobulin J chain	AW518944	Hs.76325	4.1	827 5428
	406625	stearoyl-CoA desaturase (delta-9-desatu	Y13647	Hs.119597	4.1	28 29 4811
	400259	NM_017432*:Homo sapiens prostate tumor		Hs.19555	4.1	4610
70	438209	aryl-hydrocarbon receptor nuclear trans	AL120659	Hs.6111	4.1	3309 7301
	446570	ESTs	AV659177	Hs.127160	4.1	3858 7779
	400252	NM_004651*:Homo sapiens ubiquitin speci		Hs.171501	4.1	4609
	442739	cytosolic acyl coenzyme A thioester hyd	NM_007274	Hs.8 679	4.1	3581 3582 7550
	419488	nucleophosmin/nucleoplasmin 3	AA316241	Hs.90691	4.1	1342 5822
75	452866	Homo sapiens cDNA: FLJ21243 fis, clone	R26969	Hs.268016	4.1	4361 8191
	452689	transferrin	F33868	Hs.284176	4.1	4342 8176
	409012	DKFZP434I216 protein	AL117435	Hs.49725	4.1	293 294 5013
	449717	cerebral cell adhesion molecule	AB040935	Hs.23954	4.1	4110 4111 7989
	414172	phosphatidylinositol glycan, class C	AW954324	Hs.75790	4.1	785 5393
80	428001	ESTs, Moderately similar to Transformin	H97428	Hs.219907	4.1	2389 6576
	412970	dual specificity phosphatase 10	AB026436	Hs.177534	4.1	661 662 5295
	409512	melanoma differentiation associated pro	AW979187	Hs.293591	4.1	354 5057
	428778	fibroblast growth factor receptor-like	AK000530	Hs.193326	4.1	2473 2474 6642
	444739	Homo sapiens cDNA FLJ12924 fis, clone N	N48982	Hs.38034	4.1	3720 7670
	422609	sialidase 1 (lysosomal sialidase)	Z46023	Hs.118721	4.1	1711 6093
85	418327	paired-like homeodomain transcription f	U70370	Hs.84136	4.1	1217 1218 5729
	418932	cadherin 4, type 1, R-cadherin (retinal	L34059	Hs.89484	4.0	1285 1286 5777

5	434408	ESTs	AI031771	Hs.132586	4.0	3053 7080
	412561	lymphocyte-activation gene 3	NM_002286	Hs.7 4011	4.0	603 604 5249
	408901	hypothetical protein FLJ10468	AK001330	Hs.48855	4.0	272 273 4997
	437202	nuclear transcription factor Y, gamma	AA326110	Hs.374481	4.0	3243 7240
	401552	C15001438:gil7300644[gb]AAF55793.1[AE]			4.0	4653
	435674	ESTs	H18063	Hs.13254	4.0	3144 7156
	430381	1-acylglycerol-3-phosphate O-acyltransf	NM_006411	Hs.2 40534	4.0	2684 2685 6796
	417160	proteolipid protein 1 (Pelizaeus-Merzba	N76497	Hs.355807	4.0	1086 5626
10	428409	ESTs	AW117207	Hs.98523	4.0	2438 6616
	453949	heat shock 105kD	AU077146	Hs.36927	4.0	4474 8284
	420247	hypothetical protein FLJ20979	AA256930	Hs.44680	4.0	1437 5895
	421508	absent in melanoma 2	NM_004833	Hs.1 05115	4.0	1551 1552 5977
	453983	ESTs	H94997	Hs.16450	4.0	4476 8286
15	424223	putative DNA/chromatin binding motif	AJ243706	Hs.143323	4.0	1915 1916 6240
	452068	ESTs	W76412	Hs.57877	4.0	4282 8125
	419490	granzyme A (granzyme 1, cytotoxic T-lym	NM_006144	Hs.9 0708	4.0	1343 1344 5823
	447519	ESTs	U46258	Hs.339665	4.0	3936 7844
	411492	immunoglobulin superfamily, member 4	T46848	Hs.70337	4.0	538 5195
20	425688	NGF-A binding protein 2 (ERG1 binding	U48361	Hs.159223	4.0	2124 2125 6386
	428450	KIAA0175 gene product	NM_014791	Hs.1 84339	4.0	2443 2444 6621
	411943	ESTs, Weakly similar to S44608 C02F5.6	BE502436	Hs.7962	4.0	562 5214
	425390	protein tyrosine phosphatase, non-recep	AI092634	Hs.156114	4.0	2098 6368
	423408	hypothetical protein FLJ11743	AA325517	Hs.321046	4.0	1805 6161
25	417933	thymidylate synthetase	X02308	Hs.82962	4.0	1170 1171 5692
	421666	endothelin 3	AL035250	Hs.1408	4.0	1574 1575 5991
	457639	ESTs	W02410	Hs.205555	4.0	4558 8356
	430200	geminin	BE613337	Hs.234896	4.0	2658 6777
	425172	ESTs	AA447729	Hs.12714	4.0	2062 6343
30	406908	gb:H.sapiens protein-tyrosine kinase ge	Z25437		4.0	77 78 4842
	404561	trichorhinophalangeal syndrome I gene (4.0	4751
	407604	collagen, type VIII, alpha 2	AW191962	Hs.353001	4.0	145 4891
	405411	ENSP00000252213:SODIUM BICARBONATE COTR			4.0	4781
	407856	phosphoprotein associated with GEMs	AA045281	Hs.266175	4.0	170 4914
35	438614	KIAA1305 protein	AB037726	Hs.288348	4.0	3338 3339 7326
	428309	cellular retinoic acid-binding protein	M97815	Hs.183650	4.0	2427 2428 6608
	428046	ESTs, Moderately similar to I38022 hypo	AW812795	Hs.337534	4.0	2393 6579
	448610	nel (chicken)-like 1	NM_006157	Hs.2 1602	3.9	4019 4020 7912
	409988	transcription factor AP-2 alpha (activa	N27687	Hs.334334	3.8	401 5092
40	409198	H2A histone family, member P	L19778	Hs.51011	2.4	323 324 5036

TABLE 5B:

	Pkey:	Unique Eos probeset identifier number	
45	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Pkey	CAT Number	Accession
	406782	0_0	AA430373 AA968771
50	406636	0_0	L12064 L12083 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080
	426076	1227958_1	AW962714 AA369277 AA369278
	455813	1515590_1	BE141577 BE141585 BE141587
	426413	372468_1	AW954494 AA377823 BG219617 BG195685 BG616269 AI022688
	406642	0_0	AJ245210 AJ245212 AJ245211 AJ245213
55	455169	1102920_1	AW860953 AW860957 AW860955 AW862593 AW860963 AW862595 AW860889 BF334678 AW860965 AW860890 AW860905
			AW860908 BI031718

TABLE 5C:

60	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

65	Pkey	Ref	Strand	NL_position
	404854	7143420	Plus	14260-14537
	403349	8569773	Minus	167815-168374
	402992	7767907	Minus	42137-42515
70	406367	9256126	Minus	58313-58489
	404378	8810489	Minus	133379-133526
	401797	6730720	Plus	6973-7118
	403404	9438460	Plus	22392-22598,22967-23148
	404815	5911819	Minus	64494-64691
75	404030	7671252	Plus	149362-151749
	402888	9930892	Minus	54727-54901
	403857	7708910	Minus	2524-3408
	405542	9857564	Plus	71331-72183
	404240	5002624	Minus	116132-116407,116653-116922
80	405451	7622517	Minus	145949-146227
	403402	9438460	Plus	13943-14086,15552-15845,16211-16483
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	403668	7259739	Plus	39942-40150
	403405	9438460	Plus	24174-24296
	404977	3738341	Minus	43081-43229
85	404277	1834458	Minus	91665-91946
	400543	9800021	Minus	101471-102209

	405104	8077004	Plus	55387-55519
	404721	9856648	Minus	173763-174294
	401357	9931663	Plus	143295-143425
5	402994	2996643	Minus	4727-4969
	405770	2735037	Plus	61057-62075
	404920	6289231	Plus	94213-94389
	405372	2078459	Minus	10148-10272,11205-11349,11436-11560,1178
	402876	9864669	Plus	5679-6027,7485-7584
10	400802	8567867	Minus	174571-174856
	403130	9211429	Plus	62566-62725
	403508	7630896	Plus	5570-5719
	401176	9438469	Minus	20475-20734
	401552	8099284	Minus	78877-79056
	404561	9795980	Minus	69039-70100
15	405411	3451356	Minus	17503-17778,18021-18290

TABLE 6A

20	Pkey:	Unique Eos probeset identifier number
	Gene name:	Unigene gene title
	Accession:	Exemplar Accession number, Genbank accession number
	UniGene:	Unigene number
25	RATIO:	95th percentile of rhabdomyosarcoma AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator
	SEQ ID #:	nucleic acid and protein sequences provided on CD for search purposes

	Pkey	Gene Name	Accession	UniGene	RATIO	SEQ ID #
30	418678	cancer/testis antigen (NY-ESO-1)	NM_001327	Hs.8 7225	20.0	1269 1270 5765
	429664	POU domain, class 4, transcription factor	L20433	Hs.211588	18.4	2600 2601 6734
	419078	insulinoma-associated 1	M93119	Hs.89584	17.3	1297 1298 5787
	452899	nascent helix loop helix 1	M96739	Hs.30956	17.0	4367 8196
	431727	ESTs	AW293464	Hs.162031	15.3	2814 6889
	412719	ESTs	AW016610	Hs.816	15.1	633 5270
35	419741	ubiquitin carrier protein E2-C	NM_007019	Hs.9 3002	14.5	1379 1380 5850
	416836	cholecystokinin	D54745	Hs.80247	13.8	1038 5589
	452838	preferentially expressed antigen in melanoma	U65011	Hs.30743	13.6	4357 4358 8188
	452340	ISL1 transcription factor, LIM/homeodomain	NM_002202	Hs.5 05	12.9	4317 4318 8155
40	417308	KIAA0101 gene product	H60720	Hs.81892	12.7	1094 5634
	422960	cadherin 13, H-cadherin (heart)	AW890487	Hs.355618	12.7	1762 6130
	414683	hypothetical protein MGC12702	S78296	Hs.76888	12.6	846 847 5444
	430294	guanine nucleotide binding protein 4	A1538226	Hs.32976	12.5	2677 6791
	417389	midkine (neurite growth-promoting factor)	BE260964	Hs.82045	12.3	1109 5647
	447377	transcription factor AP-2 alpha	X77343	Hs.334334	12.0	3920 3921 7831
45	434314	RAB26, member RAS oncogene family	BE392921	Hs.3797	12.0	3042 7072
	424411	crystallin, beta A2	NM_005209	Hs.1 46549	11.7	1945 1946 6262
	407168	ESTs	R45175	Hs.117183	11.7	116 4868
	446921	small inducible cytokine subfamily A (C)	AB012113	Hs.16530	11.6	3878 3879 7797
	441290	cholinergic receptor, nicotinic, alpha	W27501	Hs.89605	11.3	3507 7482
50	443184	ESTs	A1638728	Hs.135159	11.3	3607 7574
	445084	hypothetical protein FLJ14761	H38914	Hs.250848	11.2	3742 7687
	417153	collagen, type II, alpha 1 (primary osteoblast)	X57010	Hs.81343	11.2	1084 1085 5625
	457411	iroquois-class homeobox protein IRX2	AW085961	Hs.130093	11.1	4549 8349
55	425397	topoisomerase (DNA) II alpha (170kD)	J04088	Hs.156346	10.7	2099 2100 6369
	422311	cytokine receptor-like factor 1	AF073515	Hs.114948	10.6	1689 1670 6062
	407178	AP-2 beta transcription factor	AA195651	Hs.352312	10.6	118 4870
	438703	ESTs	A1803373	Hs.31599	10.3	3348 7333
	416854	Purkinje cell protein 4	H40164	Hs.80296	10.3	1041 5591
60	417900	CDC20 (cell division cycle 20, S. cerevisiae)	BE250127	Hs.82906	10.3	1165 5688
	413248	hypothetical protein DKFZp547J036	T64858	Hs.380145	10.1	690 5319
	451952	ESTs	AL120173	Hs.301663	10.1	4264 8111
	440492	hypothetical protein DKFZp547J036	R39127	Hs.380145	10.1	3469 7448
	436481	HSPC150 protein similar to ubiquitin-co	AA379597	Hs.5199	10.0	3192 7197
	423362	myosin XV	NM_016239	Hs.1 27561	9.9	1800 1801 6158
65	426784	chromogranin A (parathyroid secretory protein)	U03749	Hs.172216	9.8	2271 2272 6485
	433001	clone HQ0310 PRO0310p1	AF217513	Hs.279805	9.8	2923 2924 6977
	420092	ESTs	AA814043	Hs.88045	9.7	1415 5877
	413278	interferon-stimulated protein, 15 kDa	BE563085	Hs.833	9.7	695 5322
70	453857	Ras-induced senescence 1 (RIS1)	AL080235	Hs.35861	9.6	4449 4450 8266
	442117	ESTs; hypothetical protein for IMAGE:44	AW664964	Hs.128899	9.6	3551 7523
	450390	Human DNA sequence from clone RP11-234G N93227	Hs.348805	Hs.348805	9.6	4163 8031
	429290	neurofilament, heavy polypeptide (200kD)	AF203032	Hs.198760	9.6	2538 2539 6692
	410687	lysyl oxidase-like 1	U24389	Hs.65436	9.5	485 486 5153
75	442432	hypothetical protein FLJ23468	BE093589	Hs.38178	9.5	3563 7535
	433929	ESTs	A1375499	Hs.27379	9.4	3016 7050
	437204	ESTs, Weakly similar to I55214 salivary	AL110216	Hs.355961	9.4	3244 7241
	453240	hypothetical protein DKFZp566I133	A1969564	Hs.380132	9.4	4406 8230
	449956	Inhibitor of DNA binding 2, dominant negative	AA004852	Hs.180919	9.3	4122 8000
80	440210	ESTs	AW674562	Hs.122128	9.3	3462 7441
	438091	nuclear receptor subfamily 1, group I, member 1	AW373062	Hs.351546	9.2	3302 7295
	411666	neurofilament 3 (150kD medium)	AF106564	Hs.71346	9.1	546 5201
	418156	nuclear receptor subfamily 1, group I, member 1	W17056	Hs.83623	9.0	1198 5715
	450164	ESTs	A1239923	Hs.63931	9.0	4138 8013
85	410402	similar to mouse Ras, dexamethasone-inducible	AL022334	Hs.248222	8.9	458 459 5134
	413597	ESTs	AW302885	Hs.117183	8.9	732 5349
	435652	uncharacterized hypothalamus protein HB N32388	Hs.334370	Hs.334370	8.8	3142 7154

	432143	Homo sapiens, clone IMAGE:4178394, mRNA AL040183	Hs.123484	8.8	2845 6912
	441134	cellular retinoic acid-binding protein	W29092	Hs.346950	8.8
	430627	atonal homolog 1 (Drosophila)	U81148	Hs.247685	8.7
5	410366	hypothetical protein	AI267589	Hs.302689	8.7
	438089	nuclear receptor subfamily 1, group I,	W05391	Hs.351546	8.7
	410467	dachshund (Drosophila) homolog	AF102546	Hs.63931	8.7
	424687	matrix metalloproteinase 9 (gelatinase)	J05070	Hs.151738	8.7
	453582	hypothetical protein FLJ11937	AW854339	Hs.33476	8.5
10	452363	Homo sapiens, Similar to complement com	AI582743	Hs.94953	8.5
	439671	kinesin family member 5C	AW162840	Hs.6641	8.4
	455601	SRY (sex determining region Y)-box 2	AI368680	Hs.816	8.4
	423232	leucine-rich neuronal protein	BE244625	Hs.125742	8.3
	438831	synapsin II	BE263273	Hs.6439	8.3
15	432729	hypothetical protein FLJ20285	AK000292	Hs.130732	8.3
	408826	Homo sapiens clone HB-2 mRNA sequence	AF216077	Hs.48376	8.2
	417160	proteolipid protein 1 (Pelizaeus-Merzba	N76497	Hs.355807	8.2
	412754	amyloid beta (A4) precursor-like protei	AW160375	Hs.74565	8.2
	440650	Human DNA sequence from PAC 75N13 on ch	R44692	Hs.326801	8.2
20	412471	endothelial cell growth factor 1 (plate	M53193	Hs.73946	8.2
	409893	minichromosome maintenance deficient (S	AW247090	Hs.57101	8.2
	414219	ALL1-fused gene from chromosome 1q	W20010	Hs.75823	8.1
	420783	lectin, galactoside-binding, soluble, 7	AI659838	Hs.99923	8.1
	443247	c-Myc target JPO1	BE614387	Hs.333893	8.1
25	419236	Homo sapiens cDNA FLJ11481 fis, clone H	AA330447	Hs.135159	8.1
	443426	chromosome 20 open reading frame 1	AF098158	Hs.9329	8.1
	400411	Homo sapiens G-protein gamma 8 subunit	AF188179		8.1
	425256	collapsin response mediator protein 1	BE297611	Hs.155392	7.9
	422809	hypothetical protein FLJ10549	AK001379	Hs.121028	7.8
30	406673	major histocompatibility complex, class	M34996	Hs.198253	7.8
	444279	cholinergic receptor, nicotinic, alpha	U62432	Hs.89605	7.7
	415989	ESTs	AI267700	Hs.351201	7.7
	441390	ESTs	AI692560	Hs.355961	7.7
	407112	ESTs, Weakly similar to ALU7_HUMAN ALU	AA070801	Hs.51615	7.7
35	435099	flap structure-specific endonuclease 1	AC004770	Hs.4756	7.7
	419086	Kallmann syndrome 1 sequence	NM_000216	Hs.8 9591	7.7
	424800	MyoD family inhibitor	AL035588	Hs.153203	7.6
	448051	ephrin-A3	BE048061	Hs.37054	7.6
	420460	Homo sapiens clone HB-2 mRNA sequence	AA262331	Hs.48376	7.6
40	414945	lymphocyte antigen 6 complex, locus E	BE076358	Hs.77687	7.5
	409142	SMC4 (structural maintenance of chromos	AL136877	Hs.50768	7.5
	412107	growth factor independent 1	BE242676	Hs.73172	7.5
	444527	small inducible cytokine subfamily A (C	NM_005408	Hs.1 1383	7.5
	424468	LIM homeobox protein 3	AF156889	Hs.148427	7.5
45	413407	inositol polyphosphate phosphatase-like	AI356293	Hs.75339	7.4
	449722	cyclin B1	BE280074	Hs.23960	7.4
	412140	RAB6 interacting, kinesin-like (rabkine	AA219691	Hs.73625	7.4
	423279	ESTs	AW959861	Hs.290943	7.4
	454140	hypothetical protein FLJ10474	AB040888	Hs.41793	7.4
50	439979	hypothetical protein FLJ10430	AW600291	Hs.6823	7.4
	421307	Homo sapiens mRNA; cDNA DKFZp434B0425 (BE539976	Hs.103305	7.4
	453243	KIAA0441 gene product	AB007901	Hs.32511	7.3
	430826	POU domain, class 4, transcription fact	U10061	Hs.248019	7.3
	418375	synaptosomal-associated protein, 25kD	NM_003081	Hs.8 4389	7.3
55	453597	myo-inositol 1-phosphate synthase A1	BE281130	Hs.381118	7.3
	408915	heptacelular carcinoma novel gene-3 pr	NM_016651	Hs.4 8950	7.3
	414117	proteolipid protein 1 (Pelizaeus-Merzba	W88559	Hs.355807	7.3
	452223	hypothetical protein MGC2827	AA425467	Hs.8035	7.3
	429345	hypothetical protein	R11141	Hs.199695	7.2
60	444006	type I transmembrane protein Fn14	BE395085	Hs.334762	7.2
	408562	roundabout (axon guidance) receptor, Dro	AI436323	Hs.31141	7.2
	450663	ribonuclease H1, large subunit	H43540	Hs.25292	7.2
	448610	nel (chicken)-like 1	NM_006157	Hs.2 1602	7.2
	416322	pyrroline-5-carboxylate reductase 1	BE019494	Hs.79217	7.1
65	453392	SRY (sex determining region Y)-box 11	U23752	Hs.32964	7.1
	425770	spastic ataxia of Charlevoix-Saguenay (NM_014363	Hs.1 59492	7.1
	437036	ESTs	AI571514	Hs.133022	7.1
	450447	hypothetical protein P15-2	AF212223	Hs.25010	7.1
	424001	paternally expressed 10	W67883	Hs.137476	7.1
70	443981	KIAA0274 gene product	D87464	Hs.10037	7.1
	443071	complement component 1, q subcomponent,	AL080021	Hs.8986	7.1
	426991	Homo sapiens cDNA FLJ10574 fis, clone N	AK001536	Hs.214410	7.1
	431629	interferon, alpha-inducible protein (cl	AU077025	Hs.265827	7.0
	432731	fibronectin 1	R31178	Hs.287820	7.0
75	432409	KIAA1575 protein	AA806538	Hs.130732	7.0
	414761	enhancer of zeste (Drosophila) homolog	AU077228	Hs.77256	7.0
	418515	ESTs, Weakly similar to CNH_HUMAN CORN	AI568453	Hs.19487	7.0
	428450	KIAA0175 gene product	NM_014791	Hs.1 84339	6.9
	445016	reelin	U79716	Hs.12246	6.9
80	421777	HSPC037 protein	BE562088	Hs.108196	6.9
	443021	Ig superfamily protein	AA368546	Hs.8904	6.9
	425274	minichromosome maintenance deficient (m	BE281191	Hs.155462	6.8
	433447	neuronal pentraxin II	U29195	Hs.3281	6.8
	414416	hypothetical protein MGC2721	AW409985	Hs.76084	6.8
	451489	amyloid beta (A4) precursor protein-bin	NM_005503	Hs.2 6468	6.8
85	442285	uncharacterized hypothalamus protein HT	W28729	Hs.374989	6.8
	435977	brain-specific membrane-anchored protei	AL138079	Hs.5012	6.8

407792	putative secreted ligand homologous to	A1077715	Hs.39384	6.8	162 4906
443859	folistatin	NM_013409	Hs.9 914	6.8	3651 3652 7613
444381	hypothetical protein BC014245	BE387335	Hs.283713	6.8	3697 7652
436608	down syndrome critical region protein D	AA628980	Hs.192371	6.8	3205 7207
422363	replication factor C (activator 1) 3 (3)	T55979	Hs.115474	6.7	1673 6065
421362	hypothetical protein FLJ20043	AK000050	Hs.103853	6.7	1531 1532 5965
427239	ubiquitin carrier protein	BE270447	Hs.356512	6.7	2311 6515
410889	twist (Drosophila) homolog (acrocephalo	X91662	Hs.66744	6.7	501 502 5164
428405	cholinergic receptor, nicotinic, alpha	Y00762	Hs.2266	6.7	2436 2437 6615
416602	Protein kinase C-binding protein NELL2	NM_006159	Hs.3 67895	6.7	1017 1018 5575
407619	collagen, type IX, alpha 2	AL050341	Hs.37165	6.7	146 147 4892
432527	ESTs	AW975028	Hs.102754	6.7	2883 6944
416065	proliferating cell nuclear antigen	BE267931	Hs.78996	6.7	968 5536
425234	ESTs, Weakly similar to I38022 hypothet	AW152225	Hs.165909	6.7	2070 6349
416658	fibrillin 2 (congenital contractual ar	U03272	Hs.79432	6.7	1020 1021 5577
418399	hypothetical protein FLJ12442	AF131781	Hs.84753	6.6	1232 1233 5738
450676	ESTs	AI147155	Hs.279727	6.6	4180 8045
409633	ESTs	AW449822	Hs.55200	6.6	371 5068
419405	ESTs	AI377043	Hs.42189	6.6	1333 5816
437044	differentially expressed in Fanconi's a	AL035864	Hs.69517	6.5	3233 7232
435732	leucine rich repeat and death domain co	AF229178	Hs.123136	6.5	3147 3148 7159
438076	ESTs	W88525	Hs.18816	6.5	3298 7291
453439	guanine nucleotide binding protein 4	AI572438	Hs.32976	6.5	4419 8241
410359	ESTs	R38624	Hs.106313	6.5	455 5131
431183	KDEL (Lys-Asp-Glu-Leu) endoplasmic reti	NM_006855	Hs.250696	6.4	2756 2757 6845
452097	a disintegrin-like and metalloprotease	AB002364	Hs.27916	6.4	4287 4288 8130
450748	ESTs	AI733093	Hs.247686	6.4	4189 8053
409731	thymosin, beta, identified in neuroblas	AA125985	Hs.56145	6.4	386 5080
412577	CD163 antigen	Z22968	Hs.74076	6.4	608 609 5252
418113	SRY (sex determining region Y)-box 4	AI272141	Hs.83484	6.4	1194 5711
411789	Adican	AF245505	Hs.72157	6.4	553 554 5207
422515	multifunctional polypeptide similar to	AW500470	Hs.117950	6.3	1693 6079
439522	Homo sapiens, clone MGC:15766, mRNA, co	AA405968	Hs.58219	6.3	3404 7387
453139	Human DNA sequence from clone RP11-234G	AA330620	Hs.348805	6.3	4394 8220
433036	ESTs	AA574091	Hs.105964	6.3	2929 6981
434284	ankyrin 1, erythrocytic	N63745	Hs.183805	6.3	3041 7071
409799	phosphoserine phosphatase-like	D11928	Hs.76845	6.3	387 5081
452701	glutamine-fructose-6-phosphate transami	NM_005110	Hs.3 0332	6.3	4345 4346 8178
424308	minichromosome maintenance deficient (S	AW975531	Hs.154443	6.3	1932 6250
426075	ESTs, Weakly similar to 2109260A B cell	AW513691	Hs.270149	6.3	2170 6417
437696	hypothetical protein dJ37E16.5	Z83844	Hs.5790	6.3	3281 7274
413995	synixin 1A (brain)	BE048146	Hs.75671	6.3	761 5373
421016	transcription factor 3 (E2A immunogloblu	AA504583	Hs.101047	6.3	1497 5937
412014	ESTs, Weakly similar to A46010 X-linked	AI620650	Hs.43761	6.3	566 5218
457869	Homo sapiens, alpha-1 (VI) collagen	AU077186	Hs.108885	6.3	4561 8359
452056	Homo sapiens, clone IMAGE:4054156, mRNA	AW955065	Hs.101150	6.2	4280 8123
436199	hypothetical protein FLJ14503	R38946	Hs.127951	6.2	3175 7180
427400	hypothetical protein FLJ11939	AW245084	Hs.94229	6.2	2325 6525
449052	ESTs	AW029507	Hs.161102	6.2	4062 7946
453041	Homo sapiens cDNA FLJ11918 fis, clone H	AI680737	Hs.289068	6.2	4384 8211
439753	hypothetical protein from EUROIMAGE 216	BE262233	Hs.7423	6.2	3429 7412
430167	FEV protein	Y08976	Hs.234759	6.2	2655 2656 6775
451766	ephrin-B3	NM_001406	Hs.2 6988	6.2	4255 4256 8104
456508	ESTs, Weakly similar to AF208855 1 BM-0	AA502764	Hs.123469	6.2	4521 8325
456534	phospholipase C, beta 3, neighbor pseud	X91195	Hs.100623	6.2	4522 8326
408349	homeo box C10	BE546947	Hs.44276	6.2	213 4949
429903	cyclin-dependent kinase 5, regulatory s	AL134197	Hs.93597	6.2	2616 6746
439668	frizzled (Drosophila) homolog 8	AI091277	Hs.302634	6.2	3414 7397
431070	transcription factor 19 (SC1)	AW408164	Hs.249184	6.2	2744 6837
410530	ATPase, H transporting, lysosomal (vacu	M25809	Hs.64173	6.1	469 470 5141
434859	collapsin response mediator protein-5;	BE255080	Hs.299315	6.1	3083 7104
450414	KIAA1716 protein	AI907735	Hs.21446	6.1	4165 8033
402994	NM_002463*:Homo sapiens myxovirus (infl			6.1	4701
450701	hypothetical protein XP_098151 (leucine	H39960	Hs.288467	6.1	4183 8048
414747	centromere protein F (350/400kD, mitosi	U30872	Hs.77204	6.1	861 862 5455
449514	protein predicted by clone 23627	AW970440	Hs.23642	6.1	4093 7975
440774	ESTs	AI420611	Hs.153934	6.1	3486 7462
418406	cytokeratin 20	X73501	Hs.84905	6.0	1235 1236 5740
452319	transducin-like enhancer of split 1, ho	M99435	Hs.28935	6.0	4313 4314 8152
447414	neuroblastoma (nerve tissue) protein	D82343	Hs.74376	6.0	3924 3925 7834
419991	eyes absent (Drosophila) homolog 1	AJ000098	Hs.94210	6.0	1404 1405 5869
432290	Homo sapiens cDNA FLJ10237 fis, clone H	AK001099	Hs.274273	6.0	2882 6926
418322	cyclin-dependent kinase inhibitor 3 (CD	AA284166	Hs.84113	6.0	1214 5727
452242	glycosyltransferase	R50956	Hs.159993	6.0	4305 8145
427375	metallocarboxypeptidase CPX-1	AL035460	Hs.177536	6.0	2320 2321 6522
406634	GDP dissociation inhibitor 1	AA386235	Hs.74576	6.0	31 4813
418140	microfibrillar-associated protein 2	BE613836	Hs.83551	6.0	1196 5713
436190	gb:Homo sapiens cDNA FLJ10197 fis, clon	AK001059	Hs.3821	6.0	3173 3174 7179
426509	pentaxin-related gene, rapidly induced	M31166	Hs.2050	6.0	2243 2244 6468
438162	deleted in bladder cancer chromosome re	NM_014618	Hs.6 090	6.0	3306 3307 7299
414915	myxovirus (influenza) resistance 1, hom	NM_002462	Hs.7 6391	6.0	888 889 5473
452291	CDC7 (cell division cycle 7, S. cerevis	AF015592	Hs.28853	6.0	4310 4311 8150
429415	procollagen C-endopeptidase enhancer	NM_002593	Hs.2 02097	6.0	2557 2558 6706
409012	DKFZP434I216 protein	AL117435	Hs.49725	5.9	293 294 5013
443210	hypothetical protein MGC13168	AI692649	Hs.9451	5.9	3609 7576
456658	Homo sapiens PAC clone RP4-751H13 from	AI660203	Hs.112158	5.9	4527 8330

414812	monokine induced by gamma interferon	X72755	Hs.77367	5.9	874 875 5464
424439	ligase I, DNA, ATP-dependent	AA579635	Hs.1770	5.9	1950 6265
441689	ESTs	AI123705	Hs.289068	5.9	3533 7505
415947	mutS (E. coli) homolog 2 (colon cancer,	U04045	Hs.78934	5.9	960 961 5529
420238	ESTs, Weakly similar to 2109260A B cell	AA256783	Hs.12549	5.9	1436 5894
434449	hypothetical protein FLJ22041 similar t	AW953484	Hs.3849	5.9	3057 7083
414732	minichromosome maintenance deficient (S	AW410976	Hs.77152	5.9	859 5453
410102	ESTs; homologue of PEM-3 [Clona savigny	AW248508	Hs.279727	5.8	422 5107
443912	ESTs	R37257	Hs.184780	5.8	3657 7618
429163	gb:am20a10.s1 Soares_NFL_T_GBC_S1	Homo AA884766		5.8	2521 6678
435793	KIAA1313 protein	AB037734	Hs.4993	5.8	3152 3153 7162
435978	Homo sapiens PR-domain zinc finger prot	AF272899	Hs.135118	5.8	3167 3168 7175
422283	CDC45 (cell division cycle 45, S.cerevi	AW411307	Hs.114311	5.8	1668 6061
452833	KIAA0124 protein	BE559681	Hs.30736	5.8	4355 8186
409327	collagen, type IX, alpha 3	L41162	Hs.53563	5.8	341 342 5047
400263	Eos Control		Hs.75309	5.8	4613
447733	MAD2 (mitotic arrest deficient, yeast,	AF157482	Hs.19400	5.8	3955 3956 7860
417115	small nuclear ribonucleoprotein polypep	AW952792	Hs.334612	5.8	1081 5622
444371	forkhead box M1	BE540274	Hs.239	5.8	3696 7651
453830	ESTs	AA534296	Hs.20953	5.8	4445 8263
419550	KIAA0128 protein; septin 2	D50918	Hs.90998	5.8	1348 1349 5827
457211	ESTs, Weakly similar to S51797 vasodila	AW972565	Hs.32399	5.8	4543 8344
435141	Rec8p, a meiotic recombination and sls	AA862498	Hs.4767	5.8	3108 7126
447499	protocadherin beta 16	AW262580	Hs.147674	5.8	3934 7842
427528	minichromosome maintenance deficient (S	AAU077143	Hs.179565	5.8	2341 6537
417933	thymidylate synthetase	X02308	Hs.82962	5.8	1170 1171 5692
439963	platelet-activating factor acetylhydrol	AW247529	Hs.6793	5.8	3441 7423
438821	ESTs	AA826425	Hs.192375	5.8	3355 7339
431049	hypothetical protein FLJ22548 similar t	AA846576	Hs.103267	5.8	2743 6836
444783	anillin (Drosophila Scraps homolog), ac	AK001468	Hs.62180	5.8	3722 3723 7672
415857	Homo sapiens cDNA FLJ11381 fis, clone H	AA866115	Hs.127797	5.8	952 5523
409062	Homo sapiens mRNA; cDNA DKFZp564B182	(F AL157488	Hs.50150	5.8	301 5018
418478	cyclin-dependent kinase inhibitor 2A (m	U38945	Hs.1174	5.7	1245 1246 5747
440209	neurexin 3	H05049	Hs.247837	5.7	3461 7440
428342	Homo sapiens cDNA FLJ13458 fis, clone P	AI739168	Hs.349283	5.7	2432 6611
407136	Homo sapiens cDNA FLJ11533 fis, clone H	T64896	Hs.287420	5.7	113 4865
406367	NM_022357;Homo sapiens putative metallo			5.7	4804
428949	hypothetical protein DKFZp434J0617	AA442153	Hs.104744	5.7	2490 6655
433075	sortilin 1	NM_002959	Hs.3 51872	5.7	2936 2937 6987
428289	complement component 2	M26301	Hs.2253	5.7	2421 2422 6603
438915	Williams-Beuren syndrome chromosome reg	AA280174	Hs.355711	5.7	3365 7348
413882	ESTs	AA132973	Hs.184492	5.7	750 5364
449789	hypothetical protein DKFZp566i133	AA004300	Hs.380132	5.7	4116 7994
418574	M-phase phosphoprotein 9	N28754	Hs.351230	5.7	1258 5757
425295	ESTs	AA431366	Hs.37251	5.7	2085 6360
407824	Homo sapiens cDNA FLJ14388 fis, clone H	AA147884	Hs.9812	5.7	166 4910
424840	extra spindle poles, S. cerevisiae, hom	D79987	Hs.153479	5.7	2011 2012 6306
448775	nudix (nucleoside diphosphate linked mo	AB025237	Hs.388	5.7	4036 4037 7927
420005	ESTs	AW271106	Hs.133294	5.7	1407 5871
425048	ESTs	H05468	Hs.164502	5.7	2040 6327
412978	homeo box C6	AI431708	Hs.820	5.7	665 5298
409698	short stature homeobox 2	AF022654	Hs.55967	5.6	378 379 5074
406964	FGENES predicted novel secreted protein	M21305		5.6	87 88 4847
441016	ESTs	AW138653	Hs.25845	5.6	3494 7470
437898	ESTs	W81260	Hs.43410	5.6	3293 7286
446619	secreted phosphoprotein 1 (osteopontin,	AU076643	Hs.313	5.6	3861 7782
414312	ESTs	AA155694	Hs.191060	5.6	800 5407
435708	ESTs	AI362949	Hs.6439	5.6	3146 7158
453665	ESTs, Weakly similar to SFRB_HUMAN SPLI	AA626250	Hs.326184	5.6	4434 8253
438944	KIAA1444 protein	AA302517	Hs.92732	5.6	3368 7351
421506	thymidine kinase 1, soluble	BE302796	Hs.105097	5.6	1550 5976
432562	DKFZP586G1122 protein	BE531048	Hs.278422	5.6	2887 6948
434022	ESTs	R18374	Hs.117956	5.6	3024 7057
428046	ESTs, Moderately similar to I38022 hypo	AW812795	Hs.337534	5.6	2393 6579
446021	ribosomal protein L4	BE389213	Hs.286	5.6	3811 7740
422094	F-box only protein 5	AF129535	Hs.272027	5.5	1642 1643 6041
447200	Homo sapiens cDNA FLJ14028 fis, clone H	BE543146	Hs.281434	5.5	3899 7815
424837	N-acetyltransferase, homolog of S. cere	BE276113	Hs.333034	5.5	2010 6305
406851	major histocompatibility complex, class	AA609784	Hs.352392	5.5	71 4838
432247	ESTs	AA531287	Hs.105805	5.5	2859 6923
451407	fibroblast growth factor 12B	AA131376	Hs.343809	5.5	4230 8085
418216	AF15q14 protein	AA662240	Hs.283099	5.5	1208 5721
434149	hypothetical protein MGC5469	Z43829	Hs.244624	5.5	3030 7063
426265	ESTs	AA421069	Hs.97896	5.5	2189 6432
428058	ESTs	AI821625	Hs.191602	5.5	2395 6581
414430	ubiquitin carboxyl-terminal esterase L1	AI346201	Hs.76118	5.5	815 5419
450693	ESTs	AW450461	Hs.203965	5.5	4182 8047
419260	protein kinase Njmu-R1	H08819	Hs.334851	5.5	1323 5807
424440	ESTs	AA340743	Hs.133208	5.5	1951 6266
408196	SRY (sex determining region Y)-box 22	AL034548	Hs.43627	5.5	199 200 4940
439456	hypothetical protein FLJ20980	AI752409	Hs.109314	5.5	3400 7383
422871	collagen, type XI, alpha 2	AL031228	Hs.121509	5.5	1753 1754 6123
418255	ESTs	AW135405	Hs.37251	5.5	1209 5723
420805	reticulon 1	L10333	Hs.99947	5.4	1480 1481 5926
448277	hypothetical protein FLJ13044	BE622827	Hs.99486	5.4	3991 7890
437741	putative transmembrane protein; homolog	BE561610	Hs.5809	5.4	3283 7276

413945	CD14 antigen	NM_000591	Hs.7 5627	5.4	758 759 5371
424870	ESTs	T15545	Hs.244624	5.4	2014 6308
425157	phospholipid transfer protein	NM_006227	Hs.2 83007	5.4	2057 2058 6340
429038	seizure related gene 6 (mouse)-like	AL023513	Hs.194766	5.4	2504 2505 6666
441954	Fancor anemia, complementation group G	A1744935	Hs.8047	5.4	3542 7514
409608	cadherin, EGF LAG seven-pass G-type rec	AF231023	Hs.55173	5.4	367 368 5065
443907	TYRO protein tyrosine kinase binding pr	AU076484	Hs.9963	5.4	3656 7617
410342	Fc fragment of IgE, high affinity I, re	R31350	Hs.743	5.4	453 5129
445472	Homo sapiens mRNA for KIAA0293 gene, pa	AB006631	Hs.12784	5.4	3773 3774 7711
408096	dihydrofolate reductase	BE250162	Hs.83765	5.4	189 4931
429612	pituitary tumor-transforming 1	AF062649	Hs.252587	5.4	2586 2587 6726
448103	hypothetical protein FLJ11362	AA968672	Hs.8929	5.4	3976 7878
436748	collagen, type VI, alpha 2	BE159107	Hs.159263	5.4	3212 7213
443883	serine (or cysteine) proteinase inhibit	AA114212	Hs.9930	5.4	3653 7614
433570	ESTs, Weakly similar to S55916 ribosoma	A1580053	Hs.109007	5.4	2988 7027
424905	NIMA (never in mitosis gene a)-related	NM_002497	Hs.1 53704	5.4	2022 2023 6315
452106	ESTs	A1141031	Hs.21342	5.4	4289 8131
422799	neuraxophilin 4	A1933199	Hs.120911	5.4	1738 6113
450755	ESTs	AA010984	Hs.159464	5.3	4190 8054
408901	hypothetical protein FLJ10468	AK001330	Hs.48855	5.3	272 273 4997
407756	ubiquitin specific protease 18	AA116021	Hs.38260	5.3	159 4903
423961	perostin (OSF-2os)	D13666	Hs.136348	5.3	1878 1879 6215
434669	core histone macroH2A2.2	AF151534	Hs.92023	5.3	3068 3069 7093
446839	mitotic spindle coiled-coil related pro	BE091926	Hs.16244	5.3	3873 7793
437162	thyroid hormone receptor coactivating p	AW005505	Hs.5464	5.3	3239 7237
450149	Zic family member 2 (odd-paired Drosoph	AW969781	Hs.132863	5.3	4136 8011
423354	calcium channel, voltage-dependent, alp	AB011130	Hs.127436	5.3	1798 1799 6157
452402	peroxisome proliferative activated rece	A1138530	Hs.22216	5.3	4327 8162
401621	NM_025193:Homo sapiens 3 beta-hydroxy-d			5.3	4656
408212	hypothetical protein	AA297567	Hs.43728	5.3	206 4945
447519	ESTs	U46258	Hs.339655	5.3	3936 7844
446674	solute carrier family 4 (anion exchange	AA563892	Hs.350401	5.3	3868 7788
438086	nuclear receptor subfamily 1, group I,	AA336519	Hs.83623	5.3	3300 7293
432154	ESTs	A1701523	Hs.112577	5.3	2846 6913
424949	core-binding factor, runt domain, alpha	AF052212	Hs.153934	5.3	2030 6321
421508	absent in melanoma 2	NM_004833	Hs.1 05115	5.3	1551 1552 5977
457060	beta tubulin 1, class VI	AA402364	Hs.303023	5.3	4538 8339
412926	macrophage myristoylated alanine-rich C	A1879076	Hs.75061	5.3	655 5290
456364	Homo sapiens, clone IMAGE:3163559, mRNA	AA234315	Hs.58093	5.3	4520 8324
448966	phosphoinositol 3-phosphate-binding pro	AW372914	Hs.86149	5.3	4053 7938
451811	hypothetical protein MGC1136	AA663485	Hs.8719	5.3	4259 8106
447425	acylphosphatase 1, erythrocyte (common)	A1963747	Hs.18573	5.3	3927 7836
406663	immunoglobulin heavy constant mu	U24683		5.3	39 40 4818
420596	polymerase (DNA directed), epsilon 2	NM_002692	Hs.9 9185	5.3	1467 1468 5917
434851	ESTs	AA806164	Hs.116502	5.3	3082 7103
422728	MAD (mothers against decapentaplegic, D	AW937826	Hs.103262	5.2	1729 6107
418827	HT021	BE327311	Hs.47166	5.2	1275 5770
440700	guanine nucleotide binding protein (G p	AW952281	Hs.296184	5.2	3481 7458
424223	putative DNA/chromatin binding motif	AJ243706	Hs.143323	5.2	1915 1916 6240
420301	paired box gene 5 (B-cell lineage speci	AA767526	Hs.22030	5.2	1442 5899
425348	cadherin-like 24	AL137477	Hs.155912	5.2	2091 2092 6364
406837	immunoglobulin kappa constant	R70292	Hs.156110	5.2	69 4836
432191	hypothetical protein, clone Telethon/lt	AA043193	Hs.273186	5.2	2851 6916
409625	sphingomyelin phosphodiesterase 2, neut	AI394338	Hs.55235	5.2	369 5066
410407	carbonic anhydrase IX	X66839	Hs.63287	5.2	460 461 5135
439653	hypothetical protein FLJ20373	AW021103	Hs.6631	5.2	3413 7396
401797	Target Exon			5.2	4663
443063	ESTs	A1031852	Hs.65239	5.2	3596 7564
415197	hypothetical protein TAJ-alpha	D82272	Hs.283615	5.2	919 5495
426215	stanniocalcin 2	AW963419	Hs.155223	5.2	2187 6430
400419	Target	AF084545		5.2	22 23 4626
435124	ESTs	AA725362	Hs.75514	5.2	3107 7125
416140	roundabout (axon guidance receptor, Dro	A1918035	Hs.301198	5.2	978 5545
407719	Homo sapiens mRNA for FLJ00065 protein, AW	963866	Hs.44021	5.2	152 4897
438115	ESTs	A1564020	Hs.122014	5.2	3304 7297
411251	HHGP protein	R19774	Hs.22835	5.2	520 5180
407910	fibronectin leucine rich transmembrane	AA650274	Hs.41296	5.2	180 4922
441362	RAD51 (S. cerevisiae) homolog (E coli R	BE614410	Hs.23044	5.2	3512 7486
433332	Homo sapiens clone TCCCTA00151 mRNA seq	AI367347	Hs.44898	5.2	2971 7012
432215	ribonucleotide reductase M1 polypeptide	AU076609	Hs.2934	5.2	2853 6918
417089	Homo sapiens cDNA: FLJ21909 fis, clone	H52280	Hs.18612	5.1	1077 5619
408495	ESTs	W68796	Hs.237731	5.1	232 4963
417222	hypothetical protein MGC2383	A1525424	Hs.42053	5.1	1089 5629
428977	cyclin B2	AK001404	Hs.194698	5.1	2496 6659
414011	asparagine synthetase	AA307680	Hs.75692	5.1	766 5377
436679	ESTs, Weakly similar to unnamed protein	A1127483	Hs.120451	5.1	3210 7211
431958	cadherin 3, type 1, P-cadherin (placent	X63629	Hs.2877	5.1	2834 2835 6904
422997	DNA replication factor	BE018212	Hs.122908	5.1	1766 6133
425322	protein kinase, DNA-activated, catalyti	U63630	Hs.155637	5.1	2089 2090 6363
432383	Homo sapiens cDNA FLJ20137 fis, clone C	AK000144	Hs.274449	5.1	2868 6931
424825	procollagen-lysine, 2-oxoglutarate 5-di	AF207069	Hs.153357	5.1	2005 2006 6302
423897	DKFZP434N178 protein	AB033062	Hs.134970	5.1	1863 1864 6205
407103	hypothetical protein MGC13170	AA424881	Hs.256301	5.1	110 4862
422765	baculoviral IAP repeat-containing 5 (su	AW409701	Hs.1578	5.1	1734 6110
431797	hypothetical protein FLJ20280	BE169641	Hs.270134	5.1	2822 6896
428752	ESTs	A1962660	Hs.98788	5.1	2469 6639

407192	gib:af12e02.s1 Soares_testis_NHT Homo sa	AA609200	Hs.366318	5.1	119 4871
435080	hypothetical protein FLJ14428	AB31760	Hs.155111	5.1	3103 7122
428479	cell division cycle 2, G1 to S and G2 t	Y00272	Hs.334562	5.1	2447 2448 6623
427820	inhibitor of DNA binding 2, dominant ne	BE222494	Hs.180919	5.1	2374 6563
403857	Target Exon			5.1	4730
448111	Interferon-induced protein with tetratr	AA053486	Hs.20315	5.1	3978 7880
416908	coagulation factor XIII, A1 polypeptide	AA333990	Hs.80424	5.1	1044 5594
426317	ESTs	AW022609	Hs.50745	5.1	2431 6610
434349	neurobeachin	NM_015678	Hs.3 821	5.1	3045 3046 7074
451752	KIAA1171 protein	AB032997	Hs.353087	5.1	4252 4253 8102
414132	ESTs	AB01235	Hs.48480	5.0	778 5387
404208	C6001282:gil4504223 ref NP_000172.1 gi			5.0	4740
444565	ESTs	W32889	Hs.154329	5.0	3707 7659
426919	ELAV (embryonic lethal, abnormal vision	ALD41228	Hs.166109	5.0	2284 6495
414245	WAS protein family, member 1	BE148072	Hs.75850	5.0	791 5399
447217	neuropilin 2	BE465754	Hs.17778	5.0	3904 7819
434629	glioma-amplified sequence-41	AA789081	Hs.4029	5.0	3064 7090
431689	UDP-Gal:betaGlcNAc beta 1,3-galactosylt	AA305688	Hs.267695	5.0	2810 6888
421875	ESTs	AA299607	Hs.98969	5.0	1606 6016
420164	ESTs	AW339037	Hs.349096	5.0	1423 5884
426788	SWI/SNF related, matrix associated, act	U66615	Hs.172280	5.0	2273 2274 6486
436574	ESTs	AW293527	Hs.126465	5.0	3202 7204
415052	mesenchyme homeo box 2 (growth arrest-s	NM_005924	Hs.77858	5.0	904 905 5485
406868	Immunoglobulin heavy constant gamma 3 (AA505445	Hs.300697	5.0	72 4839
433285	ESTs	AW975944	Hs.237396	5.0	2967 7008
412446	ESTs	AJ768015	Hs.352375	5.0	586 5235
404030	NM_015669*:Homo sapiens protocadherin b			5.0	4735
414359	cadherin 11, type 2, OB-cadherin (osteo	M62194	Hs.75929	5.0	808 5413
412507	EphA4	L36645	Hs.73964	5.0	596 597 5243
448524	hypothetical protein DKFZp762K2015	AB032948	Hs.21356	5.0	4012 4013 7908
420397	centrosomal protein 1	NM_007018	Hs.9 7437	5.0	1449 5904
419488	nucleophosmin/nucleoplasmin 3	AA316241	Hs.90691	5.0	1342 5822
459305	ESTs	AW007781	Hs.249858	5.0	4591 8387
429138	NS1-binding protein	AB020657	Hs.197298	5.0	2515 2516 6674
453511	AP-2 beta transcription factor	AL031224	Hs.33102	5.0	4422 4423 8244
443780	activating transcription factor 5	NM_012068	Hs.9 754	5.0	3643 3644 7606
415701	gamma-glutamyl hydrolase (conjugase, fo	NM_003878	Hs.78619	5.0	940 941 5514
453818	hypothetical protein FLJ13449	BE256832	Hs.10711	5.0	4443 8261
449230	melanoma cell adhesion molecule	BE613348	Hs.356392	5.0	4074 7956
408161	hypothetical protein MGC3032	AW952912	Hs.300383	5.0	195 4937
427337	Fc fragment of IgG, low affinity IIb,	Z46223	Hs.176663	5.0	2318 2319 6521
453271	ESTs	AA903424	Hs.6786	5.0	4409 8232
436291	protein regulator of cytokinesis 1	BE568452	Hs.344037	5.0	3180 7185
436477	ESTs	AA719989	Hs.107894	5.0	3191 7196
427747	serine/threonine kinase 12	AW411425	Hs.180655	4.9	2365 6557
418241	LIM domain only 1 (rhombotin 1)	M26682	Hs.1149	4.9	1207 1208 5722
458692	ESTs	BE549905	Hs.231754	4.9	4579 8376
428865	BarH-like homeobox 1	BE544095	Hs.164960	4.9	2485 6651
432715	ESTs, Weakly similar to KIAA1074 protei	AA247152	Hs.44566	4.9	2901 6959
437608	ESTs, Weakly similar to ALU1_HUMAN ALU	AA761605	Hs.292308	4.9	3274 7268
429493	ESTs	AL134708	Hs.145998	4.9	2573 6717
424408	collagen, type V, alpha 1	AJ754813	Hs.146428	4.9	1943 6260
424624	Ca2+-dependent activator protein for sec	AB032947	Hs.151301	4.9	1978 1979 6283
411263	kinesin-like 6 (mitotic centromere-asso	BE297802	Hs.69360	4.9	523 5182
417084	ESTs	H08370	Hs.57937	4.9	1076 5618
423811	homeo box C4	AW299598	Hs.50895	4.9	1854 6198
446142	ESTs	AJ754693	Hs.145968	4.9	3820 7748
413199	ELAV (embryonic lethal, abnormal vision	M62843	Hs.75236	4.9	687 688 5317
434175	ESTs	AW979081	Hs.165469	4.9	3032 7065
423673	matrix metalloproteinase 12 (macrophage	BE003054	Hs.1695	4.9	1837 6186
422938	centromere protein A (17kD)	NM_001809	Hs.1 594	4.9	1759 1760 6128
448498	ESTs	AA418276	Hs.375003	4.9	4007 7904
454033	homeo box HB9	AF107457	Hs.37035	4.9	4483 8292
414809	transferrin receptor (p90, CD71)	AJ434899	Hs.77356	4.9	873 5463
424415	enolase 2, (gamma, neuronal)	NM_001975	Hs.1 46580	4.9	1947 1948 6263
410711	KIAA0318 protein	AB002316	Hs.65746	4.9	489 490 5155
452724	cyclin E2	R84810	Hs.30464	4.9	4347 8179
419585	actin-like 6	T08459	Hs.259831	4.9	1359 5833
439453	thyroid hormone receptor Interactor 13	BE264974	Hs.6566	4.9	3399 7382
434355	ESTs	AA630865	Hs.186556	4.9	3049 7076
418203	CDC28 protein kinase 2	X54942	Hs.83758	4.9	1202 1203 5719
430552	nuclear autoantigenic sperm protein (h)	AA176374	Hs.243886	4.9	2709 6812
424954	tumor protein p53 (Li-Fraumeni syndrome	NM_000546	Hs.1 846	4.9	2031 2032 6322
446291	Interferon, gamma-inducible protein 30	BE397753	Hs.14623	4.8	3833 7760
448381	Homo sapiens mRNA; cDNA DKFZp434A1010 (D61580	Hs.21036	4.8	3996 7895
453884	KIAA0186 gene product	AA355925	Hs.36232	4.8	4460 8274
427407	ADP-ribosyltransferase (NAD; poly (ADP-	BE268649	Hs.177766	4.8	2326 6526
433202	KIAA1465 protein	AB040898	Hs.233335	4.8	2951 2952 6998
417911	chaperonin containing TCP1, subunit 6A	AA333387	Hs.82916	4.8	1166 5689
453883	cofactor required for Sp1 transcription	AJ638516	Hs.347524	4.8	4459 8273
406698	major histocompatibility complex, class	X03068	Hs.73931	4.8	51 52 4824
437007	ESTs, Weakly similar to I38022 hypothet	AA741300	Hs.202599	4.8	3230 7229
414341	KIAA0182 protein	D80004	Hs.75909	4.8	804 805 5410
452908	neuronal Shc adaptor homolog	AB001451	Hs.30965	4.8	4369 4370 8198
407811	cysteine knot superfamily 1, BMP antago	AW190902	Hs.40098	4.8	164 4908
446681	kendrin	AJ003624	Hs.15896	4.8	3869 7789

	448663	hypothetical protein MGC14797	BE614599	Hs.356501	4.8	4023 7915
	409529	Cdc42 guanine exchange factor (GEF) 9	AB007884	Hs.54697	4.8	355 356 5058
	406687	matrix metalloproteinase 11 (stromelysin)	M31126	Hs.352054	4.8	49 50 4823
5	401827	Target Exon			4.8	4664
	416801	sal (Drosophila)-like 2	X98834	Hs.79971	4.8	1032 5585
	409125	axonal transport of synaptic vesicles	R17268	Hs.343567	4.8	308 5024
	407785	ESTs, Weakly similar to A43932 mucin 2	AW207285	Hs.98279	4.8	160 4904
	400262	Eos Control		Hs.75309	4.8	4612
10	424878	ESTs	H57111	Hs.221132	4.8	2017 6311
	411089	cell division cycle 2-like 1 (PITSLRE p	AA456454	Hs.214291	4.8	513 5173
	450377	KIAA1265 protein	AB033091	Hs.355925	4.8	4160 4161 8029
	428293	solute carrier family 1 (neutral amino	BE250944	Hs.183556	4.8	2424 6605
	416111	chromatin assembly factor 1, subunit A	AA033813	Hs.79018	4.8	975 5542
	411296	growth suppressor 1	BE207307	Hs.10114	4.8	524 5183
15	405770	NM_002362:Homo sapiens melanoma antigen			4.8	4796
	436252	Homo sapiens cDNA FLJ11562 fis, clone H	AI539519	Hs.142827	4.8	3179 7184
	407871	ESTs	AA045368	Hs.98317	4.8	174 4917
	421524	GNF family receptor alpha 1	AA312082	Hs.105445	4.8	1556 5980
20	413670	hypothetical protein, expressed in oste	AB000115	Hs.75470	4.8	735 736 5352
	410261	schwannomin-interacting protein 1	AF145713	Hs.61490	4.8	439 440 5119
	433487	histone deacetylase 2	U31814	Hs.3352	4.8	2983 2984 7023
	431019	forkhead box G1B	NM_005249	Hs.2714	4.8	2740 2741 6834
	447321	Homo sapiens cDNA FLJ14028 fis, clone H	AW271217	Hs.281434	4.8	3915 7827
25	425308	receptor tyrosine kinase-like orphan re	M97639	Hs.155585	4.8	2087 2088 6362
	433013	actn 2 (conductin, actl)	AI697890	Hs.127337	4.8	2927 6979
	419682	paired-like homeodomain transcription f	H13139	Hs.92282	4.8	1368 5841
	431863	spindlin	AA188185	Hs.289043	4.8	2829 6901
	406311	NM_021979*:Homo sapiens heat shock 70kD			4.7	4803
30	405754	Target Exon			4.7	4795
	424078	paternally expressed 3	AB006625	Hs.139033	4.7	1893 1894 6225
	423011	adrenergic, alpha-2C-, receptor	NM_000683	Hs.1 23022	4.7	1767 1768 6134
	458933	RAN binding protein 1	AI638429	Hs.24763	4.7	4584 8381
	435523	membrane-spanning 4-domains, subfamily	T62849	Hs.11090	4.7	3131 7147
35	453990	ESTs	AW014847	Hs.233331	4.7	4478 8288
	408539	fibulin 1	AA421528	Hs.349607	4.7	237 4968
	417944	collagen, type V, alpha 2	AU077196	Hs.82985	4.7	1172 5693
	400235	NM_005336:Homo sapiens high density lip		Hs.177516	4.7	4604
40	410868	Homo sapiens cDNA FLJ11490 fis, clone H	T06529	Hs.98518	4.7	500 5163
	439452	B-cell CLL/lymphoma 11B (zinc finger pr	AA918317	Hs.57987	4.7	3398 7381
	451987	Homo sapiens cDNA FLJ14967 fis, clone T	AA815092	Hs.77554	4.7	4267 8114
	410781	ESTs	AI375672	Hs.165028	4.7	495 5159
	458207	U2 small nuclear ribonucleoprotein auxi	T28472	Hs.7655	4.7	4569 8366
	448633	tubulin, gamma 1	AA311426	Hs.21635	4.7	4021 7913
45	426287	calpain 6	AF029232	Hs.169172	4.7	2194 2195 6436
	430280	interleukin 7 receptor	AA361258	Hs.237868	4.7	2673 6787
	423449	ESTs	AI497900	Hs.57937	4.7	1808 6164
	414034	early development regulator 1 (homolog	U89277	Hs.305985	4.7	771 772 5381
	443715	cyclin E1	AI583187	Hs.9700	4.7	3638 7601
50	412006	ESTs	AW451618	Hs.380683	4.7	565 5217
	420162	cyclin-dependent kinase 4	BE378432	Hs.95577	4.7	1422 5883
	408660	ESTs, Moderately similar to PC4259 ferr	AA525775	Hs.89040	4.7	247 4977
	427701	nuclear autoantigenic sperm protein (hi	AA411101	Hs.243886	4.7	2362 6555
	410006	eukaryotic translation initiation facto	AW732308	Hs.57783	4.7	405 5095
55	411773	protease, serine, 21 (testisin)	NM_006799	Hs.7 2026	4.7	551 552 5206
	437597	SCG10-like-protein	AA730767	Hs.285753	4.7	3273 7267
	458079	Homo sapiens similar to RIKEN cDNA 2810	AI796870	Hs.381220	4.7	4566 8363
	425801	gb:HSC14H051 normalized infant brain cD	Z43151	Hs.343666	4.7	2144 6397
	428392	secretory granule, neuroendocrine prote	H10233	Hs.2265	4.7	2434 6613
60	443623	complement component 1, q subcomponent,	AA345519	Hs.9641	4.7	3631 7594
	443802	KIAA1291 protein	AW504924	Hs.9805	4.7	3647 7609
	449267	ESTs	AI638640	Hs.220624	4.7	4077 7959
	436703	RNA binding motif protein, X chromosome	AW880614	Hs.374352	4.7	3211 7212
	400991	Target Exon			4.7	4641
65	442573	branched chain aminotransferase 1, cyto	H93366	Hs.7567	4.7	3570 7541
	450296	hepatocyte growth factor-regulated tyro	AL041949	Hs.24756	4.7	4153 8023
	411962	gb:zk85d12.r1 Soares_pregnant uterus_Nb	AA099050		4.7	563 5215
	440516	cadherin 2, type 1, N-cadherin (neurona	S42303	Hs.161	4.7	3472 3473 7451
	429024	complement-c1q tumor necrosis factor-re	AI652297	Hs.119302	4.7	2502 6664
70	414561	Homo sapiens amino acid transport syste	AI064813	Hs.195155	4.7	831 5432
	402992	Target Exon			4.7	4700
	417312	leukemia-associated phosphoprotein p18	AW888411	Hs.250811	4.7	1095 5635
	437437	hypothetical protein DKFZp762L0311	AA226869	Hs.351623	4.7	3262 7257
	450534	KIAA0470 gene product	AI570189	Hs.25132	4.6	4175 8040
75	429183	KIAA0704 protein	AB014604	Hs.197955	4.6	2526 2527 6681
	421707	lectomedin-2	NM_014921	Hs.1 07054	4.6	1581 1582 5995
	433159	kinesin-like protein 2	AB035898	Hs.150587	4.6	2947 2948 6996
	408949	putative ribonuclease III	AF189011	Hs.49163	4.6	280 281 5003
	407366	gb:Homo sapiens cig33 mRNA, partial seq	AF026942	Hs.17518	4.6	137 4885
80	442932	bromodomain adjacent to zinc finger dom	AA457211	Hs.8858	4.6	3591 7559
	450336	Homo sapiens cDNA: FLJ23296 fis, clone	AA046814	Hs.288928	4.6	4155 8025
	448044	gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapie	AI458682		4.6	3972 7874
	445564	KIAA1034 protein	AB028957	Hs.12896	4.6	3784 3785 7718
	450356	KIAA1674	BE149824	Hs.132888	4.6	4156 8026
	406137	NM_000179*:Homo sapiens mutS (E. coli)			4.6	4802
85	423731	gb:EST06706 Infant Brain, Bento Soares	T08814	Hs.31599	4.6	1839 6188
	425003	apurinic/apyrimidinic endonuclease(APEX	AF119046	Hs.154149	4.6	2038 2039 6326

	405268	ENSP00000223174*:KIAA0783 PROTEIN.		4.6	4776
	408989	KIAA0746 protein	AW361666	Hs.49500	290 5010
	426400	Homo sapiens clone 25121 neuronal olfac	M78361	Hs.169743	2218 6452
5	423419	ESTs	R55336	Hs.23539	1806 6162
	453753	ubiquitin specific protease 1	BE252983	Hs.35086	4437 8256
	439070	ESTs	AJ733278	Hs.7621	3375 7358
	426095	ESTs	AJ278023	Hs.89986	2172 6419
	406076	Homo sapiens mRNA; cDNA DKFZp547P134 (f		4.6	4800
10	408393	ESTs	AW015318	Hs.143509	219 4953
	439246	membrane-associated tyrosine- and threo	AJ498072	Hs.351474	3386 7369
	435013	NM_020142:Homo sapiens NADH:ubiquinone	H91923	Hs.110024	3096 7115
	408190	ATPase, Class I, type 8B, member 2	AB032963	Hs.43577	197 198 4939
	426110	replication factor C (activator 1) 1 (1	NM_002913	Hs.1 66563	2174 2175 6421
15	420058	Homo sapiens cDNA FLJ10561 fis, clone	N AK001423	Hs.94694	1411 5874
	418045	ESTs	AJ972919	Hs.118837	1183 5701
	424005	vang (van gogh, Drosophila)-like 2	AB033041	Hs.137507	1883 1884 6218
	416209	MAD2 (mitotic arrest deficient, yeast,	AA236776	Hs.79078	982 5549
	453905	LIM domain kinase 1	NM_002314	Hs.3 6566	4462 4463 8276
	429986	sine oculis homeobox (Drosophila) homol	AF092047	Hs.227277	2632 2633 6759
20	414706	KIAA0097 gene product	AW340125	Hs.76989	854 5449
	435832	Bruno (Drosophila)-like 4, RNA binding	AA425688	Hs.41641	3155 7164
	429574	hypothetical protein MGC861	BE268321	Hs.208912	2580 6722
	424192	P311 protein	U30521	Hs.142827	1911 1912 6238
25	432101	EphA3	AJ918950	Hs.123642	2841 6909
	403650	dynein, cytoplasmic, light polypeptide		4.6	4726
	426118	polymerase (DNA directed), epsilon	AF128542	Hs.166846	2176 2177 6422
	435232	cyclin-dependent kinase inhibitor 2C (p	NM_001262	Hs.4 854	3114 3115 7132
	452017	prostate cancer associated protein 7	AF109302	Hs.27495	4270 8117
30	453922	budding uninhibited by benzimidazoles 1	AF053306	Hs.36708	4467 4468 8279
	423853	slit (Drosophila) homolog 1	AB011537	Hs.133466	1855 1856 6199
	442904	thymopoietin	AW575008	Hs.11355	3588 7556
	420911	O-linked N-acetylglucosamine (GlcNAc) t	U77413	Hs.100293	1491 1492 5934
	438833	ESTs	BE612940	Hs.88252	3358 7342
35	447284	hypothetical protein FLJ10204	AK001066	Hs.18029	3912 3913 7825
	452732	Homo sapiens, clone IMAGE:3535294, mRNA	BE300078	Hs.80449	4348 8180
	444170	ESTs	AW613879	Hs.102408	3683 7640
	435256	cytokine-like protein C17	AF193766	Hs.13872	3116 3117 7133
	422239	SMT3 (suppressor of mit two 3, yeast) h	AJ878922	Hs.180139	1662 6057
40	406836	immunoglobulin kappa constant	AW514501	Hs.156110	68 4835
	448985	carbonic anhydrase XI	AA324885	Hs.22777	4054 7939
	404632	NM_022490:Homo sapiens hypothetical pro		4.5	4754
	410768	Homo sapiens clone 23700 mRNA sequence	AF038185	Hs.66187	494 5158
	434862	ESTs	AA652272	Hs.197320	3084 7105
45	448772	L-tryptophan/alpha-aminoadipate aminotr	AW390822	Hs.380782	4035 7926
	418565	phosphoinositol 3-phosphate-binding pro	AK001529	Hs.86149	1256 1257 5756
	418607	KIAA1402 protein	AL137426	Hs.86392	1260 5759
	429455	CD209 antigen	AJ472111	Hs.278694	2563 6710
	447478	fibronectin type 3 and SPRY domain-cont	BE618843	Hs.28144	3932 7840
50	416640	neuron-specific protein	BE262478	Hs.13406	1019 5576
	452792	KIAA1344 protein	AB037765	Hs.30652	4351 4352 8183
	423181	ESTs	AA323415	Hs.278385	1779 6144
	444664	map kinase phosphatase-like protein MK-	N26362	Hs.11615	3711 7663
	429320	ESTs, Weakly similar to I78885 serine/t	AA449838	Hs.119334	2545 6697
55	422575	hypothetical protein FLJ20539	AK000546	Hs.118552	1705 1706 6089
	438293	stromal antigen 2	L08437	Hs.8217	3314 7305
	453096	ESTs	AW294631	Hs.351270	4391 8217
	452277	KIAA1223 protein	AL049013	Hs.28783	4308 8148
60	424927	hypothetical protein C321D2.4	AW973666	Hs.153850	2029 6320
	417576	phosphoribosylglycnamide formyltransfe	AA339449	Hs.82285	1134 5662
	440510	ESTs, Weakly similar to ISHUS protein	H08427	Hs.309165	3471 7450
	430066	signal recognition particle 72kD	AJ929659	Hs.237825	2647 6769
	422382	KIAA0166 gene product	D79988	Hs.115778	1674 1675 6066
	452461	transcription factor	N78223	Hs.108106	4333 8167
65	422684	H2A histone family, member Z	BE561617	Hs.119192	1726 6105
	416980	high-mobility group (nonhistone chromos	AA381133	Hs.80684	1054 5601
	414907	polo (Drosophila)-like kinase	X90725	Hs.77597	886 887 5472
	433706	ESTs	AW947250	Hs.151604	3001 7037
	417777	ESTs, Weakly similar to I78885 serine/t	AJ823763	Hs.7055	1156 5679
70	417731	polymerase (DNA directed), delta 3	D26018	Hs.82502	1152 1153 5676
	447417	KIAA1602 protein	AW732858	Hs.143067	3926 7835
	421302	neurtin	T34462	Hs.103291	1527 5962
	456940	ESTs	H46986	Hs.31881	4534 8336
	447250	protein phosphatase 1G (formerly 2C), m	AJ878909	Hs.17883	3906 7821
75	409139	ESTs, Highly similar to IRX1_HUMAN IROQ	AJ681917	Hs.3321	311 5026
	405326	Target Exon		4.5	4777
	400340	homeo box 11-like 2	AJ223798		12 13 4621
	433149	hypothetical protein HES6	BE257672	Hs.42949	2946 6995
	431301	ESTs	AA502384	Hs.151529	2773 6858
80	419131	ESTs	AA406293	Hs.109526	1306 5794
	412314	downstream of: G protein-coupled recept	AA825247	Hs.356084	581 5230
	414175	hypothetical protein DKFZp761D112	AJ308876	Hs.103849	786 5394
	431830	small inducible cytokine subfamily A (C	Y16645	Hs.271387	2827 2828 6900
	438937	ESTs	AW952654	Hs.73964	3367 7350
	418199	ESTs	AA884555	Hs.86603	1201 5718
85	440080	ESTs	AW051597	Hs.143707	3449 7431
	441020	ESTs	W79283	Hs.35962	3495 7471

	443725	growth arrest and DNA-damage-inducible, AW245680	Hs.9701	4.5	3639 7602
	425219	cytosolic ovarian carcinoma antigen 1 AF207881	Hs.155185	4.5	2067 2068 6347
	422128	gb:QV0-OT0033-010400-182-a07 OT0033 Hom AW881145	Hs.6456	4.5	1650 6047
5	454075	Kruppel-like zinc finger protein GLIS2 R43826	Hs.16313	4.5	4489 8297
	412432	ESTs AA126311	Hs.9879	4.4	585 6234
	406672	major histocompatibility complex, class M26041	Hs.198253	4.4	43 44 4820
	442328	ESTs, Weakly similar to ALU4_HUMAN ALU AI952430	Hs.150614	4.4	3556 7528
	414883	CDC28 protein kinase 1 AA926960	Hs.348669	4.4	885 5471
10	413004	interleukin enhancer binding factor 2, T35901	Hs.75117	4.4	667 5300
	424394	RNA binding motif protein, X chromosome BE277024	Hs.146381	4.4	1941 6258
	454561	hepatitis delta antigen-interacting protein AI984144	Hs.66713	4.4	4502 8308
	420129	ESTs AA255760	Hs.122994	4.4	1417 5879
	424410	ESTs W79027	Hs.271762	4.4	1944 6261
15	411562	hypothetical protein DKFZp586E1923 AL050201	Hs.70769	4.4	541 5198
	422516	multifunctional polypeptide similar to BE258862	Hs.117950	4.4	1694 6080
	452160	cysteine sulfinic acid decarboxylase-related BE378541	Hs.355568	4.4	4292 8134
	412659	olfactomedin related ER localized protein AW753865	Hs.74376	4.4	627 5265
	439239	ESTs AJ031540	Hs.235331	4.4	3385 7368
20	407896	Zic family member 1 (odd-paired Drosophila D76435	Hs.41154	4.4	176 177 4919
	408805	vaccinia related kinase 1 H69912	Hs.48269	4.4	262 4989
	414839	DNA (cytosine-5)-methyltransferase 1 X63692	Hs.77462	4.4	880 881 5467
	424451	protein tyrosine phosphatase, non-receptor M83738	Hs.147663	4.4	1955 1956 6269
	425368	cullin 4B AB014595	Hs.155976	4.4	2096 2097 6367
25	425159	carbamoyl-phosphate synthetase 2, aspartate NM_004341	Hs.154868	4.4	2059 2060 6341
	422795	KIAA1283 protein AB033109	Hs.375610	4.4	1736 1737 6112
	414725	ring finger protein 21, Interferon-response AA769791	Hs.350518	4.4	858 5452
	422244	karyopherin (importin) beta 3 Y08890	Hs.113503	4.4	1665 1666 6059
	454060	ephrin-A3 U14187	Hs.37054	4.4	4485 4486 8294
30	416507	transcription factor Dp-1 AL045364	Hs.79353	4.4	1009 5569
	430439	DKFZP434B061 protein AL133561	Hs.380155	4.4	2695 2696 6803
	429656	neurofilament, light polypeptide (68kD) X05608	Hs.211584	4.4	2598 2599 6733
	420174	ESTs AI824144	Hs.199749	4.4	1427 5887
	420440	mammaglobin 2 NM_002407	Hs.9 7644	4.4	1450 1451 5905
35	433211	MARK H11850	Hs.12808	4.4	2955 7000
	421102	protocadherin beta 6 AI470093	Hs.283085	4.4	1506 5945
	450746	general transcription factor II, I D82673	Hs.278589	4.4	4187 8051
	414733	minichromosome maintenance deficient (S BE514535	Hs.77171	4.4	860 5454
	426512	Meis1 (mouse) homolog AW511656	Hs.170177	4.4	2245 6469
40	414760	chromobox homolog 1 (Drosophila HP1) beta BE298063	Hs.77254	4.4	864 5457
	434256	ESTs AI378817	Hs.191847	4.4	3036 7068
	450553	hypothetical protein MGC3232 AW850613	Hs.8715	4.4	4176 8041
	449433	ESTs, Weakly similar to S26650 DNA-binding AI672096	Hs.9012	4.4	4086 7968
	430027	KIAA0980 protein AB023197	Hs.227743	4.4	2639 2640 6763
45	402861	Wilms' tumor 1-associating protein		4.4	4695
	449989	multiple endocrine neoplasia I U93237	Hs.240443	4.4	4124 4125 8002
	424616	intercellular adhesion molecule 5, tele U72671	Hs.151250	4.4	1975 1976 6281
	414528	ESTs AA148950	Hs.188836	4.4	828 5429
	414133	ESTs AW022188	Hs.109526	4.3	779 5388
50	411893	ESTs R82845	Hs.273789	4.3	558 5211
	410099	KIAA0036 gene product AA081630	Hs.167	4.3	421 5106
	422565	singed (Drosophila)-like (sea urchin family BE259035	Hs.118400	4.3	1701 6086
	410054	Homo sapiens cDNA: FLJ23005 fis, clone AL120050	Hs.58220	4.3	413 5101
	437330	Homo sapiens mRNA; cDNA DKFZp761J1112 (AL353944	Hs.50115	4.3	3253 7250
55	457986	Homo sapiens, clone IMAGE:4299555, mRNA AA781745	Hs.126920	4.3	4565 8362
	447660	ESTs AW160386	Hs.163667	4.3	3946 7853
	412800	polymerase (DNA directed), delta 2, region AW950852	Hs.74598	4.3	644 5281
	409326	choreoacanthocytosis gene; KIAA0986 pro AK000273	Hs.53542	4.3	340 5046
	437623	chromosome condensation-related SMC-ass D63880	Hs.5719	4.3	3275 3276 7269
60	426990	Homo sapiens mRNA for KIAA1750 protein, AL044315	Hs.173094	4.3	2293 6501
	405387	NM_022170: Homo sapiens Williams-Beuren		4.3	4779
	413644	ESTs, Weakly similar to Z195_HUMAN ZINC BE154910	Hs.278793	4.3	733 5350
	457313	transcriptional coactivator AF047002	Hs.241520	4.3	4544 4545 8345
	416084	deoxythymidylate kinase (thymidylate kinase L16991	Hs.79006	4.3	972 973 5540
65	429150	smoothed (Drosophila) homolog AF120103	Hs.197366	4.3	2519 2520 6677
	453028	RecQ protein-like 4 AB006532	Hs.31442	4.3	4381 4382 8209
	425776	parathyroid hormone receptor 2 U25128	Hs.159499	4.3	2138 2139 6394
	433895	mitogen-activated protein kinase kinase AI287912	Hs.3628	4.3	3014 7048
	435554	early B-cell factor AF208502	Hs.32425	4.3	3136 3137 7150
70	419356	hypothetical protein FLJ22316 AI656166	Hs.7331	4.3	1332 5815
	452744	Homo sapiens mRNA; cDNA DKFZp434E082 (AI267652	Hs.246107	4.3	4350 8182
	409703	2'-5'-oligoadenylate synthetase 3 (100 NM_006187	Hs.5 6009	4.3	381 382 5076
	408847	ESTs AW290997	Hs.190153	4.3	268 4993
	436114	ESTs, Highly similar to NRG3_HUMAN PRO- AA778232	Hs.19515	4.3	3171 7177
75	425870	ESTs R13406	Hs.56782	4.3	2153 6405
	433411	RNA binding motif protein 4 AI658666	Hs.352381	4.3	2975 7016
	443123	putative transcription regulation nucleotide AA094538	Hs.272808	4.3	3603 7570
	413431	ubiquitin-conjugating enzyme E2N (homolog AW246428	Hs.75355	4.3	715 5335
	414136	SMC2 (structural maintenance of chromosomes AA812434	Hs.119023	4.3	780 5389
80	443823	hypothetical protein BE089782	Hs.9877	4.3	3649 7611
	424560	protein predicted by clone 23733 AA158727	Hs.150555	4.3	1972 6279
	445139	synaptotagmin XIII AB037848	Hs.12365	4.3	3746 3747 7691
	403668	Target Exon		4.3	4727
	412672	chromodomain helicase DNA binding protein AA158910	Hs.74441	4.3	628 5266
85	410268	six transmembrane epithelial antigen of AA316181	Hs.61635	4.3	441 5120
	422175	ESTs, Highly similar to T00391 hypothetical N79885	Hs.6382	4.3	1657 6053
	440001	ESTs AI740721	Hs.128292	4.3	3445 7427

5	454104	hypothetical protein MGC2555	BE275031	Hs.158210	4.3	4491 8299
	417588	gb:HSC22D091 normalized infant brain cD Z44510			4.3	1135 5663
	412046	RAS-related on chromosome 22	Y07847	Hs.73088	4.3	567 568 5219
	400295	AI905687:IL-BT095-190199-019 BT095 Homo W72838	Hs.348419	4.3	6 4617	
	438407	eukaryotic translation Initiation facto	AI457122	Hs.129673	4.3	3320 7310
	420759	Homo sapiens cDNA FLJ11381 fis, clone H T11832	Hs.127797	4.3	1476 5922	
	442404	ESTs	AI733500	Hs.124370	4.3	3558 7530
	421878	Homo sapiens cDNA FLJ11643 fis, clone H AA299652	Hs.111496	4.3	1607 6017	
10	435420	ESTs	AA443966	Hs.31595	4.3	3187 7192
	421040	ESTs	AA715026	Hs.135280	4.3	1498 5938
	414242	dolichyl-phosphate (UDP-N-acetylglucosa	AA749230	Hs.143509	4.3	790 5398
	427961	ESTs	AW293165	Hs.143134	4.3	2388 6575
15	436251	nucleolar protein (KKE/D repeat)	BE515065	Hs.296585	4.3	3178 7183
	424026	ribosomal protein L34 pseudogene 1	AI798295	Hs.137576	4.3	1888 6221
	423803	PDZ-73 protein	NM_005709	Hs.1 32945	4.3	1852 1853 6197
	418661	E2F transcription factor 3	NM_001949	Hs.1 189	4.3	1264 1265 5762
	454340	gb:PMO-HT0339-081199-001-h05 HT0339 Hom	AW382767	Hs.122128 4.3	4496 8303	
	443950	epithelial membrane protein 3	NM_001425	Hs.9 999	4.3	3660 3661 7621
20	448057	RAB39	BE300105	Hs.301853	4.3	3973 7875
	402260	NM_001436*:Homo sapiens fibrillarin (FB			4.3	4676
	412651	ESTs	AA115333	Hs.107968	4.3	625 5263
	421846	protein kinase C substrate 80K-H	AA017707	Hs.1432	4.3	1601 6012
	439053	chaperonin containing TCP1, subunit 2 (BE244588	Hs.6456	4.3	3374 7357
25	416565	endoplasmic reticulum resident protein	AW000960	Hs.44970	4.3	1015 5573
	434792	ESTs	AA649253	Hs.132458	4.3	3075 7099
	439512	Homo sapiens, clone IMAGE:3163559, mRNA	AA418287	Hs.58093	4.3	3403 7386
	426867	ESTs	AA460967	Hs.22668	4.3	2282 6493
	443674	ESTs	AI081330	Hs.40510	4.3	3635 7598
30	431374	CTP synthase	BE258532	Hs.251871	4.3	2778 6862
	428309	cellular retinoic acid-binding protein	M97815	Hs.183650	4.3	2427 2428 6608
	452046	KIAA0802 protein	AB018345	Hs.27657	4.3	4275 4276 8120
	413273	stem-loop (histone) binding protein	U75679	Hs.75257	4.3	693 694 5321
	429984	hypothetical protein FLJ21617	AL050102	Hs.227209	4.3	2630 2631 6758
35	453880	ESTs, Weakly similar to I38022 hypothe	AI803166	Hs.135121	4.3	4458 8272
	417866	collagen, type XI, alpha 1	AW067903	Hs.82772	4.3	1162 5685
	427495	Homo sapiens cDNA FLJ11333 fis, clone P	AI799104	Hs.178705	4.3	2335 6533
	417061	Homo sapiens cDNA FLJ12033 fis, clone H	AI675944	Hs.188691	4.3	1068 5612
	446849	cleavage and polyadenylation specific f	AU076617	Hs.16251	4.2	3874 7794
40	400250	Eos Control		Hs.3352	4.2	4608
	429918	ESTs	AW873986	Hs.119383	4.2	2619 6748
	448390	hypothetical protein	AL035414	Hs.21068	4.2	3999 7897
	433234	KIAA1495 protein	AB040928	Hs.65366	4.2	2961 2962 7005
	412795	special AT-rich sequence binding protei	BE241753	Hs.74592	4.2	643 5280
45	422830	hypothetical protein DKFZp434P0111	AC007954	Hs.121371	4.2	1746 1747 6118
	421937	hematological and neurological expresse	AI878857	Hs.109706	4.2	1617 6024
	427716	karyopherin (importin) beta 1	L38951	Hs.180446	4.2	2363 2364 6556
	402330	Target Exon			4.2	4678
	412939	eukaryotic translation elongation facto	AW411491	Hs.75069	4.2	657 5292
50	449436	hypothetical protein DKFZp434I2117	AA860329	Hs.279307	4.2	4087 7969
	420582	Homo sapiens chromosome 19, cosmid	R283 BE047878	Hs.99093	4.2	1464 5915
	413313	glycyl-tRNA synthetase	NM_002047	Hs.2 93885	4.2	699 700 5325
	406534	Target Exon			4.2	4809
	422173	phorbol-in-like protein MDS019 (CEM15)	BE385828	Hs.250619	4.2	1656 6052
55	417037	antigen identified by monoclonal antibo	BE083936	Hs.80976	4.2	1063 5608
	418583	hypothetical protein	AA604379	Hs.86211	4.2	1259 5758
	418196	KIAA1708 protein	AI745649	Hs.26549	4.2	1199 5716
	429399	ESTs	AA452244	Hs.16727	4.2	2556 6705
	450172	signal transduction protein (SH3 contai	NM_005864	Hs.2 4587	4.2	4139 4140 8014
60	446627	hypothetical protein SBB148	AI973016	Hs.15725	4.2	3862 7783
	418956	KIAA0788 protein	AA234831	Hs.348493	4.2	1287 5778
	438626	ESTs	AI198059	Hs.26370	4.2	3342 7328
	419335	hypothetical protein FLJ12888	AW960146	Hs.284137	4.2	1330 5813
	444153	hypothetical protein FLJ10748	AK001610	Hs.10414	4.2	3680 3681 7638
65	421949	G8 protein	N47378	Hs.109798	4.2	1620 6026
	417410	PC4 and SFRS1 interacting protein 1	AF063020	Hs.82110	4.2	1114 1115 5651
	438662	cleavage and polyadenylation specific f	AA223599	Hs.6351	4.2	3345 7330
	454390	KIAA0906 protein	AB020713	Hs.56966	4.2	4497 4498 8304
	430130	Homo sapiens mRNA; cDNA DKFZp761G02121	AL137311	Hs.234074 4.2	2650 2651 6772	
70	425966	cyclin F	NM_001761	Hs.1 973	4.2	2158 2159 6409
	430030	lectin, galactoside-binding, soluble, 1	BE300094	Hs.227751	4.2	2641 6764
	436045	DKFZP564O0423 protein	AB037723	Hs.5028	4.2	3169 3170 7176
	429250	tryptophan rich basic protein	H56585	Hs.198308	4.2	4541 6688
	428099	ESTs	AA421288	Hs.149025	4.2	2397 6583
75	408932	TP53TG3 protein	AW594172	Hs.278513	4.2	277 5000
	434371	KIAA1283 protein	AA631362	Hs.120866	4.2	3050 7077
	412723	hypothetical protein AF301222	AA648459	Hs.335951	4.2	634 5271
	445162	piccolo (presynaptic cytomatrix protein	AB011131	Hs.12376	4.2	3749 3750 7693
	410211	zinc finger protein	NM_014347	Hs.2 96365	4.2	431 432 5114
80	420230	forkhead box C1	AL034344	Hs.284186	4.2	1434 1435 5893
	458300	ribosomal protein L31	AW580932	Hs.164170	4.2	4572 8370
	432618	hypothetical protein MGC2705	AA557284	Hs.172330	4.2	2893 6952
	416224	reticulocalbin 2, EF-hand calcium bindi	NM_002902	Hs.7 9088	4.2	983 984 5550
	421917	KIAA1020 protein	AB028943	Hs.109445	4.2	1612 1613 6021
	456759	delta (Drosophila)-like 3	BE259150	Hs.127792	4.2	4528 8331
85	404420	C8001064*:g[1]6754928[ref][NP_035989.1] o			4.2	4748
	426981	KIAA0530 protein	AL044675	Hs.173081	4.2	2292 6500

	419900	ESTs	AI469960	Hs.170598	4.2	1392 5860
	420028	carbohydrate (N-acetylglucosamine-6-O)	AB014680	Hs.8786	4.2	1408 1409 5872
	408633	PRO2000 protein	AW963372	Hs.222088	4.2	245 4975
5	440716	ESTs	AW105245	Hs.307082	4.2	3485 7461
	440491	ESTs, Weakly similar to 2109260A B cell	R35252	Hs.130558	4.2	3468 7447
	425848	vaiyl-IRNA synthetase 2	BE242709	Hs.159637	4.2	2150 6402
	413097	ankyrin repeat-containing protein	BE383876	Hs.75196	4.2	681 5312
	424649	embryonic ectoderm development	BE242035	Hs.151461	4.2	1983 6286
10	408621	chromosome 11 open reading frame 8	AI970672	Hs.46638	4.2	244 4974
	445255	synaptosomal-associated protein, 91 kDa	NM_014841	Hs.1 2477	4.2	3753 3754 7696
	406648	major histocompatibility complex, class	AA563730	Hs.277477	4.2	38 4817
	424130	Homo sapiens mRNA; cDNA DKFZp586L141 (f AL050136	Hs.140945	4.2	1903 6232	
	438253	hypothetical protein from EUROIMAGE 210	X65230	Hs.38004	4.2	3311 3312 7303
	413010	transcription factor 6-like 1 (mitochon	AA393273	Hs.75133	4.2	668 5301
15	430390	KIAA0969 protein	AB023186	Hs.343666	4.2	2686 2687 6797
	441495	ESTs	AW294603	Hs.127039	4.2	3521 7494
	452256	Homo sapiens cDNA FLJ10071 fis, clone	H AK000933	Hs.28661	4.2	4306 8146
	423198	cell division cycle 25A	M81933	Hs.1634	4.2	1780 1781 6145
20	431393	ESTs, Highly similar to cytokine recept	AW971493	Hs.134269	4.2	2780 6864
	418283	cathepsin K (pseudodysostosis)	S79895	Hs.83942	4.2	1210 1211 5724
	447078	ESTs	AW885727	Hs.9914	4.2	3888 7805
	443698	hypothetical protein FLJ12529	AW961106	Hs.169100	4.2	3636 7599
	436957	ESTs	AA902488	Hs.122952	4.2	3228 7227
25	443898	Sec61 gamma	AW804296	Hs.9950	4.2	3655 7616
	432265	SCG10-like-protein	BE382679	Hs.285753	4.1	2860 6924
	400205	NM_006265*:Homo sapiens RAD21 (S. pombe		Hs.81848	4.1	4598
	441478	ESTs, Weakly similar to I38022 hypothet	AW957372	Hs.46791	4.1	788 5396
	435593	DKFZP586J1624 protein	R88872	Hs.4964	4.1	3141 7153
30	402233	NM_030760*:Homo sapiens endothelial dif			4.1	4674
	409200	KIAA0076 gene product	AL042914	Hs.51039	4.1	325 5037
	408772	ESTs	W88532	Hs.254562	4.1	256 4985
	438930	hypothetical protein AL110115	AW843633	Hs.343261	4.1	3366 7349
	441749	ESTs	AW450805	Hs.199316	4.1	3536 7508
35	411395	KIAA1802 protein	AA889673	Hs.7542	4.1	532 5190
	441094	MYC-associated zinc finger protein (pur	U33819	Hs.7647	4.1	3497 3498 7473
	453896	KIAA1853 protein	AW293483	Hs.255205	4.1	4461 8275
	446073	hypothetical protein MGC5508	BE261001	Hs.13662	4.1	3818 7746
	408056	ephrin-A4	AA312329	Hs.42331	4.1	188 4930
40	430200	geminin	BE613337	Hs.234896	4.1	2658 6777
	408547	ESTs	AA574291	Hs.57837	4.1	238 4969
	408433	ras-related C3 botulinum toxin substrat	AW162931	Hs.45002	4.1	221 4955
	443837	spindle pole body protein	AI984625	Hs.9884	4.1	3650 7612
	436415	proliferation-associated 2G4, 38kD	BE265254	Hs.343258	4.1	3186 7191
45	427087	uncharacterized hypothalamus protein HT	BE073913	Hs.173515	4.1	2301 6508
	409596	KIAA0410 gene product	BE244200	Hs.90421	4.1	364 5063
	441955	ESTs	AA972327	Hs.368431	4.1	3543 7515
	445674	transcription factor CA150	BE410347	Hs.13063	4.1	3790 7722
	412620	ESTs	T58171	Hs.12253	4.1	617 5258
50	429617	B-cell CLL/lymphoma 7A	X89984	Hs.211563	4.1	2589 2590 6728
	441742	ESTs, Highly similar to A59266 unconven	H21075	Hs.31802	4.1	3534 7506
	414280	zyxin	BE410769	Hs.75873	4.1	796 5403
	423062	ESTs	NM_003655	Hs.5 637	4.1	1774 1775 6140
	452092	hypothetical protein FLJ11210	BE245374	Hs.27842	4.1	4285 8128
55	413048	mannose receptor, C type 1	M93221	Hs.75182	4.1	672 673 5305
	450785	Homo sapiens, alpha-1 (VI) collagen	AA852713	Hs.108885	4.1	4193 8056
	419594	topoisomerase (DNA) II binding protein	AA013051	Hs.91417	4.1	1360 5834
	450705	Iroquois homeobox protein 2A (IRX-2A)	U90304	Hs.25351	4.1	4185 4186 8050
	411078	CocOA/Crisp	AI222020	Hs.182364	4.1	512 5172
60	419452	PTK7 protein tyrosine kinase 7	U33635	Hs.90572	4.1	1340 1341 5821
	446215	SH3 domain binding glutamic acid-rich p	AW821329	Hs.14368	4.1	3825 7753
	449969	Homo sapiens cDNA FLJ14337 fis, clone P	AW295142	Hs.180187	4.1	4123 8001
	437762	synaptotagmin I	T78028	Hs.154679	4.1	3284 7277
	421931	gamma-aminobutyric acid (GABA) A recept	NM_000814	Hs.1440	4.1	1615 1616 6023
65	411943	ESTs, Weakly similar to S44608 C02F5.6	BE502436	Hs.7962	4.1	562 5214
	410160	ESTs	AI124557	Hs.368306	4.1	427 5111
	448072	ESTs	AI459306	Hs.349096	4.1	3974 7876
	418154	nuclear receptor subfamily 1, group I,	BE165866	Hs.352403	4.1	1197 5714
	409869	GDP dissociation inhibitor 1	BE259015	Hs.74576	4.1	393 5085
70	444759	ESTs	AW105011	Hs.371157	4.1	3721 7671
	422599	non-metastatic cells 1, protein (NM23A)	BE387202	Hs.118638	4.1	1710 6092
	421753	ATP-binding cassette, sub-family B (MDR	BE314828	Hs.107911	4.1	1587 5999
	405516	ENSP00000200457*:Thyroid receptor inter			4.1	4785
	454024	hypothetical protein FLJ23403	AA993527	Hs.293907	4.1	4481 8290
75	416959	ubiquitin-conjugating enzyme E2A (RAD6	D28459	Hs.80612	4.1	1050 1051 5599
	452187	transcription factor Dp-2 (E2F dimeriza	AA400200	Hs.379018	4.1	4293 8135
	449568	KIAA1598 protein	AL157479	Hs.23740	4.1	4096 7977
	453173	KIAA0442 protein	AB007902	Hs.32168	4.1	4397 4398 8223
	414702	cell division cycle 34	L22005	Hs.76932	4.1	852 853 5448
80	427857	hypothetical protein FLJ22865	AL133017	Hs.288679	4.1	2377 6566
	423589	ESTs	AA328082	Hs.361361	4.1	1822 6175
	448186	Homo sapiens cDNA FLJ14208 fis, clone N	AA262105	Hs.4094	4.1	3982 7883
	426269	Homo sapiens mRNA; cDNA DKFZp566A1046 (H15302	Hs.168950	4.1	2190 6433
	431192	ESTs, Weakly similar to SP62_HUMAN SPLI	AI670056	Hs.137274	4.1	2759 6847
	417164	heterogeneous nuclear ribonucleoprotein	AA338283	Hs.81361	4.1	1087 5627
85	436639	fibroblast growth factor 9 (glia-activa	D14838	Hs.111	4.1	3207 3208 7209
	434775	ESTs	AA648983	Hs.370514	4.1	3074 7098

448807	ESTs	AI571940	Hs.7549	4.1	4041 7930
442990	hypothetical protein MGC11321	AA197226	Hs.19347	4.1	3592 7560
424756	lamin B receptor	AW504657	Hs.152931	4.0	1997 6296
449458	ESTs	AI805078	Hs.208261	4.0	4089 7971
438203	ESTs	BE540090	Hs.7345	4.0	3308 7300
416737	LIM domain protein	AF154335	Hs.79691	4.0	1028 1029 5582
447397	E-1 enzyme	BE247676	Hs.18442	4.0	3923 7833
417871	ESTs	AA521368	Hs.24252	4.0	1163 5686
452063	ESTs, Weakly similar to TWST_HUMAN TWIS	R53185	Hs.32366	4.0	4281 8124
437987	mel transforming oncogene (derived from	BE277414	Hs.5947	4.0	3294 7287
417259	chondroitin sulfate proteoglycan 2 (ver	AW903838	Hs.81800	4.0	1092 5632
421057	Homo sapiens cDNA: FLJ22063 fis, clone	T58283	Hs.120638	4.0	1501 5940
416188	v-myc avian myelocytomatosis viral onco	BE157260	Hs.79070	4.0	979 5546
448950	CGI-152 protein	AF288687	Hs.9275	4.0	4050 4051 7936
418385	Homo sapiens, clone IMAGE:3357127, mRNA	AW590613	Hs.301040	4.0	1225 5734
431431	Human DNA sequence from clone RP3-403A1	AL096711	Hs.118744	4.0	2784 6868
423662	B-cell CLL/lymphoma 11A (zinc finger pr	AK001035	Hs.130881	4.0	1835 1836 6185
430287	ESTs, Weakly similar to LEU5_HUMAN LEUK	AW182459	Hs.125759	4.0	2676 6790
449281	hypothetical protein MGC15668	AI808699	Hs.162717	4.0	4078 7960
441551	ESTs	AA318224	Hs.296141	4.0	3524 7497
438501	phosphoinositol 3-phosphate-binding pro	Z44110	Hs.86149	4.0	3328 7318
443262	interleukin enhancer binding factor 3,	AF167570	Hs.256583	4.0	3613 3614 7580
451999	DEAD/H (Asp-Glu-Ala-Asp/His) box polype	AW176401	Hs.380623	4.0	4268 8115
424441	H2A histone family, member X	X14850	Hs.147097	4.0	1952 1953 6267
414493	retinoblastoma-binding protein 2	AL133921	Hs.76272	4.0	826 5427
424720	SWI/SNF related, matrix associated, act	M89907	Hs.152292	4.0	1990 1991 6292
422326	eukaryotic translation initiation facto	AI114875	Hs.78592	4.0	1672 6064
448196	hypothetical protein FLJ10520	BE543313	Hs.77510	4.0	3983 7884
401153	Target Exon			4.0	4645
433180	K562 cell-derived leucine-zipper-like p	AB038651	Hs.31854	4.0	2949 2950 6997
435931	RNA binding motif protein 9	AI077464	Hs.351478	4.0	3163 7171
428677	troponin I, cardiac	AI657119	Hs.351582	4.0	2462 6634
447898	6.2 kd protein	AW969638	Hs.380920	4.0	3966 7868
419752	ESTs, Moderately similar to ZN91_HUMAN	AA249573	Hs.152618	4.0	1386 5854
413254	isocitrate dehydrogenase 3 (NAD) gamma	U40272	Hs.75253	4.0	691 692 5320
439490	ESTs, Weakly similar to A46302 PTB-asso	AW249197	Hs.100043	4.0	3401 7384
433808	ART-4 protein	NM_014062	Hs.3 566	4.0	3005 3006 7041
418327	paired-like homeodomain transcription f	U70370	Hs.84136	4.0	1217 1218 5729
416283	vascular endothelial growth factor C	NM_005429	Hs.7 9141	4.0	985 986 5551
432974	ESTs	BE348793	Hs.233331	4.0	2919 6973
426423	single-stranded-DNA-binding protein	NM_012446	Hs.1 69833	4.0	2222 2223 6455
435937	ESTs	AA830893	Hs.119769	4.0	3164 7172
447082	thioredoxin-like	T85314	Hs.54629	4.0	3889 7806
423896	ESTs	AA332216	Hs.130584	4.0	1862 6204
424176	hypothetical protein	AL137273	Hs.142307	4.0	1909 1910 6237
437464	Homo sapiens mRNA; cDNA DKFZp547J047	(f AA323296	Hs.97837	4.0	3266 7261
427472	transposon-derived Buster3 transposase-	AA522539	Hs.131250	4.0	2333 6531
437546	T-box 1	AW074836	Hs.173984	4.0	3270 7264
414682	Inhibitor of DNA binding 3, dominant ne	AL021154	Hs.76884	4.0	844 845 5443
446566	membrane-spanning 4-domains, subfamily	H95741	Hs.17914	4.0	3857 7778
413433	transcription factor 4	NM_003199	Hs.3 26198	4.0	716 717 5336
449349	hypothetical protein FLJ21939 similar t	AI825386	Hs.381224	4.0	4083 7965
413408	DEAD/H (Asp-Glu-Ala-Asp/His) box polype	R51793	Hs.1440	4.0	714 5334
413823	ESTs	AI341417	Hs.29408	4.0	747 5362
409995	ESTs	AW960597	Hs.129206	4.0	402 5093
435466	G protein beta subunit-like	BE619165	Hs.29203	4.0	3128 7144
409392	ESTs	AA973020	Hs.59710	4.0	346 5050
435557	ESTs, Moderately similar to I54374 gene	AA864704	Hs.67197	4.0	3138 7151
422436	KIAA0756 protein	AB018299	Hs.13349	4.0	1682 1683 6071

TABLE 6B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Pkey	CAT Number	Accession
429163	1238297_1	AW974271 AA592975 AA447312 AA884766
411962	2307710_1	AA099050 AA099526 T47733
448044	1111791_1	AW867082 AI458682 H24240 R18426 R14537
417588	33114_3	R24958 Z44510 T82024 R00714

TABLE 6C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402994	2996643	Minus	4727-4969
406367	9256126	Minus	58313-58489
401621	8570184	Minus	193-608
401797	6730720	Plus	6973-7118
403857	7708910	Minus	2524-3408

	404208	3080468	Minus	105346-105573
	404030	7671252	Plus	149362-151749
	401827	2262095	Plus	94725-94860,98452-98660
5	405770	2735037	Plus	61057-62075
	406311	9211559	Minus	137114-139033
	405754	3688349	Plus	19448-19610,20242-20699
	400991	8096825	Plus	159197-159320
	402992	7767907	Minus	42137-42515
10	406137	9166422	Minus	30487-31058
	405268	4156151	Minus	24404-24521
	406076	9123123	Plus	89972-90319
	403650	8705512	Plus	71272-71414
	404632	9796668	Plus	45096-45229
15	405326	4375975	Plus	10633-10709,30805-30893,38078-38253,5511
	402861	2814366	Minus	14933-15231,15387-15627
	405387	6587915	Minus	3769-3833,5708-5895
	403668	7259739	Plus	39942-40150
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
20	402330	4464283	Minus	15325-15380,15484-15588,15842-15915
	406534	7711477	Plus	40463-40586,41191-41336,41856-41986,4300
	404420	7407952	Minus	129817-130586
	402233	7690102	Plus	90281-91477
	405516	9454624	Plus	112707-112876,113676-113854
25	401153	9438289	Plus	30582-30801

TABLE 7A

30	Pkey:	Unique Eos probeset identifier number
	Gene name:	Unigene gene title
	Accession:	Exemplar Accession number, Genbank accession number
	UniGene:	Unigene number
	RATIO:	95th percentile of soft tissue sarcoma AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator
35	SEQ ID #:	nucleic acid and protein sequences provided on CD for search purposes

	Pkey	Gene Name	Accession	UniGene	RATIO	SEQ ID #
	413778	myosin, light polypeptide 2, regulatory	AA090235	Hs.75535	45.0	740 5356
	428087	troponin C2, fast	AA100573	Hs.182421	42.8	2396 6582
40	407245	titin	X90568	Hs.172004	42.7	132 133 4881
	425545	Homo sapiens, clone MGC:12401, mRNA, co	N98529	Hs.158295	34.0	2114 6379
	426752	titin	X69490	Hs.172004	34.0	2266 2267 6482
	409601	keratin 1 (epidermolytic hyperkeratosis)	AF237621	Hs.80828	32.2	365 366 5064
45	412519	troponin T1, skeletal, slow-	AA196241	Hs.73980	31.6	598 5244
	406704	myosin, heavy polypeptide 7, cardiac mu	M21665	Hs.929	29.8	55 56 4826
	409169	(clone PWHLC2-24) myosin light chain 2	F00991	Hs.50889	29.3	316 5029
	428221	ATPase, Ca transporting, cardiac muscle	U96781	Hs.183075	28.0	2408 2409 6592
	400440	nebulin	X83957	Hs.83870	26.0	24 25 4627
50	422633	enolase 3, (beta, muscle)	X56832	Hs.118804	25.7	1716 1717 6098
	407013	gb:Human nebulin mRNA, partial cds	U35637	Hs.83870	25.5	94 95 4851
	422867	cartilage oligomeric matrix protein (ps	L32137	Hs.1584	25.1	1751 1752 6122
	406706	myosin, heavy polypeptide 1, skeletal m	X03740	Hs.231581	24.8	59 60 4828
	417070	titin	Z19077	Hs.172004	24.6	1070 5614
55	424687	matrix metalloproteinase 9 (gelatinase	J05070	Hs.151738	23.6	1986 1987 6289
	426300	delta-like homolog (Drosophila)	U15979	Hs.169228	22.3	2196 2197 6437
	406707	myosin, heavy polypeptide 2, skeletal m	S73840	Hs.931	22.2	61 62 4829
	412129	troponin T3, skeletal, fast	M21984	Hs.73454	22.1	571 572 5222
	431204	cytochrome c oxidase subunit Via polype	F28841	Hs.250760	21.4	2760 6848
60	422640	troponin C, slow	M37984	Hs.118845	21.0	1718 1719 6099
	421296	perilipin	NM_002666	Hs.1 03253	20.3	1525 1526 5861
	416931	adipose most abundant gene transcript 1	D45371	Hs.80485	19.9	1047 1048 5597
	418205	troponin I, skeletal, fast	L21715	Hs.83760	19.5	1204 1205 5720
	405001	interleukin enhancer binding factor 1			19.4	4767
65	441134	cellular retinoic acid-binding protein	W29092	Hs.346950	19.4	3500 7475
	410621	titin	AA194329	Hs.172004	19.3	481 5149
	421773	ESTs	W69233	Hs.112457	18.7	1588 6000
	420139	lipase, hormone-sensitive	NM_005357	Hs. 95351	18.4	1419 1420 5881
	417153	collagen, type II, alpha 1 (primary ost	X57010	Hs.81343	17.9	1084 1085 5625
70	422069	titin-cap (teletthin)	AJ010063	Hs.343603	17.9	1635 1636 6037
	417435	carbonic anhydrase III, muscle specific	NM_005181	Hs.8 2129	17.2	1121 1122 5655
	427899	serum amyloid A1	AA829286	Hs.336462	17.1	2384 6571
	452838	preferentially expressed antigen in mel	U65011	Hs.30743	16.9	4357 4358 8188
	410223	calsequestrin 1 (fast-twitch, skeletal	S73775	Hs.60708	16.8	433 434 5115
75	408591	mammaglobin 1	AF015224	Hs.46452	16.6	241 242 4972
	446523	sarcolipin	NM_003063	Hs.3 34629	16.4	3852 3853 7774
	418533	myosin-binding protein C, fast-type	NM_004533	Hs.8 5937	16.3	1253 1254 5764
	420197	ESTs, Weakly similar to A57291 cytokine	AW139647	Hs.88134	16.1	1429 5889
	416373	ESTs, Weakly similar to S12658 cysteine	AA195845	Hs.73680	16.1	996 5559
	404977	Insulin-like growth factor 2 (somatomed			16.0	4766
80	424688	myosin, light polypeptide 3, alkali; ve	AA216287	Hs.1815	16.0	1988 6290
	431205	tropomodulin 4 (muscle)	AA194560	Hs.250763	15.8	2761 6849
	418391	troponin I, skeletal, slow	NM_003281	Hs.8 4673	15.5	1228 1229 5736
	409096	sarcomeric muscle protein	AA194412	Hs.50550	15.2	302 5019
85	403088	NM_003319:Homo sapiens titin (TTN), mR			15.1	4707
	424982	phosphorylase, glycogen; muscle (McArdl U94777		Hs.351580	15.1	2036 2037 6325
	447205	ESTs, Moderately similar to T17372 plas	BE617015	Hs.11006	14.9	3900 7816

5	418390	titin immunoglobulin domain protein (my	AF133820	Hs.84665	14.8	1226 1227 5735
	421566	early growth response 2 (Krox-20 (Dros	NM_000399	Hs.1 395	14.7	1563 1564 5984
	406964	FGFES predicted novel secreted protein	M21305		14.5	87 88 4847
	429359	matrix metalloproteinase 14 (membrane-l	W00482	Hs.2399	14.5	2551 6702
	419138	ryanodine receptor 1 (skeletal)	U48508	Hs.89631	13.9	1309 1310 5796
	431360	loricrin	NM_000427	Hs.2 51680	13.9	2776 2777 6861
	419648	thyroid hormone responsive SPOT14 (rat)	T73661	Hs.91877	13.8	1366 5839
	427666	calmodulin-like skin protein (CLSP)	A1791495	Hs.180142	13.7	2356 6550
10	431089	ESTs, Weakly similar to unknown protein	BE041395	Hs.374629	13.7	2745 6838
	426429	myosin-binding protein C, slow-type	X73114	Hs.169849	13.6	2224 2225 6456
	439496	Homo sapiens, Similar to RIKEN cDNA 111	BE616501	Hs.32343	13.5	3402 7385
	408493	phosphoglycerate mutase 2 (muscle)	BE206854	Hs.46039	13.4	231 4962
	420783	lectin, galactoside-binding, soluble, 7	_A1659838	Hs.99923	13.3	1478 5924
15	400499	C10001858:gil6679124[ref]NP_032759.1	n		13.3	4628
	407102	glycerol-3-phosphate dehydrogenase 1 (s	AA007629	Hs.348601	13.2	109 4861
	422424	prostate differentiation factor	A186431	Hs.296638	13.2	1681 6070
	424399	A1905687:IL-BT095-190199-019 BT095	Homo A1905687	Hs.348419	12.9	1942 6259
	417389	midkine (neurite growth-promoting facto	BE260964	Hs.82045	12.8	1109 5647
20	430411	bone gamma-carboxyglutamate (gla) prote	X51699	Hs.2558	12.7	2691 2692 6800
	437206	ESTs, Weakly similar to I38344 titin, c	AW975934	Hs.172004	12.6	3245 7242
	434352	small muscle protein, X-linked	AF129505	Hs.86492	12.6	3047 3048 7075
	430681	ESTs	AW969675	Hs.291232	12.5	2719 6819
25	453857	Ras-induced senescence 1 (RIS1)	AL080235	Hs.35861	12.5	4449 4450 8266
	445263	KIAA1560 protein	H57646	Hs.42586	12.4	3755 7697
	429973	ESTs	A423317	Hs.164680	12.4	2628 6756
	406687	matrix metalloproteinase 11 (stromelysi	M31126	Hs.352054	12.3	49 50 4823
	414152	thrombospondin 4	NM_003248	Hs.7 5774	12.2	782 783 5391
	446619	secreted phosphoprotein 1 (osteopontin,	AU076643	Hs.313	12.2	3861 7782
30	429997	apolipoprotein B mRNA editing enzyme, c	NM_006789	Hs.2 27457	12.2	2636 2637 6761
	403593	Target Exon			12.1	4725
	444381	hypothetical protein BC014245	BE387335	Hs.283713	12.1	3697 7652
	419050	adenosine monophosphate deaminase 1 (is	NM_000036	Hs.89570	12.1	1293 1294 5784
	416378	ankyrin repeat domain 2 (stretch respon	AW044467	Hs.73708	12.1	997 5560
35	427809	tipoprotein lipase	M26380	Hs.180878	12.0	2373 6562
	450701	hypothetical protein XP_098151 (leucine	H39960	Hs.288467	11.7	4183 8048
	408915	heptacellular carcinoma novel gene-3 pr	NM_016651	Hs.4 8950	11.6	274 275 4998
	453331	ESTs	AI240665	Hs.352537	11.6	4413 8236
	436519	myozenin	AJ278124	Hs.238756	11.5	3196 3197 7200
40	418072	Human DNA sequence from clone RP3-353C1	F35210	Hs.86507	11.5	1190 5707
	443727	ESTs	Z25389	Hs.18459	11.4	3640 7603
	417866	collagen, type XI, alpha 1	AW067903	Hs.82772	11.3	1162 5685
	446921	small inducible cytokine subfamily A (C	AB012113	Hs.16530	11.3	3878 3879 7797
	408536	ESTs	AW381532	Hs.135188	11.1	236 4967
45	411102	triadin	AA401295	Hs.23926	11.1	515 5175
	416349	myomesin (M-protein) 2 (165kD)	X69089	Hs.79227	11.1	991 992 5556
	418399	hypothetical protein FLJ12442	AF131781	Hs.84753	10.9	1232 1233 5738
	444329	hypothetical protein FLJ12921	W73753	Hs.209637	10.8	3693 7648
	443514	ESTs	BE464288	Hs.25475	10.8	3624 7588
50	416559	ESTs	AI039195	Hs.128060	10.8	1012 5571
	419875	proenkephalin	AA853410	Hs.93557	10.7	1391 5859
	429259	Plakophilin	AA420450	Hs.380088	10.7	2535 6689
	417308	KIAA0101 gene product	H60720	Hs.81892	10.7	1094 5634
	409944	four and a half LIM domains 3	BE297925	Hs.57687	10.7	399 5090
55	400651	ENSP0000228031::COPPER CHAPERONE FOR S			10.7	4636
	428769	ESTs	AW207175	Hs.105771	10.6	2470 6640
	418678	cancer/testis antigen (NY-ESO-1)	NM_001327	Hs.8 7225	10.5	1269 1270 5765
	450787	aquaporin 7	AB006190	Hs.25475	10.4	4194 4195 8057
	418054	lysyl oxidase-like 2	NM_002318	Hs.8 3354	10.4	1184 1185 5702
60	401781	Target Exon			10.4	4662
	428405	cholinergic receptor, nicotinic, alpha	Y00762	Hs.2266	10.3	2436 2437 6615
	409178	kallikrein 5	BE393948	Hs.50915	10.3	319 5032
	410687	lysyl oxidase-like 1	U24389	Hs.65436	10.2	485 486 6153
	425292	37 kDa leucine-rich repeat (LRR) protei	NM_005824	Hs.1 55545	10.2	2083 2084 6359
65	413011	biglycan	AW068115	Hs.821	10.1	669 5302
	427335	G antigen 7B	AA448542	Hs.278444	10.1	2317 6520
	422887	ESTs	AI751848	Hs.49215	10.1	1755 6124
	432874	melanoma inhibitory activity	W94322	Hs.279651	10.0	2913 6968
	419741	ubiquitin carrier protein E2-C	NM_007019	Hs.9 3002	10.0	1379 1380 5850
70	418004	aldehyde dehydrogenase 3 family, member	U37519	Hs.87539	9.9	1174 1175 5695
	419301	tenomodulin protein	AA236166	Hs.132957	9.9	1328 5811
	442117	ESTs; hypothetical protein for IMAGE:44	AW664964	Hs.128899	9.9	3551 7523
	422060	ESTs, Moderately similar to ALU5_HUMAN	R20893	Hs.325823	9.9	1633 6035
	437330	Homo sapiens mRNA; cDNA DKFZp761J1112 (AL353944	Hs.50115	9.9	3253 7250
75	417515	ataxia-telangiectasia group D-associate	L24203	Hs.82237	9.9	1129 1130 5659
	408202	DKFZP586L151 protein	AA227710	Hs.43658	9.9	202 4942
	428471	stratifin	X57348	Hs.184510	9.9	2445 2446 6622
	411021	titin	F00055	Hs.172004	9.8	508 5169
	428848	leptin (murine obesity homolog)	NM_000230	Hs.1 94236	9.8	2481 2482 6649
80	421512	myomegalin	AB007923	Hs.265848	9.8	1554 1555 5979
	456115	titin	F01082	Hs.172004	9.8	4515 8320
	446962	muscle specific ring finger protein 1	AI351421	Hs.279709	9.7	3884 7801
	417405	ESTs	W28657	Hs.5307	9.7	1112 5649
	426600	VEGF nerve growth factor inducible	NM_003378	Hs.1 71014	9.6	2255 2256 6475
85	450375	a disintegrin and metalloproteinase dom	AA009647	Hs.352537	9.6	4159 8028
	420067	Homo sapiens mRNA; cDNA DKFZp564O222 (I	TS2431	Hs.94795	9.6	1414 5876
	421823	ESTs	N40850	Hs.28625	9.6	1600 6011

	431211	gap junction protein, beta 2, 26kD (con	M86849	Hs.323733	9.6	2762 2763 6850
	431830	small inducible cytokine subfamily A (C	Y16645	Hs.271387	9.4	2827 2828 6900
	423961	perostin (OSF-2os)	D13666	Hs.136348	9.4	1878 1879 6215
5	409028	Z-band alternatively spliced PDZ-motif	AB014513	Hs.49998	9.4	296 297 5015
	421552	secreted frizzled-related protein 4	AF026692	Hs.105700	9.4	1559 1560 5982
	429892	myomesin 1 (skelemin) (185kD)	NM_003803	Hs.2 504	9.4	2614 2615 6745
	429500	hexabrachion (tenascin C, cytactin)	X78565	Hs.289114	9.4	2574 2575 6718
	416982	creatine kinase, mitochondrial 2 (sarco	J05401	Hs.80691	9.3	1055 1056 5602
10	418156	nuclear receptor subfamily 1, group I,	W17056	Hs.83623	9.3	1198 5715
	434449	hypothetical protein FLJ22041 similar t	AW953484	Hs.3849	9.3	3057 7083
	435370	ESTs	AI864074	Hs.225838	9.2	3120 7136
	420208	silver (mouse homolog) like	BE276055	Hs.95972	9.2	1431 5891
	422871	collagen, type XI, alpha 2	AL031228	Hs.121509	9.2	1753 1754 6123
15	401780	NM_005557*Homo sapiens keratin 16 (loc			9.1	4661
	438089	nuclear receptor subfamily 1, group I,	W05391	Hs.351546	9.1	3301 7294
	422311	cytokine receptor-like factor 1	AF073515	Hs.114948	9.0	1669 1670 6062
	429134	ESTs	AA446953	Hs.99004	9.0	2514 6673
	445234	ESTs	AW137636	Hs.146059	9.0	3751 7694
20	427639	Homo sapiens, clone MGC:18257, mRNA, co	AW444530	Hs.350860	9.0	2353 6547
	428748	Ksp37 protein	AW593206	Hs.98785	8.9	2468 6638
	412560	CCR4-NOT transcription complex, subunit	R24601	Hs.350495	8.9	602 5248
	418140	microfibrillar-associated protein 2	BE613836	Hs.83551	8.9	1196 5713
	428698	KIAA1866 protein	AA852773	Hs.334838	8.9	2463 6635
25	411789	Adican	AF245505	Hs.72157	8.9	553 554 5207
	434326	reticulin 2	NM_005619	Hs.3 803	8.9	3043 3044 7073
	420798	keratin 10 (epidermolytic hyperkeratosis)	W93774	Hs.99936	8.9	1479 5925
	430713	eukaryotic translation elongation facto	AA351647	Hs.2642	8.8	2726 6824
	451681	ESTs, Weakly similar to AA64_HUMAN 64	K Z28564	Hs.255950	8.8	4245 8097
	424408	collagen, type V, alpha 1	AI754813	Hs.146428	8.8	1943 6260
30	428305	cartilage linking protein 1	AA446628	Hs.2799	8.7	2426 6607
	414482	endothelin receptor type A	S57498	Hs.76252	8.7	824 825 5426
	428957	WNT1 inducible signaling pathway protei	NM_003881	Hs.1 94679	8.7	2491 2492 6656
	412472	ESTs	AW975398	Hs.293836	8.7	593 5240
35	410001	kallikrein 11	AB041036	Hs.57771	8.7	403 404 5094
	428398	ESTs	AI249368	Hs.98558	8.7	2435 6614
	418113	SRY (sex determining region Y)-box 4	AI272141	Hs.83484	8.7	1194 5711
	428289	complement component 2	M26301	Hs.2253	8.7	2421 2422 6603
	411296	growth suppressor 1	BE207307	Hs.10114	8.7	524 5183
40	438091	nuclear receptor subfamily 1, group I,	AW373062	Hs.351546	8.6	3302 7295
	436555	ESTs, Weakly similar to 2003319A ankyri	AI972007	Hs.304646	8.6	3200 7202
	410079	glycogenin 2	U94362	Hs.380757	8.6	418 419 5104
	419550	KIAA0128 protein; septin 2	D50918	Hs.90998	8.6	1348 1349 5827
	452023	KIAA1173 protein	AB032999	Hs.27566	8.6	4271 4272 8118
45	415989	ESTs	AI267700	Hs.351201	8.6	962 5530
	424086	lysyl oxidase	AI351010	Hs.102267	8.5	1896 6227
	422511	collagen, type XVII, alpha 1	AU076442	Hs.117938	8.5	1692 6078
	412326	small inducible cytokine A3 (homologous	R07566	Hs.73817	8.5	582 5231
	416783	monocyte to macrophage differentiation-	AA206186	Hs.79889	8.5	1031 5584
50	413554	secretogranin II (chromogranin C)	AA319146	Hs.75426	8.5	729 5346
	407112	ESTs, Weakly similar to ALU7_HUMAN ALU	AA070801	Hs.51615	8.5	111 4863
	418064	S100 calcium-binding protein, beta (neu	BE387287	Hs.83384	8.5	1188 5705
	406673	major histocompatibility complex, class	M34996	Hs.198253	8.5	90 91 4821
	416658	fibrillin 2 (congenital contractural ar	U03272	Hs.79432	8.5	1020 1021 5577
55	435101	ESTs	AI743156	Hs.131064	8.5	3106 7124
	424800	MyoD family inhibitor	AL035588	Hs.153203	8.4	2002 2003 6300
	420103	aldehyde dehydrogenase 1 family, member	AA382259	Hs.95197	8.4	1416 5878
	414219	ALL-1-fused gene from chromosome 1q	W20010	Hs.75823	8.3	789 5397
	420813	prolactin-induced protein	X51501	Hs.99949	8.3	1482 1483 5927
60	423044	protocadherin 18	AA320829	Hs.97266	8.3	1772 6138
	418026	fatty acid binding protein 4, adipocyte	BE379727	Hs.83213	8.3	1179 5698
	433430	ESTs	AI863735	Hs.369982	8.3	2977 7018
	409633	ESTs	AW449822	Hs.55200	8.3	371 5068
	443426	chromosome 20 open reading frame 1	AF098158	Hs.9329	8.3	3621 3622 7586
65	445537	EGF-like-domain, multiple 6	AJ245671	Hs.12844	8.2	3780 3781 7716
	411852	ESTs, Weakly similar to T00329 hypothet	AA528140	Hs.107515	8.2	555 5208
	445016	reelin	U79716	Hs.12246	8.2	3738 3739 7684
	415672	ESTs	N53097	Hs.193579	8.2	937 5511
	408349	homeo box C10	BE546947	Hs.44276	8.1	213 4949
70	456063	retinol-binding protein 4, interstitial	NM_006744	Hs.7 6481	8.1	4511 4512 8317
	422087	matrix metalloproteinase 2 (gelatinase	X58968	Hs.111301	8.1	1641 6040
	423778	flavin containing monooxygenase 2	Y09267	Hs.132821	8.1	1846 1847 6193
	413902	CD36 antigen (collagen type I receptor,	AU076743	Hs.75613	8.1	752 5366
	449722	cyclin B1	BE280074	Hs.23960	8.1	4112 7990
75	423024	ESTs, Moderately similar to ALU5_HUMAN	AA593731	Hs.325823	8.1	1770 6136
	449048	similar to S68401 (cattle) glucose indu	Z45051	Hs.22920	8.1	4061 7945
	421690	calbindin 2, (29kD, calretinin)	AW162667	Hs.106857	8.0	1580 5994
	409103	XAGE-1 protein	AF251237	Hs.112208	8.0	304 305 5021
	426991	Homo sapiens cDNA FLJ10674 fis, clone	N AK001536	Hs.214410	8.0	2294 6502
80	457869	Homo sapiens, alpha-1 (VI) collagen	AU077186	Hs.108885	8.0	4561 8359
	450300	ESTs, Highly similar to ITH4_HUMAN INTE	AL041440	Hs.58210	8.0	4154 8024
	452862	ADAMTS2 (a disintegrin-like and metal	AW378065	Hs.8687	8.0	4360 8190
	403071	NM_003319*Homo sapiens titin (TTN), mR			8.0	4702
	412719	ESTs	AW016610	Hs.816	8.0	633 5270
85	447377	transcription factor AP-2 alpha	X77343	Hs.334334	7.9	3920 3921 7831
	430686	desmoglein 1	NM_001942	Hs.2 633	7.9	2721 2722 6821
	425397	topoisomerase (DNA) II alpha (170kD)	J04088	Hs.156346	7.9	2099 2100 6369

	452620	ESTs	AA436504	Hs.119286	7.9	4338 8172
	423575	intron of perostin (OSF-2os)	C18863	Hs.163443	7.9	1820 6173
	453817	ESTs	AW755253	Hs.379636	7.9	4442 8260
	442082	calyculin-2	R41823	Hs.7413	7.8	3550 7522
5	442376	Homo sapiens cDNA FLJ12228 fis, clone M W95588	Hs.129982	7.8	3557 7529	
	423739	ESTs	AA398155	Hs.97600	7.8	1842 6190
	440042	ESTs	AI073387	Hs.133898	7.8	3448 7430
	435523	membrane-spanning 4-domains, subfamily T62849	Hs.11090	7.8	3131 7147	
10	431048	cell death-inducing DFFA-like effector	R50253	Hs.249129	7.8	2742 6835
	409632	serine (or cysteine) proteinase inhibit	W74001	Hs.55279	7.8	370 5067
	417689	KIAA0128 protein; septin 2	AA828347	Hs.90998	7.8	1148 5673
	422148	histidine-rich calcium-binding protein	M60052	Hs.1480	7.7	1651 1652 6048
	433447	neuronal pentraxin II	U29195	Hs.3281	7.7	2980 2981 7021
	423201	growth hormone receptor	NM_000163	Hs.125180	7.7	1782 1783 6146
15	443071	complement component 1, q subcomponent,	AL080021	Hs.8986	7.7	3598 7566
	425071	deiodinase, iodothyronine, type II	NM_013989	Hs.154424	7.7	2043 2044 6330
	419407	hypothetical protein FLJ21276	AW410377	Hs.41502	7.7	1334 5817
	420212	calcium channel, voltage-dependent, L1	NM_000069	Hs.1294	7.6	1432 1433 5892
20	439688	hypothetical protein FLJ12921	AW445181	Hs.209637	7.6	3418 7401
	445033	cyclin-dependent kinase inhibitor 2B (p	AV652402	Hs.72901	7.6	3740 7685
	454140	hypothetical protein FLJ10474	AB040888	Hs.41793	7.6	4493 4494 8301
	414443	platelet-derived growth factor receptor	AI077268	Hs.76144	7.5	817 5421
	415702	gb:HSPD18414 HM3 Homo sapiens cDNA clon F28877	Hs.73680	7.5	942 5515	
25	421335	ARS component B	X99977	Hs.103505	7.5	1529 1530 5964
	417333	bromodomain and PHD finger containing,	AL157545	Hs.173179	7.5	1096 5636
	439755	B7 homolog 3	AW748482	Hs.77873	7.5	3430 7413
	407604	collagen, type VIII, alpha 2	AW191962	Hs.353001	7.5	145 4891
	412140	RAB6 Interacting, kinesin-like (rakline	AA219691	Hs.73625	7.5	573 5223
30	412473	ESTs	F23393	Hs.153060	7.5	594 5241
	414386	haploglobin	X00442	Hs.75990	7.5	810 811 5415
	424734	ESTs	AI217685	Hs.96844	7.5	1992 6293
	409327	collagen, type IX, alpha 3	L41162	Hs.53563	7.5	341 342 5047
	413566	sprouty (Drosophila) homolog 4	AW604451	Hs.381153	7.5	730 5347
35	420202	putative lymphocyte G0/G1 switch gene	AL036557	Hs.95910	7.5	1430 5890
	414821	Fc fragment of IgG, high affinity Ia, r	M63835	Hs.77424	7.5	876 877 5465
	418045	ESTs	AI972919	Hs.118837	7.5	1183 5701
	417849	nidogen 2	AW291587	Hs.82733	7.4	1161 5684
	444301	asporin (LRR class 1)	AK000136	Hs.10760	7.4	3691 3692 7647
40	422627	transforming growth factor, beta-induce	BE336857	Hs.118787	7.4	1715 6097
	406664	glycerol-3-phosphate dehydrogenase 1 (s	L34041	Hs.348601	7.4	83 84 4819
	417900	CDC20 (cell division cycle 20, S. cerev	BE250127	Hs.82906	7.4	1165 5688
	415655	ESTs	W05433	Hs.352293	7.4	932 5506
	403081	NM_003319*:Homo sapiens titin (TTN), mR			7.4	4704
	417045	Homo sapiens ORF1	F01180	Hs.332030	7.4	1066 5610
45	414002	FBJ murine osteosarcoma viral oncogene	NM_006732	Hs.75678	7.4	763 764 5375
	413132	protein kinase (cAMP-dependent, catalyt	NM_006823	Hs.75209	7.3	683 684 5314
	453392	SRX (sex determining region Y)-box 11	U23752	Hs.32964	7.3	4416 4417 8239
	438746	Human melanoma-associated antigen p97 (AI885815	Hs.184727	7.3	3353 7337
50	407228	hemoglobin, beta	M25079	Hs.155376	7.3	124 125 4876
	409142	SMC4 (structural maintenance of chromos	AL136877	Hs.50758	7.3	312 313 5027
	421458	carbohydrate (keratan sulfate Gal-6) su	NM_003654	Hs.104576	7.3	1543 1544 5972
	411000	ESTs, Weakly similar to S38383 SEB4B pr	N40449	Hs.201619	7.3	505 5167
	425234	ESTs, Weakly similar to I38022 hypothet	AW152225	Hs.165909	7.3	2070 6349
55	422168	S100 calcium-binding protein A7 (psoria	AA586894	Hs.112408	7.3	1654 6050
	433122	ESTs	AB019391	Hs.58049	7.3	2941 6991
	414085	aldehyde dehydrogenase 1 family, member	AA114016	Hs.75746	7.3	775 5384
	420376	protocadherin 18	AL137471	Hs.97266	7.3	1447 1448 5903
	443021	Ig superfamily protein	AA368546	Hs.8904	7.3	3593 7561
60	400295	AI905687:IL-BT095-190199-019 BT095 Homo	W72838	Hs.348419	7.3	6 4617
	457411	iroquois-class homeobox protein IRX2	AW085961	Hs.130093	7.3	4549 8349
	439285	hypothetical protein FLJ20093	AL133916	Hs.47860	7.3	3389 7372
	428981	ESTs, Weakly similar to ALU2_HUMAN ALU	BE313077	Hs.93135	7.2	2497 6660
	421155	lysyl oxidase	H87879	Hs.102267	7.2	1512 5950
65	431553	cartilage linking protein 1	X78075	Hs.2799	7.2	2792 6874
	414175	hypothetical protein DKFZp761D112	AI308876	Hs.103849	7.2	786 5394
	421143	immunoglobulin superfamily containing I	AB024536	Hs.102171	7.2	1510 1511 5949
	407619	collagen, type IX, alpha 2	AL050341	Hs.37165	7.2	146 147 4892
	412978	homeo box C6	AI431708	Hs.820	7.2	665 5298
70	428824	ESTs	W23624	Hs.173059	7.2	2477 6645
	422048	spondin 2, extracellular matrix protein	NM_012445	Hs.288126	7.2	1631 1632 6034
	407788	S100 calcium-binding protein A2	BE514982	Hs.38991	7.2	161 4905
	447499	protocadherin beta 16	AW262580	Hs.147674	7.2	3934 7842
	417376	LIM protein (similar to rat protein kin	AA253314	Hs.154103	7.2	1107 5645
	459702	gb:an03c03.x1 Stratagene schizo brain S	AI204995		7.2	4596 8393
75	407172	gb:ya92c05.s1 Stratagene placenta (9372	T54095	Hs.379019	7.2	117 4869
	452701	glutamine-fructose-6-phosphate transami	NM_005110	Hs.30332	7.1	4345 4346 8178
	426509	pentaxin-related gene, rapidly induced	M31166	Hs.2050	7.1	2243 2244 6468
	401203	Target Exon			7.1	4647
	438549	trinucleotide repeat containing 3	BE386801	Hs.21858	7.1	3331 7320
80	437898	ESTs	W81260	Hs.43410	7.1	3293 7286
	408988	Homo sapiens clone TUA8 Cri-du-chat reg	AL119844	Hs.49476	7.1	289 5009
	430699	ESTs, Weakly similar to RET2_HUMAN RET1	AW969847	Hs.292718	7.1	2723 6822
	452683	progesterone membrane binding protein	AI089575	Hs.374574	7.1	4341 8175
	425682	ribosomal protein L3-like	NM_005061	Hs.159191	7.1	2122 2123 6385
85	409361	sine oculis homeobox (Drosophila) homol	NM_005982	Hs.54416	7.1	344 345 5049
	439979	hypothetical protein FLJ10430	AW600291	Hs.6823	7.1	3442 7424

	432191	hypothetical protein, clone Telethon/lt	AA043193	Hs.273186	7.0	2851 6916
	450098	hypothetical protein FLJ21080	W27249	Hs.8109	7.0	4134 8009
	419745	slug (chicken homolog), zinc finger pro	AF042001	Hs.93005	7.0	1381 1382 5851
	433001	clone HQ0310 PRO0310p1	AF217513	Hs.279905	7.0	2923 2924 6977
5	437395	hypothetical protein DKFZp762M136	AL365408	Hs.351747	7.0	3258 3259 7254
	449969	Homo sapiens cDNA FLJ14337 fis, clone P	AW295142	Hs.180187	7.0	4123 8001
	450447	hypothetical protein P15-2	AF212223	Hs.25010	7.0	4168 4169 8036
	412104	Homo sapiens, Similar to RIKEN cDNA 221	AW205197	Hs.240951	7.0	569 5220
	425154	collagen, type IX, alpha 1	NM_001851	Hs.1 54850	7.0	2055 2056 6339
10	421579	stem cell growth factor; lymphocyte sec	NM_002975	Hs.1 05927	7.0	1567 1568 5987
	414359	cadherin 11, type 2, OB-cadherin (osteo	M62194	Hs.75929	7.0	808 5413
	418532	neurotrophic tyrosine kinase, receptor,	F00797	Hs.374321	7.0	1252 5753
	445417	a disintegrin-like and metalloprotease	AK001058	Hs.12680	6.9	3766 7705
	412577	CD163 antigen	Z22968	Hs.74076	6.9	608 609 5252
15	432239	matrix metalloproteinase 13 (collagenas	X81334	Hs.2936	6.9	2856 2857 6921
	409007	Homo sapiens mRNA; cDNA DKFZp434G0827	(AL122107	Hs.49599	6.9	292 5012
	452392	comeodesmosin	L20815	Hs.507	6.9	4323 4324 8160
	437275	ESTs, Weakly similar to A47582 B-cell g	AW976035	Hs.292396	6.9	3251 7248
	414831	protein kinase, cAMP-dependent, regulat	M31158	Hs.77439	6.9	878 879 5466
20	419631	popeye protein 3	AW188117	Hs.356642	6.9	1365 5838
	447033	Predicted gene: Eos cloned; secreted w/	AI357412	Hs.167601	6.9	3885 7802
	416431	titin	AW384459	Hs.172004	6.9	1003 5565
	426369	Kreisler (mouse) maf-related leucine zi	AF134157	Hs.169487	6.9	2213 2214 6448
	417074	guanidinacetate N-methyltransferase	Z49878	Hs.81131	6.9	1071 1072 5615
25	426310	neuropeptide Y receptor Y1	NM_000909	Hs.1 69266	6.9	2199 2200 6439
	439751	Homo sapiens mRNA full length insert cD	AA196090	Hs.50794	6.9	3428 7411
	429441	lipophilin B (uteroglobin family member	AJ224172	Hs.204096	6.9	2560 2561 6708
	437191	serine protease inhibitor, Kazal type,	NM_006846	Hs.3 31555	6.9	3241 3242 7239
	417079	Interleukin 1 receptor antagonist	U65590	Hs.81134	6.9	1073 1074 5616
30	400419	Target	AF084545		6.8	22 23 4626
	414812	monokine induced by gamma interferon	X72755	Hs.77367	6.8	874 875 5464
	415657	ESTs	F32261	Hs.133004	6.8	934 5508
	409041	Hypothetical protein, XP_051860 (KIAA11	AB033025	Hs.50081	6.8	299 300 5017
	427747	serine/threonine kinase 12	AW411425	Hs.180655	6.8	2365 6557
35	442432	hypothetical protein FLJ23468	BE093589	Hs.38178	6.8	3563 7535
	453859	myogenic factor 6 (herculin)	NM_002469	Hs.3 5937	6.8	4451 4452 8267
	407711	KIAA1808 protein	AI085846	Hs.25522	6.8	151 4896
	450506	fibroblast activation protein, alpha	NM_004460	Hs.4 18	6.8	4170 4171 8037
40	421307	Homo sapiens mRNA; cDNA DKFZp434B0425	(BE539976	Hs.103305	6.8	1528 5963
	433235	contactin 3 (plasmacytoma associated)	AB040929	Hs.35089	6.8	2963 2964 7006
	452401	tumor necrosis factor, alpha-induced pr	NM_007115	Hs.2 9352	6.8	4325 4326 8161
	449238	muscle-specific RING-finger protein 3	AA428229	Hs.331561	6.8	4075 7957
	449717	cerebral cell adhesion molecule	AB040935	Hs.23954	6.8	4110 4111 7989
	428722	tissue inhibitor of metalloproteinase 4	U76456	Hs.190787	6.8	2464 2465 6636
45	418506	Unknown protein for MGC:29643 (formerly	AA084248	Hs.372651	6.8	1247 5748
	451497	Wnt inhibitory factor-1	H83294	Hs.284122	6.8	4235 8089
	410929	ESTs	H47233	Hs.30643	6.8	504 5166
	418728	ESTs	AW970937	Hs.293843	6.8	1271 5766
	451917	Homo sapiens unknown mRNA	AW391351	Hs.50820	6.8	4261 8108
50	450390	Human DNA sequence from clone RP11-234G	N93227	Hs.348805	6.8	4163 8031
	452363	Homo sapiens, Similar to complement com	AI582743	Hs.94953	6.7	4322 8159
	448719	trinucleotide repeat containing 3	AA033627	Hs.21858	6.7	4028 7920
	408486	sodium channel, voltage-gated, type IV,	L04236	Hs.46038	6.7	228 229 4960
	412755	ESTs, Weakly similar to P4HA_HUMAN PROL	BE144306	Hs.179891	6.7	637 5274
55	417944	collagen, type V, alpha 2	AU077196	Hs.82985	6.7	1172 5693
	422386	heparan sulfate (glucosamine) 3-O-sulfo	AF105374	Hs.115830	6.7	1676 1677 6067
	415656	ESTs	W84346	Hs.84673	6.7	933 5507
	424162	ESTs, Weakly similar to ALU2_HUMAN ALU	AA336229	Hs.93135	6.7	1907 6235
	403087	NM_003319; Homo sapiens titin (TTN), mR			6.7	4706
60	424420	prostaglandin E synthase	BE614743	Hs.146688	6.7	1949 6264
	408204	protein tyrosine phosphatase type IVA,	AA454501	Hs.43666	6.7	203 4943
	407792	putative secreted ligand homologous to	AI077715	Hs.39384	6.7	162 4906
	425247	matrix metalloproteinase 11 (stromelysi	NM_005940	Hs.1 55324	6.7	2072 2073 6351
	406837	immunoglobulin kappa constant	R70292	Hs.156110	6.7	69 4836
65	448520	doublecortin and CaM kinase-like 1	AB002367	Hs.21355	6.7	4010 4011 7907
	409698	short stature homeobox 2	AF022654	Hs.55967	6.7	378 379 5074
	433839	ESTs, Weakly similar to ALU1_HUMAN ALU	F35430	Hs.146070	6.7	3008 7043
	437220	GS1999full	AL117542	Hs.334305	6.7	3247 7244
	414716	Kv channel-interacting protein 2	AF199598	Hs.97044	6.6	856 857 5451
70	422667	ESTs	H25642	Hs.132821	6.6	1723 6102
	433138	semaphorin sem2	AB029496	Hs.59729	6.6	2944 2945 6994
	407824	Homo sapiens cDNA FLJ14388 fis, clone H	AA147884	Hs.9812	6.6	166 4910
	442573	branched chain aminotransferase 1, cyto	H93366	Hs.7567	6.6	3570 7541
	411396	ESTs	C04646	Hs.85428	6.6	533 5191
75	406519	C10001858:gil6679124[ref]NP_032759.1]	n		6.6	4808
	410361	guanylate binding protein 1, interferon	BE391804	Hs.62661	6.6	456 5132
	446051	ephrin-A3	BE048061	Hs.37054	6.6	3816 7744
	452223	hypothetical protein MGC2827	AA425467	Hs.8035	6.6	4302 8142
80	429609	cell adhesion molecule with homology to	AF002246	Hs.210863	6.6	2584 2585 6725
	431183	KDEL (Lys-Asp-Glu-Leu) endoplasmic ret	NM_006855	Hs.250696	6.6	2755 2757 6845
	418478	cyclin-dependent kinase inhibitor 2A (m	U38945	Hs.1174	6.6	1245 1246 5747
	417366	small proline-rich protein 1B (cornifin	BE185289	Hs.1076	6.6	1104 5642
	420981	peroxisome proliferative activated rece	L40904	Hs.100724	6.6	1495 1496 5936
	432131	muscle disease-related protein	AB033021	Hs.272564	6.6	2843 2844 6911
85	444371	forkhead box M1	BE540274	Hs.239	6.5	3696 7651
	421508	absent in melanoma 2	NM_004833	Hs.1 05115	6.5	1551 1552 5977

	409012	DKFZP434I216 protein	AL117435	Hs.49725	6.5	293 294 5013
	417027	tradin	AA192306	Hs.23926	6.5	1062 5607
	426363	transforming growth factor, beta 3	M58524	Hs.2025	6.5	2210 2211 6446
5	451766	ephrin-B3	NM_001406	Hs.2 6988	6.5	4255 4256 8104
	402621	Target Exon			6.5	4684
	410270	tumor endothelial marker 1 precursor	AF279142	Hs.195727	6.5	442 443 5121
	453041	Homo sapiens cDNA FLJ11918 fis, clone	HA1680737	Hs.289068	6.5	4384 8211
	452063	ESTs, Weakly similar to TWST_HUMAN TWIS R53185	Hs.32366	6.5	4281 8124	
10	425308	receptor tyrosine kinase-like orphan re	M97639	Hs.155585	6.5	2087 2088 6362
	438915	Williams-Beuren syndrome chromosome reg	AA280174	Hs.355711	6.5	3365 7348
	414315	gb:HSB65D052 STRATAGENE Human skeletal	Z24878	6.5	803 5409	
	419833	Homo sapiens tryptophanyl-tRNA synthetase	AA251131	Hs.220697	6.5	1388 5856
	406646	major histocompatibility complex, class	M33600	Hs.375570	6.5	36 37 4816
15	446142	ESTs	AI754693	Hs.145968	6.5	3820 7748
	410611	KIAA1628 protein	AW954134	Hs.20924	6.5	480 5148
	431103	pleiotrophin (heparin binding growth fa	M57399	Hs.44	6.5	2748 2749 6840
	441636	Homo sapiens mRNA; cDNA DKFzP566E183 (f	AA081846	Hs.7921	6.5	3530 7502
	409731	thymosin, beta, identified in neuroblas	AA125985	Hs.56145	6.4	385 5080
20	443184	ESTs	AI638728	Hs.135159	6.4	3607 7574
	456508	ESTs, Weakly similar to AF208855 1 BM-0	AA502764	Hs.123469	6.4	4521 8325
	423563	protein kinase (cAMP-dependent, catalo	R34734	Hs.75209	6.4	1817 6171
	416391	mesoderm specific transcript (mouse) ho	AI878927	Hs.79284	6.4	999 5562
	440650	Human DNA sequence from PAC 75N13 on ch	R44692	Hs.326801	6.4	3477 7455
25	407826	calpain 3, (p94)	AA128423	Hs.40300	6.4	167 4911
	424634	cartilage intermediate layer protein, n	NM_003613	Hs.1 51407	6.4	1981 1982 6285
	432408	ESTs, Weakly similar to A46010 X-linked	N39127	Hs.356235	6.4	2872 6934
	436608	down syndrome critical region protein D	AA628980	Hs.192371	6.4	3205 7207
	429415	procollagen C-endopeptidase enhancer	NM_002593	Hs.2 02097	6.4	2557 2558 6706
30	429294	Homo sapiens cDNA: FLJ22463 fis, clone	AA095971	Hs.198793	6.4	2540 6693
	406387	Target Exon			6.4	4805
	427337	Fc fragment of IgG, low affinity IIb,	Z46223	Hs.176663	6.4	2318 2319 6521
	431866	angiotensin-like 2	NM_012098	Hs.8 025	6.4	2830 2831 6902
	418059	gb:zn56d05.s1 Stratagene muscle 937209	AA211586	6.4	1186 5703	
35	421778	actin related protein 2/3 complex, subu	AA428000	Hs.283072	6.4	1591 6003
	432731	fibronectin 1	R31178	Hs.287820	6.4	2904 6961
	448390	hypothetical protein	AL035414	Hs.21068	6.4	3999 7897
	434149	hypothetical protein MGC5469	Z43829	Hs.244624	6.4	3030 7063
	431457	integrin, alpha 11	NM_012211	Hs.2 56297	6.4	2787 2788 6870
40	444006	type I transmembrane protein Fn14	BE395085	Hs.334762	6.3	3668 7627
	447414	neuroblastoma (nerve tissue) protein	D82343	Hs.74376	6.3	3924 3925 7834
	410234	fructose-1,6-bisphosphatase 2	NM_003837	Hs.6 1255	6.3	435 436 5116
	418986	ESTs	AI123555	Hs.293821	6.3	1288 5779
	418883	acid phosphatase 5, tartrate resistant	BE387036	Hs.1211	6.3	1281 5774
45	451934	ESTs	AI540842	Hs.61082	6.3	4262 8109
	429451	heme oxygenase (decycling) 1	BE409861	Hs.202833	6.3	2562 6709
	422106	Fc fragment of IgG binding protein	D84239	Hs.111732	6.3	1646 1647 6044
	420576	KIAA1858 protein	AA297634	Hs.54925	6.3	1463 5914
	435793	KIAA1313 protein	AB037734	Hs.4993	6.3	3152 3153 7162
50	409882	heat shock 27kD protein family, member	AJ243191	Hs.56874	6.3	395 396 5087
	445107	ESTs, Weakly similar to I38022 hypothet	AI208121	Hs.147313	6.3	3744 7689
	417675	similar to murine leucine-rich repeat p	AI808607	Hs.3781	6.3	1144 5670
	435406	calcium/calmodulin-dependent protein ki	F26698	Hs.4884	6.3	3124 7140
	415885	KIAA0161 gene product	D79983	Hs.78894	6.3	953 954 5524
55	408925	glycerol-3-phosphate dehydrogenase 1 (s	L34041	Hs.348601	6.3	83 84 4845
	433577	ESTs	AW007080	Hs.284192	6.3	2989 7028
	422746	glypican 3	NM_004484	Hs.1 19651	6.3	1732 1733 6109
	453575	peptidyl arginine deiminase, type II	AB023211	Hs.33455	6.3	4425 4426 8246
	448030	membrane-spanning 4-domains, subfamily	N30714	Hs.325960	6.3	3971 7873
60	426935	collagen, type I, alpha 1	NM_000088	Hs.1 72928	6.3	2288 2289 6498
	430643	MEGF10 protein	AW970065	Hs.287425	6.3	2717 6817
	408562	roundabout (axon guidance receptor, Dro	AI436323	Hs.31141	6.3	240 4971
	420005	ESTs	AW271106	Hs.133294	6.3	1407 5871
	429930	ESTs	AI580809	Hs.352364	6.3	2623 6751
65	451811	hypothetical protein MGC1136	AA663485	Hs.8719	6.3	4259 8106
	453514	ESTs	AA036675	Hs.50918	6.3	4424 8245
	416208	ESTs, Weakly similar to MUC2_HUMAN MUC1	AW291168	Hs.41295	6.2	981 5548
	441188	ESTs	AW292830	Hs.255609	6.2	3503 7478
	440274	scrapie responsive protein 1	R24595	Hs.7122	6.2	3464 7443
70	410889	twist (Drosophila) homolog (acrocephalo	X91662	Hs.66744	6.2	501 502 5164
	447733	MAD2 (mitotic arrest deficient, yeast,	AF157482	Hs.19400	6.2	3955 3956 7860
	419290	spinal cord-derived growth factor-B	AI128114	Hs.112885	6.2	1327 5810
	408212	hypothetical protein	AA297567	Hs.43728	6.2	206 4945
	424481	proteolipid protein 1 (Pelizaeus-Merzba	R19453	Hs.1787	6.2	1960 6272
75	434096	pleomorphic adenoma gene-like 1	AW662958	Hs.75825	6.2	3029 7062
	413031	phosphofructokinase, muscle	BE515051	Hs.75160	6.2	671 5304
	453880	ESTs, Weakly similar to I38022 hypothet	AI803166	Hs.135121	6.2	4458 8272
	424870	ESTs	T15545	Hs.244624	6.2	2014 6308
	418203	CDC28 protein kinase 2	X54942	Hs.83758	6.2	1202 1203 5719
80	457211	ESTs, Weakly similar to S51797 vasodila	AW972565	Hs.32399	6.2	4543 8344
	417068	hypothetical protein MGC3169	AA451910	Hs.85852	6.2	1069 5613
	412471	endothelial cell growth factor 1 (plate	M63193	Hs.73946	6.2	591 592 5239
	436252	Homo sapiens cDNA FLJ11562 fis, clone H	AI539519	Hs.142827	6.2	3179 7184
	443907	TYRO protein tyrosine kinase binding pr	AU076484	Hs.9963	6.2	3656 7617
	424455	calcium channel, voltage-dependant, gam	AA452006	Hs.147989	6.2	1957 6270
85	414555	phospholipase A2, group IIA (platelets,	N98569	Hs.76422	6.2	830 5431
	429299	hypothetical protein MGC13102	AI620463	Hs.347408	6.2	2541 6694

5	410102	ESTs; homologue of PEM-3 [Clona savigny AW248508	Hs.279727	6.2	422 5107	
	425256	collapsin response mediator protein 1	BE297611	Hs.155392	6.2	2074 6352
	416322	pyrroline-5-carboxylate reductase 1	BE019494	Hs.79217	6.2	989 5554
	428450	KIAA0175 gene product	NM_014791	Hs.1 84339	6.2	2443 2444 6621
	448731	ESTs	AI522273	Hs.173179	6.2	4030 7922
10	452046	KIAA0802 protein	AB018345	Hs.27657	6.2	4275 4276 8120
	411411	ESTs, Weakly similar to KIAA1330 protei	AA345241	Hs.55950	6.2	537 5194
	410295	nidogen (enactin)	AA741357	Hs.356624	6.2	450 5127
	424825	procollagen-lysine, 2-oxoglutarate 5-di	AF207069	Hs.153357	6.1	2005 2006 6302
	430250	chloride intracellular channel 5	NM_016929	Hs.2 83021	6.1	2666 2667 6783
15	407811	cysteine knot superfamily 1, BMP antago	AW190902	Hs.40098	6.1	164 4908
	458079	Homo sapiens similar to RIKEN cDNA 2810 A1795870	Hs.381220	6.1	4566 8363	
	401797	Target Exon		6.1	4663	
	411962	gb:zk85d12.r1 Soares_pregnant_uterus_Nb AA099050		6.1	563 5215	
	443780	activating transcription factor 5	NM_012068	Hs.9 754	6.1	3643 3644 7606
20	417930	Homo sapiens mRNA for KIAA1870 protein, H81136	Hs.334604	6.1	1169 5691	
	419987	osteomodulin	NM_005014	Hs.9 4070	6.1	1402 1403 5868
	413945	CD14 antigen	NM_000591	Hs.7 5627	6.1	758 759 5371
	450785	Homo sapiens, alpha-1 (VI) collagen	AA852713	Hs.108885	6.1	4193 8056
	444784	ectonucleotide pyrophosphatase/phosphod	D12485	Hs.11951	6.1	3724 3725 7673
25	432842	hypothetical protein MGC4485	AW674093	Hs.334822	6.1	2911 6966
	452281	Homo sapiens cDNA FLJ11041 fis, clone P T93500	Hs.28792	6.1	4309 8149	
	443883	serine (or cysteine) proteinase inhibit	AA114212	Hs.9930	6.1	3653 7614
	433075	sortilin 1	NM_002959	Hs.3 51872	6.1	2936 2937 6987
	440704	insulin-like growth factor binding prot	M69241	Hs.162	6.0	3482 3483 7459
30	414312	ESTs	AA155694	Hs.191060	6.0	800 5407
	421913	osteoglycin (osteoinductive factor, mim	AI934365	Hs.109439	6.0	1611 6020
	413278	interferon-stimulated protein, 15 kDa	BE563085	Hs.833	6.0	695 5322
	414657	protein phosphatase 1, regulatory (inhi	AA424074	Hs.76780	6.0	843 5442
	448595	KIAA0644 gene product	AB014544	Hs.21572	6.0	4015 4016 7910
35	418067	cystatin E/M	AI127958	Hs.83393	6.0	1189 5706
	444931	general transcription factor IIIA	AV652066	Hs.75113	6.0	3735 7681
	443105	chondroitin sulfate proteoglycan 4 (mel	X96753	Hs.9004	6.0	3600 3601 7568
	430439	DKFZP434B061 protein	AL133561	Hs.380155	6.0	2695 2696 6803
	412006	ESTs	AW451618	Hs.380683	6.0	565 5217
40	452106	ESTs	AI141031	Hs.21342	6.0	4289 8131
	416072	growth associated protein 43	AL110370	Hs.79000	6.0	969 5537
	441327	hypothetical protein FLJ10751	AK001706	Hs.7778	6.0	3509 3510 7484
	406663	immunoglobulin heavy constant mu	U24683		6.0	39 40 4818
	439706	ESTs, Weakly similar to DAP1_HUMAN DEAT AW872527	Hs.59761	6.0	3421 7404	
45	416433	ESTs	AI658904	Hs.84673	6.0	1004 5566
	423225	Thy-1 cell surface antigen	AA852604	Hs.125359	6.0	1786 6148
	421487	serine/threonine kinase 23	AF027406	Hs.104865	6.0	1548 1549 5975
	429903	cyclin-dependent kinase 5, regulatory s	AL134197	Hs.93597	6.0	2616 6746
	407896	Zic family member 1 (odd-paired Drosoph	D76435	Hs.41154	6.0	176 177 4919
50	403903	C5001632*.gij10645308[gbl]AAG21430.1JACO		6.0	4731	
	425398	hypothetical protein similar to tenasci	AL049689	Hs.156369	6.0	2101 2102 6370
	420059	RAB23, member RAS oncogene family	AF161486	Hs.94769	6.0	1412 1413 5875
	413436	sphingosine kinase 1	AF238083	Hs.68061	6.0	721 722 5339
	418299	Integrin, beta 2 (antigen CD18 (p95), I	AA279530	Hs.83968	6.0	1212 5725
55	427239	ubiquitin carrier protein	BE270447	Hs.356512	6.0	2311 6515
	428248	ESTs	AI126772	Hs.40479	6.0	2414 6596
	403086	NM_003319*.Homo sapiens titin (TTN), mR		5.9	4705	
	425280	phosphoenolpyruvate carboxykinase 1 (so	U31519	Hs.1872	5.9	2080 2081 6357
	449378	ESTs	AW664026	Hs.59892	5.9	4085 7967
60	417114	ESTs	AA193472	Hs.20007	5.9	1080 5621
	419968	interleukin 6 (interferon, beta 2)	X04430	Hs.93913	5.9	1399 1400 5866
	408491	ESTs	AI088063	Hs.7882	5.9	230 4961
	452291	CDC7 (cell division cycle 7, S. cerevis	AF015592	Hs.28853	5.9	4310 4311 8150
	436748	collagen, type VI, alpha 2	BE159107	Hs.159263	5.9	3212 7213
65	426928	retinol dehydrogenase 5 (11-cis and 9-c	AF037062	Hs.172914	5.9	2285 2286 6496
	402992	Target Exon		5.9	4700	
	428342	Homo sapiens cDNA FLJ13458 fis, clone P A1739168	Hs.349283	5.9	2432 6611	
	410628	ESTs, Moderately similar to similar to	AI131408	Hs.68756	5.9	483 5151
	451195	mesenchyme homeo box 1	U10492	Hs.438	5.9	4218 4219 8077
70	437446	ESTs, Moderately similar to CA1C RAT CO AA788946	Hs.101302	5.9	3264 7259	
	424001	paternally expressed 10	W67883	Hs.137476	5.9	1882 6217
	417632	glycoprotein M6B	R20855	Hs.379090	5.9	1141 6667
	430171	skin-specific protein	AF086289	Hs.234766	5.9	2657 6776
	419682	paired-like homeodomain transcription f	H13139	Hs.92282	5.9	1368 5841
75	422567	glypican 6	AF111178	Hs.118407	5.9	1702 1703 6087
	409430	splicing factor, arginine/serine-rich 5	R21945	Hs.346735	5.9	348 5052
	453271	ESTs	AA903424	Hs.6786	5.8	4409 8232
	429207	ESTs	AA447941	Hs.123423	5.8	2532 6686
	442295	Homo sapiens cDNA FLJ11469 fis, clone H A1827248	Hs.224398	5.8	3555 7527	
80	424440	ESTs	AA340743	Hs.133208	5.8	1951 6266
	413795	ESTs	AL040178	Hs.142003	5.8	743 5358
	424806	MSTP031 protein	AA382523	Hs.105689	5.8	2004 6301
	401771	Target Exon		5.8	4660	
	450421	ADP-ribosyltransferase 3	C03188	Hs.24976	5.8	4166 8034
85	426457	chimerin (chimaerin) 1	AW894667	Hs.380138	5.8	2229 6459
	429670	protein kinase C, theta	L01087	Hs.211593	5.8	2602 2603 6735
	456034	gb:U1-H-B13-ala-a-12-0-U1.s1 NCI_CGAP_S AW450979		5.8	4510 8316	
	421485	hypothetical protein FLJ10134	AA243499	Hs.104800	5.8	1547 5974
	447217	neuropilin 2	BE465754	Hs.17778	5.8	3904 7819
	410366	hypothetical protein	AI267589	Hs.302689	5.8	457 5133

	444143	ESTs, Moderately similar to A56194 thro	AW747996	Hs.160999	5.8	3679 7637
	447770	frizzled (Drosophila) homolog 4	AB032417	Hs.19545	5.8	3961 3962 7864
	427418	LAT1-3TM protein	AA402587	Hs.356667	5.7	2327 6527
5	439039	ESTs	AI656707	Hs.48713	5.7	3373 7356
	416908	coagulation factor XIII, A1 polypeptide	AA333990	Hs.80424	5.7	1044 5594
	427474	aggrecaan 1 (chondroitin sulfate proteog	U13192	Hs.2159	5.7	2334 6532
	414285	ESTs	AA312914	Hs.71719	5.7	798 5405
	406868	immunoglobulin heavy constant gamma 3 (AA505445	Hs.300697	5.7	72 4839
10	423858	Homo sapiens mRNA; cDNA DKFZp434B0650 (AL137326	Hs.133483	5.7	1858 6201
	414142	hemiscentin (fibulin 6)	AW368397	Hs.334485	5.7	781 5390
	438704	ESTs	AA35060	Hs.6705	5.7	3349 7334
	432693	ESTs	AW449630	Hs.293790	5.7	2900 6958
	456534	phospholipase C, beta 3, neighbor pseud	X91195	Hs.100623	5.7	4522 8326
	440594	ESTs	AW445167	Hs.126036	5.7	3475 7453
15	409125	axonal transport of synaptic vesicles	R17268	Hs.343567	5.7	308 5024
	410867	fibrillin 1 (Marfan syndrome)	X63556	Hs.750	5.7	498 499 5162
	452360	ESTs	AI742082	Hs.98539	5.7	4321 8158
	406714	hemoglobin, gamma G	AJ219304	Hs.266959	5.7	63 4830
20	426968	amphiphysin (Stiff-Mann syndrome with b	U07616	Hs.173034	5.7	2290 2291 6499
	439551	ESTs	W72062	Hs.11112	5.7	3406 7389
	439668	frizzled (Drosophila) homolog 8	AJ091277	Hs.302634	5.7	3414 7397
	403074	NM_003319*:Homo sapiens titin (TTN), mR			5.7	4703
	453596	hypothetical protein FLJ14834	AA441838	Hs.62905	5.7	4428 8248
25	444367	hypothetical protein FLJ22390	H54892	Hs.10974	5.7	3695 7650
	422491	neurexin	AA338548	Hs.117546	5.7	1691 6077
	418283	cathepsin K (pseudosynthesis)	S79895	Hs.83942	5.7	1210 1211 5724
	417605	regulator of G-protein signalling 3	AF006609	Hs.82294	5.7	1138 1139 5665
	404030	NM_015669*:Homo sapiens protocadherin b			5.7	4735
30	433124	hypothetical protein SMAP31	U51712	Hs.13775	5.7	2942 6992
	409553	semaphorin Y	AF055020	Hs.54937	5.7	359 360 5060
	419693	FXD domain-containing ion transport re	AA133749	Hs.301350	5.7	1371 5844
	408829	heparan sulfate (glucosamine) 3-O-sulfo	NM_006042	Hs.4 8384	5.7	264 265 4991
	420486	caveolin 3	AF036365	Hs.98303	5.7	1456 1457 5909
35	428418	ESTs	AI368826	Hs.8768	5.7	2441 6619
	425240	phosphoglucosyltransferase 1	AA306495	Hs.1869	5.6	2071 6350
	452242	glycosyltransferase	R50956	Hs.159993	5.6	4305 8145
	410132	Microfibril-associated glycoprotein-2	NM_003480	Hs.3 00946	5.6	425 426 5110
	421848	collagen, type VI, alpha 1	X15880	Hs.108885	5.6	1602 1603 6013
40	425157	phospholipid transfer protein	NM_006227	Hs.2 83007	5.6	2057 2058 6340
	448672	ESTs	AI955511	Hs.89582	5.6	4025 7917
	419405	ESTs	AJ377043	Hs.42189	5.6	1333 5816
	439737	Homo sapiens mRNA full length insert cD	AI751438	Hs.41271	5.6	3427 7410
	427452	protein phosphatase	NM_016364	Hs.1 78170	5.6	2330 2331 6529
45	433635	hypothetical protein MGC12921	AI074502	Hs.134292	5.6	2994 7032
	417511	chordin-like	AL049176	Hs.82223	5.6	1125 1126 5657
	415701	gamma-glutamyl hydrolase (conjugase, fo	NM_003878	Hs.78619	5.6	940 941 5514
	438866	tissue inhibitor of metalloproteinase 2	U44385	Hs.6441	5.6	3360 3361 7344
	453341	adenylyl cyclase-associated protein 2	AI758912	Hs.296341	5.6	4414 8237
50	418867	msh (Drosophila) homeo box homolog 2	D31771	Hs.89404	5.6	1277 1278 5772
	421948	keratin 6A	L42583	Hs.334309	5.6	1618 1619 6025
	435080	hypothetical protein FLJ14428	AI831760	Hs.155111	5.6	3103 7122
	412430	fumarylacetoacetate hydrolase (fumaryl	AW675064	Hs.73875	5.6	584 5233
	427019	hypothetical protein FLJ10970	AA001732	Hs.173233	5.6	2296 6504
55	449318	Homo sapiens, Similar to RIKEN cDNA 573	AW236021	Hs.78531	5.6	4080 7962
	431347	insulin-like growth factor 2 (somatomed	AJ133461	Hs.251664	5.6	2774 6859
	414020	small inducible cytokine A4 (homologous	NM_002984	Hs.7 5703	5.5	767 768 5378
	427527	immunoglobulin heavy constant mu	AI809057	Hs.153261	5.5	2340 6536
	410036	caldesmon 2 (cardiac muscle)	R57171	Hs.57975	5.5	412 5100
60	435520	HNOEL-iso protein	AA297990	Hs.9315	5.5	3130 7146
	409893	minichromosome maintenance deficient (S	AW247090	Hs.57101	5.5	397 5088
	426485	platelet-derived growth factor receptor	NM_006207	Hs.1 70040	5.5	2238 2239 6465
	418322	cyclin-dependent kinase inhibitor 3 (CD	AA284166	Hs.84113	5.5	1214 5727
	413670	hypothetical protein, expressed in oste	AB000115	Hs.75470	5.5	735 736 5352
65	405681	C3000593*:gll10120319[embjCAC08185.1]			5.5	4793
	421362	hypothetical protein FLJ20043	AK000050	Hs.103853	5.5	1531 1532 5965
	424125	inhibin, beta B (activin AB beta polype	M31669	Hs.1735	5.5	1900 1901 6230
	453830	ESTs	AA534296	Hs.20953	5.5	4445 8263
	403857	Target Exon			5.5	4730
70	431706	adenylyl cyclase-associated protein 2	AI816086	Hs.296341	5.5	2811 6887
	430044	ESTs	AA464510	Hs.152812	5.5	2842 6765
	441611	ESTs	AW590829	Hs.133463	5.5	3528 7500
	453828	ESTs	AW970960	Hs.293821	5.5	4444 8262
	413435	carboxypeptidase E	X51405	Hs.75360	5.5	719 720 5338
75	411358	KIAA1691 protein	R47479	Hs.94761	5.5	527 5186
	419621	Homo sapiens clone B18 unknown mRNA	AF052497	Hs.91626	5.5	1361 5835
	416491	parathyroid hormone receptor 1	U17418	Hs.1019	5.5	1005 1006 5567
	400297	hypothetical protein DKFZp564O1278	AI127076	Hs.288381	5.5	7 4618
	426075	ESTs, Weakly similar to 2109260A B cell	AW513691	Hs.270149	5.5	2170 6417
80	434715	ESTs	BE005346	Hs.116410	5.5	3070 7094
	443163	ESTs	AI082610	Hs.132079	5.5	3605 7572
	432485	CDW52 antigen (CAMPATH-1 antigen)	N90866	Hs.276770	5.5	2877 6939
	425262	GS3955 protein	D87119	Hs.155418	5.5	2076 2077 6354
	433323	ESTs	AA805132	Hs.159142	5.5	2970 7011
85	441020	ESTs	W79283	Hs.35962	5.5	3495 7471
	419086	Kallmann syndrome 1 sequence	NM_000216	Hs.8 9591	5.4	1300 1301 5789
	420058	Homo sapiens cDNA FLJ10561 fis, clone N	AK001423	Hs.94694	5.4	1411 5874

408901	hypothetical protein FLJ10468	AK001330	Hs.48855	5.4	272 273 4997
406836	immunoglobulin kappa constant	AW514501	Hs.156110	5.4	68 4835
453649	ATPase, Na ⁺ transporting, alpha 2 () po	Y07494	Hs.34114	5.4	4432 4433 8252
410581	tumor endothelial marker 7 precursor	AA018982	Hs.125036	5.4	478 5146
448988	gamma-aminobutyric acid (GABA) A recept	Y09763	Hs.22785	5.4	4055 4056 7940
419750	Homo sapiens cDNA FLJ14236 fis, clone N	AL079741	Hs.183114	5.4	1385 5853
431070	transcription factor 19 (SC1)	AW408164	Hs.249184	5.4	2744 6837
430147	hairly/enhancer-of-split related with YR	R60704	Hs.234434	5.4	2652 6773
441689	ESTs	AI123705	Hs.289068	5.4	3533 7505
416406	lipoma HMGIC fusion partner-like 2	D86961	Hs.79299	5.4	1001 1002 5564
443595	PPAR(gamma) angiopotelin related protei	AF169312	Hs.9613	5.4	3626 3627 7590
438203	ESTs	BE540090	Hs.7345	5.4	3308 7300
419235	neurotrophin	AW470411	Hs.288433	5.4	1320 5804
407785	ESTs, Weakly similar to A43932 mucin 2	AW207285	Hs.98279	5.4	160 4904
447471	sprouty (Drosophila) homolog 2	AF039843	Hs.18676	5.4	3930 3931 7839
432247	ESTs	AA531287	Hs.105805	5.4	2859 6923
447343	ESTs, Highly similar to S02392 alpha-2-	AA256641	Hs.236894	5.4	3916 7828
412507	EphA4	L36645	Hs.73964	5.4	596 597 5243
414416	hypothetical protein MGC2721	AW409985	Hs.76084	5.4	813 5417
427596	extracellular glycoprotein EMILIN-2 pre	AA449506	Hs.270143	5.4	2350 6544
408660	ESTs, Moderately similar to PC4259 ferr	AA525775	Hs.89040	5.4	247 4977
447261	extracellular link domain-containing 1	NM_006691	Hs.17917	5.4	3908 3909 7823
417421	nuclear receptor subfamily 4, group A,	AL138201	Hs.82120	5.4	1118 5653
426855	Homo sapiens mRNA; cDNA DKFZp566P013	(f AL117427	Hs.172778	5.4	2279 6491
451952	ESTs	AL120173	Hs.301663	5.3	4264 8111
447297	protease, cysteine, 1 (legumain)	BE617970	Hs.18069	5.3	3914 7826
414459	CCAAT/enhancer binding protein (C/EBP),	Y11525	Hs.76171	5.3	818 819 5422
444412	Homo sapiens clone HH409 unknown mRNA	AI147652	Hs.216381	5.3	3700 7655
422809	hypothetical protein FLJ10549	AK001379	Hs.121028	5.3	1741 1742 6115
448498	ESTs	AA418276	Hs.375003	5.3	4007 7904
441104	ESTs	AI382357	Hs.143903	5.3	3499 7474
427400	hypothetical protein FLJ11939	AW245084	Hs.94229	5.3	2325 6525
422765	baculoviral IAP repeat-containing 5 (su	AW409701	Hs.1578	5.3	1734 6110
441362	RAD51 (S. cerevisiae) homolog (E coli R	BE614410	Hs.23044	5.3	3512 7486
400288	Integrin, alpha 5 (fibronectin receptor	X06256	Hs.149609	5.3	1 2 4614
438086	nuclear receptor subfamily 1, group I,	AA336519	Hs.83623	5.3	3300 7293
452355	G protein-coupled receptor 34	N54926	Hs.29202	5.3	4320 8157
452056	Homo sapiens, clone IMAGE:4054156, mRNA	AW955065	Hs.101150	5.3	4280 8123
414531	allograft inflammatory factor 1	T69387	Hs.76364	5.3	829 5430
406698	major histocompatibility complex, class	X03068	Hs.73931	5.3	51 52 4824
445084	hypothetical protein FLJ14761	H38914	Hs.250848	5.3	3742 7687
418110	hypothetical protein FLJ22202	R43523	Hs.217754	5.3	1193 5710
408018	ESTs	AI912976	Hs.187497	5.3	185 4927
417160	proteolipid protein 1 (Pelizaeus-Merzba	N76497	Hs.355807	5.3	1086 5626
427099	odd Oz/ten-m homolog 2 (Drosophila, mou	AB032953	Hs.173560	5.3	2302 2303 6509
453079	LIM protein (similar to rat protein kin	AW160480	Hs.154103	5.3	4387 8214
422100	ADP-ribosylation factor-like 7	AI096988	Hs.111554	5.3	1644 6042
424078	paternally expressed 3	AB006625	Hs.139033	5.3	1893 1894 6225
426413	gb:EST90805 Synovial sarcoma Homo sapie	AA377823		5.3	2219 6453
407366	gb:Homo sapiens cig33 mRNA, partial seq	AF026942	Hs.17518	5.3	137 4885
428046	ESTs, Moderately similar to I38022 hypo	AW812795	Hs.337534	5.3	2393 6579
422562	AE-binding protein 1	AI862060	Hs.118397	5.3	1700 6085
416140	roundabout (axon guidance receptor, Dro	AI918035	Hs.301198	5.3	978 5545
421016	transcription factor 3 (E2A immunoglobu	AA504583	Hs.101047	5.3	1497 5937
417259	chondroitin sulfate proteoglycan 2 (ver	AW903838	Hs.81800	5.3	1092 5632
413199	ELAV (embryonic lethal, abnormal vision	M62843	Hs.75236	5.3	687 688 5317
435256	cytokine-like protein C17	AF193766	Hs.13872	5.3	3116 3117 7133
410738	litin	AA197128	Hs.172004	5.3	491 5156
453935	ESTs	AI633770	Hs.42572	5.3	4470 8281
408753	SH3 domain binding glutamic acid-rich p	AI337192	Hs.47438	5.3	254 4983
432098	cytochrome P450 retinoid metabolizing p	AF252297	Hs.91546	5.2	2839 2840 6908
432503	ESTs	AA551196	Hs.188952	5.2	2878 6940
439999	ras homolog gene family, member E	AA115811	Hs.6838	5.2	3444 7426
425065	Homo sapiens, clone IMAGE:3603836, mRNA	AA371906	Hs.294151	5.2	2042 6329
428834	ESTs	AW899713	Hs.10338	5.2	2479 6647
450923	ESTs	AW043951	Hs.38449	5.2	4203 8063
412563	ESTs, Weakly similar to I38022 hypothe	Z25372	Hs.350621	5.2	605 5250
428976	ras homolog gene family, member I	AL037824	Hs.194695	5.2	2495 6658
407965	heat shock 27kD protein 3	W21483	Hs.41707	5.2	183 4925
410624	ESTs, Weakly similar to alternatively s	AA180060	Hs.68751	5.2	482 5150
442080	ESTs	AW444761	Hs.72901	5.2	3549 7521
408989	KIAA0746 protein	AW361666	Hs.49500	5.2	290 5010
427700	dual specificity phosphatase 6	AA262294	Hs.180383	5.2	2361 6554
411020	macrophage receptor with collagenous st	NM_005770	Hs.67726	5.2	506 507 5168
453767	extracellular matrix protein 2, female	AB011792	Hs.35094	5.2	4439 4440 8258
414117	proteolipid protein 1 (Pelizaeus-Merzba	W88559	Hs.355807	5.2	777 5386
424651	ESTs	AI493206	Hs.120785	5.2	1984 6287
407874	Homo sapiens cDNA FLJ14059 fis, clone H	AI1766311	Hs.289047	5.2	175 4918
435977	brain-specific membrane-anchored protei	AL138079	Hs.6012	5.2	3166 7174
423013	secreted modular calcium-binding protei	AW875443	Hs.22209	5.2	1769 6135
423217	collagen, type VII, alpha 1 (epidermol	NM_000094	Hs.1640	5.2	1784 1785 6147
448569	signal transducer and activator of tran	BE382657	Hs.21486	5.2	4014 7909
428862	SRY (sex determining region Y)-box 9 (c	NM_000346	Hs.2316	5.2	2483 2484 6650
453948	ESTs	AI970797	Hs.64859	5.2	4473 8283
427871	Homo sapiens, clone IMAGE:3507281, mRNA	AW992405	Hs.352406	5.2	2380 6568
416729	Ras-related associated with diabetes	U46165	Hs.1027	5.2	1026 1027 5581

406851	major histocompatibility complex, class	AA609784	Hs.352392	5.2	71 4838
429197	ESTs, Weakly similar to T20272 hypothet	H24471	Hs.26930	5.2	2531 6685
433013	axin 2 (conductin, axil)	AI697890	Hs.127337	5.2	2927 6979
428317	ESTs	AW022609	Hs.50745	5.2	2431 6610
432290	Homo sapiens cDNA FLJ10237 fis, clone	HAK001099	Hs.274273	5.2	2852 6926
422901	ribosomal protein L44	R81936	Hs.75874	5.2	1757 6126
452698	chemokine (C-C motif) receptor 1	NM_001295	Hs.3 01921	5.2	4343 4344 8177
410099	KIAA0036 gene product	AA081630	Hs.167	5.2	421 5106
429266	ESTs	AI014510	Hs.350621	5.2	2537 6691
426527	sodium channel, voltage-gated, type I,	NM_001037	Hs.1 70238	5.2	2247 2248 6471
403291	Target Exon			5.2	4713
410494	protein S (alpha)	M36564	Hs.64016	5.1	466 467 5139
443960	hypothetical protein FLJ21986	AI093577	Hs.255416	5.1	3663 7623
441944	Homo sapiens clone 23767 and 23782 mRNA	AW855861	Hs.8025	5.1	3541 7513
429455	CD209 antigen	AI472111	Hs.278694	5.1	2563 6710
449780	ribosomal protein L44	AA443241	Hs.75874	5.1	4114 7992
429612	pituitary tumor-transforming 1	AF062649	Hs.252587	5.1	2586 2587 6726
418036	latent transforming growth factor beta	Z37976	Hs.83337	5.1	1180 1181 5699
448782	KIAA0758 protein	AL050295	Hs.362806	5.1	4038 4039 7928
436481	HSPC150 protein similar to ubiquitin-co	AA379597	Hs.5199	5.1	3192 7197
415166	carboxypeptidase Z	NM_003652	Hs.7 8068	5.1	913 914 5491
415314	glycoprotein M6B	N88802	Hs.5422	5.1	921 5497
439456	hypothetical protein FLJ20980	AI752409	Hs.109314	5.1	3400 7383
417011	ESTs, Weakly similar to 2109260A B cell	F08212	Hs.234898	5.1	1060 5605
412490	Homo sapiens cDNA: FLJ22528 fis, clone	AW803564	Hs.288850	5.1	595 5242
434868	collagen, type VI, alpha 2	R50032	Hs.159263	5.1	3085 7106
419956	cadherin 19, type 2	AL137939	Hs.40096	5.1	1398 5865
438085	ESTs	R52518	Hs.7967	5.1	3299 7292
425964	progesterone membrane binding protein	AW889928	Hs.9071	5.1	2157 6408
418400	KIAA0246 protein	BE243026	Hs.301989	5.1	1234 5739
416051	mannosidase, alpha, class 1A, member 1	AA835868	Hs.25253	5.1	966 5534
445363	tubulin-specific chaperone d	NM_005993	Hs.1 2570	5.1	3762 3763 7702
414715	amylase-1, 6-glucosidase, 4-alpha-glucanot	AA587891	Hs.904	5.1	855 5450
414945	lymphocyte antigen 6 complex, locus E	BE076358	Hs.77667	5.1	894 5477
425227	ESTs	H84455	Hs.40639	5.1	2069 6348
448357	RAB38, member RAS oncogene family	N20169	Hs.108923	5.1	3994 7893
437802	ESTs	AI475995	Hs.122910	5.1	3288 7281
408161	hypothetical protein MGC3032	AW952912	Hs.300383	5.1	195 4937
447519	ESTs	U46258	Hs.339665	5.1	3936 7844
443060	procollagen C-endopeptidase enhancer 2	D78874	Hs.8944	5.1	3594 7562
423550	ESTs	F37675	Hs.152129	5.1	1815 6169
429583	1-acylglycerol-3-phosphate O-acyltransf	NM_006412	Hs.2 09119	5.1	2581 2582 6723
400263	Eos Control		Hs.75309	5.1	4613
452436	ESTs, Moderately similar to A46010 X-li	BE077546	Hs.31447	5.1	4330 8164
411756	discoidin domain receptor family, membe	BE294350	Hs.71891	5.1	550 5205
428311	tryptophan 2,3-dioxygenase	NM_005651	Hs.1 83671	5.1	2429 2430 6609
446681	kendrin	AJ003624	Hs.15896	5.1	3869 7789
420028	carbohydrate (N-acetylglucosamine-6-O)	AB014680	Hs.8786	5.1	1408 1409 5872
451292	KIAA1295 protein	AB037716	Hs.26204	5.1	4221 4222 8079
432306	protein phosphatase 1, regulatory (inhi	Y18207	Hs.303090	5.1	2864 2865 6928
413063	chitinase 3-like 1 (cartilage glycoprot	AL035737	Hs.75184	5.1	676 5308
452689	transferrin	F33868	Hs.284176	5.1	4342 8176
444783	anillin (Drosophila Scraps homolog), ac	AK001468	Hs.62180	5.1	3722 3723 7672
402994	NM_002463*:Homo sapiens myxovirus (infl			5.1	4701
411894	GLI-Kruppel family member GLI3 (Greig c	M57609	Hs.72916	5.1	559 560 5212
445900	Homo sapiens clone 24787 mRNA sequence	AF070526	Hs.125036	5.1	3803 7733
450606	ESTs, Moderately similar to ALU6_HUMAN	AI668605	Hs.60380	5.1	4177 8042
430513	G6C protein	AJ012008	Hs.241586	5.1	2704 2705 6809
420162	cyclin-dependent kinase 4	BE378432	Hs.95577	5.1	1422 5883
420255	membrane metallo-endopeptidase (neutral	NM_007289	Hs.1298	5.0	1438 1439 5895
423556	dynein, cytoplasmic, heavy polypeptide	R72694	Hs.356692	5.0	1816 6170
417933	thymidylate synthetase	X02308	Hs.82962	5.0	1170 1171 5692
426156	natriuretic peptide receptor A/guanylat	BE244537	Hs.167382	5.0	2183 6427
427509	complement component 5 receptor 1 (C5a	M62505	Hs.2161	5.0	2338 2339 6535
451149	RNA binding motif protein 8B	AL047586	Hs.10283	5.0	4214 8073
422175	ESTs, Highly similar to T00391 hypothet	N79885	Hs.6382	5.0	1657 6053
443062	Homo sapiens mRNA full length insert cD	N77999	Hs.8963	5.0	3595 7563
435099	flap structure-specific endonuclease 1	AC004770	Hs.4756	5.0	3104 3105 7123
436291	protein regulator of cytokinesis 1	BE568452	Hs.344037	5.0	3180 7185
439070	ESTs	AI733278	Hs.7621	5.0	3375 7358
402855	NM_001839*:Homo sapiens calponin 3, aci			5.0	4694
408196	SRY (sex determining region Y)-box 22	AL034548	Hs.43627	5.0	199 200 4940
426514	bone morphogenetic protein 7 (osteogeni	BE616633	Hs.170195	5.0	2246 6470
421991	KIAA0990 protein	NM_014918	Hs.1 10488	5.0	1622 1623 6028
450755	ESTs	AA010984	Hs.159464	5.0	4190 8054
427528	minichromosome maintenance deficient (S	AU077143	Hs.179565	5.0	2341 6537
429150	smoothened (Drosophila) homolog	AF120103	Hs.197366	5.0	2519 2520 6677
449129	ESTs	AI631602	Hs.258949	5.0	4066 7950
425863	Human unidentified mRNA, partial sequen	U43604	Hs.159901	5.0	2152 6404
415447	myocilin, trabecular meshwork inducible	Z97171	Hs.78454	5.0	927 928 5503
422530	bone marrow stromal cell antigen 2	AW972300	Hs.118110	5.0	1696 6082
422481	DNAX-activation protein 10	AL050163	Hs.117339	5.0	1687 1688 6075
435232	cyclin-dependent kinase inhibitor 2C (p	NM_001262	Hs.4 854	5.0	3114 3115 7132
428309	cellular retinoic acid-binding protein	M97815	Hs.183650	5.0	2427 2428 6608
414024	gb:zm79g08.r1 Stratagene neuroepitheliu	AA134712	Hs.22410	5.0	769 5379
434355	ESTs	AA630865	Hs.186556	5.0	3049 7076

445160	sine oculis homeobox (Drosophila) homol	AI299144	Hs.101937	5.0	3748 7692
441389	endocytic receptor (macrophage mannose	AF134838	Hs.7835	5.0	3514 3515 7488
437696	hypothetical protein dJ37E16.5	ZB3844	Hs.5790	5.0	3281 7274
421483	hypothetical protein MGC11333	NM_003388	Hs.1 04717	5.0	1545 1546 5973
408826	Homo sapiens clone HB-2 mRNA sequence	AF216077	Hs.48376	5.0	263 4990
439332	Homo sapiens mRNA; cDNA DKFZp547M072 (f	AWB42747	Hs.378821	5.0	3393 7376
429170	dual specificity phosphatase 4	NM_001394	Hs.2 359	5.0	2524 2525 6680
443353	ESTs	AA001220	Hs.242947	5.0	4084 7966
443859	folistatin	NM_013409	Hs.9 914	5.0	3651 3652 7613
415052	mesenchyme homeo box 2 (growth arrest-s	NM_005924	Hs.77858	5.0	904 905 5485
435905	KIAA0456 protein	AW997484	Hs.5003	5.0	3160 7168
426304	Homo sapiens cDNA FLJ11477 fis, clone H	AA374532	Hs.124673	5.0	2198 6438
436396	wingless-type MMTV integration site fam	AI683487	Hs.152213	5.0	3184 7189
434175	ESTs	AW979081	Hs.165469	5.0	3032 7065
421506	thymidine kinase 1, soluble	BE302796	Hs.105097	5.0	1550 5976
431958	cadherin 3, type 1, P-cadherin (placant	X63629	Hs.2877	5.0	2834 2835 6904
410600	ESTs, Moderately similar to S65657 alph	AW575742	Hs.351676	5.0	479 5147
433043	lymphoid nuclear protein (LAF-4) mRNA	W57554	Hs.125019	5.0	2930 6982
422363	replication factor C (activator 1) 3 (3	T55979	Hs.115474	5.0	1673 6065
438944	KIAA1444 protein	AA302517	Hs.92732	4.9	3368 7351
411089	cell division cycle 2-like 1 (PITSLRE p	AA456454	Hs.214291	4.9	513 5173
428949	hypothetical protein DKFZp434J0617	AA442153	Hs.104744	4.9	2490 6655
407204	ESTs, Weakly similar to ALU1_HUMAN ALU	R41933	Hs.140237	4.9	121 4873
409082	Homo sapiens mRNA; cDNA DKFZp564B182 (f	AL157488	Hs.50150	4.9	301 5018
428227	small inducible cytokine subfamily B (C	AA321649	Hs.2248	4.9	2410 6593
428182	ESTs, Weakly similar to GGC1_HUMAN G	AN BE385042	Hs.293317	4.9	2403 6588
417059	extracellular matrix protein 1	AL037672	Hs.81071	4.9	1067 5611
453597	myo-inositol 1-phosphate synthase A1	BE281130	Hs.381118	4.9	4429 8249
423057	ESTs, Moderately similar to I38022 hypo	AW961597	Hs.130816	4.9	1773 6139
422684	H2A histone family, member Z	BE561617	Hs.119192	4.9	1726 6105
432101	EphA3	AI918950	Hs.123642	4.9	2841 6909
407756	ubiquitin specific protease 18	AA116021	Hs.38260	4.8	159 4903
424308	minichromosome maintenance deficient (S	AW975531	Hs.154443	4.8	1932 6250
410108	OSBP-related protein 6	AA081659	Hs.318775	4.8	423 5108
444670	hypothetical protein MGC5370	H58373	Hs.332938	4.8	3714 7666
427378	melanoma antigen, family D, 1	BE515037	Hs.177556	4.8	2322 6523
417796	ESTs	AA206141	Hs.367818	4.8	1159 5682
418216	AF15q14 protein	AA662240	Hs.283099	4.8	1206 5721
452973	ESTs	H88409	Hs.40527	4.8	4375 8203
431448	hypothetical protein DKFZp564O1278	AL137517	Hs.306201	4.8	2785 2786 6869
434747	ESTs	AA837085	Hs.372254	4.8	3073 7097
435124	ESTs	AA725362	Hs.75514	4.8	3107 7125
414053	transgelin 2	BE391635	Hs.75725	4.8	774 5383
408938	ESTs	AA059013	Hs.22607	4.8	279 5002
420238	ESTs, Weakly similar to 2109260A B cell	AA256783	Hs.12549	4.8	1436 5894
407656	Homo sapiens mRNA; cDNA DKFZp434B2119 (AW747986	Hs.37443	4.8	148 4893
410011	PFTAIRE protein kinase 1	AB020641	Hs.57856	4.8	406 407 5096
416640	neuron-specific protein	BE262478	Hs.13406	4.8	1019 5576
453983	ESTs	H94997	Hs.16450	4.8	4476 8286
420842	hypothetical protein MGC10986	AI083668	Hs.50601	4.8	1485 5929
429707	matrix metalloproteinase 23B	W76631	Hs.211819	4.8	2606 6738
447232	interleukin 10 receptor, alpha	AW499834	Hs.327	4.8	3905 7820
417370	tryptophanyl-tRNA synthetase	T28651	Hs.374466	4.8	1105 5643
406672	major histocompatibility complex, class	M26041	Hs.198253	4.8	43 44 4820
448493	ESTs	AI524124	Hs.270307	4.7	4006 7903
445302	hypothetical protein FLJ10675	AK001537	Hs.12488	4.7	3757 3758 7699
415598	ESTs	N29102	Hs.79658	4.7	4241 8093
434629	glioma-amplified sequence-41	AA789081	Hs.4029	4.7	3064 7090
439130	ESTs	AA306090	Hs.345588	4.7	3378 7361
443247	c-Myc target JPO1	BE614387	Hs.333893	4.7	3611 7578
432481	intron of collagen, type XI, alpha 1	AW451645	Hs.151504	4.7	2876 6938
417115	small nuclear ribonucleoprotein polypep	AW952792	Hs.334612	4.7	1081 5622
412564	cardiac ankyrin repeat protein	XB3703	Hs.355934	4.7	606 607 5251
429139	ESTs	F09092	Hs.66087	4.7	2517 6675
424829	nerve growth factor receptor (TNFR supe	NM_002507	Hs.1 827	4.7	2007 2008 6303
427647	Homo sapiens cDNA FLJ20653 fis, clone K	W19744	Hs.180059	4.7	2354 6548
408482	adenosine A2b receptor	NM_000676	Hs.4 5743	4.7	226 227 4959
440028	ESTs, Weakly similar to T17227 hypothet	AW473675	Hs.367649	4.7	3446 7428
432527	ESTs	AW975028	Hs.102754	4.7	2883 6944
449596	ESTs	AW293799	Hs.255238	4.6	4098 7979
454071	ESTs	AI041793	Hs.42502	4.6	4487 8295
428977	cyclin B2	AK001404	Hs.194698	4.6	2496 6659
424263	L1 cell adhesion molecule (hydrocephalu	M77640	Hs.1757	4.6	1925 1926 6246
412939	eukaryotic translation elongation facto	AW411491	Hs.75069	4.6	657 5292
410342	Fc fragment of IgE, high affinity I, re	R31350	Hs.743	4.6	453 5129
433513	ESTs	AI566356	Hs.171437	4.6	2985 7024
452613	ESTs	AA461599	Hs.23459	4.6	4337 8171
427876	ESTs	AI494291	Hs.369171	4.6	2381 6569
453139	Human DNA sequence from clone RP11-234G	AA330620	Hs.348805	4.6	4394 8220
431124	doublesex and mab-3 related transcripti	AF284221	Hs.59506	4.6	2753 2754 6843
406636	gb:Homo sapiens (clone WR4.12VL) anti-I	L12064		4.6	32 33 4814
456181	ras inhibitor	L36463	Hs.1030	4.6	4516 4517 8321
408209	ets variant gene 5 (ets-related molecu	NM_004454	Hs.4 3697	4.6	204 205 4944
418452	C-type (calcium dependent, carbohydrate	BE379749	Hs.85201	4.6	1241 5744
419726	bone morphogenetic protein 1	U50330	Hs.1274	4.6	1376 1377 5848
449077	ESTs	AW262836	Hs.252844	4.6	4063 7947

5	427585	collagen, type X, alpha 1 (Schmid metap	D31152	Hs.179729	4.6	2349 6543
	438937	ESTs	AW952654	Hs.73964	4.5	3367 7350
	433819	ESTs	AW511097	Hs.110069	4.5	3007 7042
	430223	nephroblastoma overexpressed gene	NM_002514	Hs.2 35935	4.5	2661 2662 6779
	449294	ESTs	AI651786	Hs.195045	4.5	4079 7961
	419488	nucleophosmin/nucleoplasm 3	AA316241	Hs.90691	4.5	1342 5822
	409637	Homo sapiens mRNA; cDNA DKFp434K0621 (AA323948	Hs.55407	4.5	372 5069
	417166	Paired box protein Pax-3	AA431323	Hs.42146	4.5	1088 5628
10	410407	carbonic anhydrase IX	X66839	Hs.63287	4.5	460 461 5135
	452402	peroxisome proliferative activated rece	AI138530	Hs.22216	4.5	4327 8162
	424223	putative DNA/chromatin binding motif	AJ243706	Hs.143323	4.5	1915 1916 6240
	433212	ESTs	BE218049	Hs.121820	4.5	2956 7001
	421251	enigma (LIM domain protein)	Z28913	Hs.102948	4.5	1521 5957
15	416700	cathepsin D (lysosomal aspartyl) proteas	AW498958	Hs.343475	4.5	1023 5579
	452839	ribosomal protein L44	R96290	Hs.75874	4.4	4359 8189
	445875	Homo sapiens clone 24453 mRNA sequence	AF070524	Hs.13410	4.4	3801 7731
	425848	valyl-tRNA synthetase 2	BE242709	Hs.159637	4.4	2150 6402
	451304	collagen, type XVI, alpha 1	M92642	Hs.26208	4.4	4224 4225 8081
20	435854	putative ankyrin-repeat containing prot	AJ278120	Hs.4996	4.4	3157 3158 7166
	413916	apolipoprotein C-II	N49813	Hs.75615	4.4	753 5367
	440099	DKFZP564G202 protein	AL080058	Hs.6909	4.4	3453 3454 7434
	427674	H2B histone family, member Q	NM_003528	Hs.2 178	4.4	2359 2360 6553
	423811	homeo box C4	AW299598	Hs.50895	4.4	1854 6198
25	453883	cofactor required for Sp1 transcription	AI638516	Hs.347524	4.3	4459 8273
	422515	multifunctional polypeptide similar to	AW500470	Hs.117950	4.3	1693 6079
	442173	KIAA0144 gene product	N76101	Hs.8127	4.3	3552 7524
	451763	hypothetical protein FLJ14220	AW294647	Hs.233634	4.3	4254 8103
	448961	ESTs	AI610643	Hs.187285	4.3	4052 7937
30	421815	membrane protein CH1	AW592146	Hs.108636	4.3	1598 6009
	421920	gamma-aminobutyric acid (GABA) receptor	BE551245	Hs.1438	4.3	1614 6022
	451099	interleukin 13 receptor, alpha 2	R52795	Hs.25954	4.3	4212 8071
	428865	Bart-H-like homeobox 1	BE544095	Hs.164960	4.3	2485 6651
	413385	indoleamine-pyrrole 2,3 dioxygenase	M34455	Hs.840	4.3	710 711 5331
35	421535	phosphoribosylformylglycinamide synth	AB002359	Hs.105478	4.2	1557 1558 5981
	417355	endothelin receptor type B	D13168	Hs.82002	4.2	1100 1101 5640
	432691	mitogen-activated protein kinase 7	U29725	Hs.3080	4.2	2897 2898 6956
	435652	uncharacterized hypothalamus protein HB	N32388	Hs.334370	4.2	3142 7154
	419093	spinal cord-derived growth factor-B	AI804054	Hs.112885	4.2	1304 5792
40	441544	ESTs	AW300043	Hs.127137	4.2	3523 7496
	437044	differentially expressed in Fanconi's a	AL035864	Hs.69517	4.2	3233 7232
	419236	Homo sapiens cDNA FLJ11481 fis, clone H	VAA330447	Hs.135159	4.1	1321 5805
	428242	leukemia inhibitory factor (cholinergic	H55709	Hs.2250	4.1	2411 6594
	433570	ESTs, Weakly similar to S55916 ribosome	AI580053	Hs.109007	4.1	2988 7027
45	430838	hypothetical protein FLJ12015	N46664	Hs.169395	4.1	2733 6829
	424291	ephrin-B1	AL120051	Hs.144700	4.1	1931 6249
	448425	ESTs	AI500359	Hs.371249	4.1	4004 7901
	426798	ESTs	AA385062	Hs.130260	4.1	2275 6487
	432994	ESTs	AA573452	Hs.150941	4.1	2922 6976
50	442285	uncharacterized hypothalamus protein HT	W28729	Hs.374989	4.1	3554 7526
	403171	C2001472*gi15809678[gb]AAB41848.2[U6		4.0	4710
	457458	ESTs	AW972881	Hs.276507	4.0	4552 8352
	451698	endothelin converting enzyme-like 1	Y16187	Hs.26880	3.9	4249 4250 8100
	417437	interferon regulatory factor 4	U52682	Hs.82132	3.9	1123 1124 5656
55	404815	ENSP00000251989*DJ100N22.1 (NOVEL	EGF-		3.9	4761
	452319	transducin-like enhancer of split 1, ho	M99435	Hs.28935	3.7	4313 4314 8152
	424326	ADAM-like disintegrin protease, dactyl	NM_014479	Hs.1 45296	3.7	1934 1935 6252
	407178	AP-2 beta transcription factor	AA195651	Hs.352312	3.6	118 4870
	419762	ESTs	AI608647	Hs.32374	3.5	1387 5855
60	414477	amplified in osteosarcoma	U41635	Hs.76228	3.5	822 823 5425
	412709	KIAA0027 protein	AL022327	Hs.74518	3.3	631 632 5269
	453665	ESTs, Weakly similar to SFRB_HUMAN SPL	AA626250	Hs.326184	3.1	4434 8253
	429329	ESTs	AA456140	Hs.99235	3.1	2547 6699
	429921	collagen, type XI, alpha 1	AA526911	Hs.82772	3.1	2620 6749
65	406367	NM_022357:Homo sapiens putative metallo			3.1	4804

TABLE 7B:

Pkey:	Unique Eos probeset Identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers
Pkey	CAT Number Accession
459702	539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
414315	203914_2 AA494098 Z24878 F13654 AA494040
418059	1164438_1 AA211586 F35799 F29720 AW937408 AW937387 AA211641
411962	2307710_1 AA099050 AA099526 T47733
456034	685585_1 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
426413	372468_1 AW954494 AA377823 BG219617 BG195685 BG616269 AI022688
406636	0_0 L12064 L12083 L12055 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080

TABLE 7C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
85	sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	405001	6015406	Minus	104646-104819
	404977	3738341	Minus	43081-43229
	403088	8954241	Plus	169894-170193,170504-170806
	400499	9796071	Minus	148495-148806
	403593	6862650	Minus	62554-62712,69449-69602
	400651	8117978	Minus	81488-81646
10	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	403071	8954241	Plus	136688-137096
	403081	8954241	Plus	155749-156048,156142-156459
	401203	9743387	Minus	172961-173056,173868-173928
15	403087	8954241	Plus	169511-169795
	406519	3962489	Plus	34617-34928
	402621	9930950	Plus	130806-131036
	406387	9256180	Plus	116229-116371,117512-117651
	401797	6730720	Plus	6973-7118
20	403903	7710671	Minus	101165-102597
	403086	8954241	Plus	169170-169412
	402992	7767907	Minus	42137-42515
	401771	9966243	Plus	166897-167099
	403074	8954241	Plus	143375-143561
25	404030	7671252	Plus	149362-151749
	405681	4544348	Minus	79420-79605
	403857	7708910	Minus	2524-3408
	403291	7230870	Plus	95177-95435
30	402994	2996643	Minus	4727-4969
	402855	9662953	Minus	59763-59909
	403171	9838164	Minus	74502-74703
	404815	5911819	Minus	64494-64691
	406367	9256126	Minus	58313-58489

TABLE 8A

	Pkey:	Unique Eos probeset identifier number				
	Gene name:	UniGene gene title				
40	Accession:	Exemplar Accession number, Genbank accession number				
	UniGene:	UniGene number				
	RATIO:	95th percentile of soft tissue sarcoma AIs divided by the 50th percentile of normal soft tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator				
45	SEQ ID #:	nucleic acid and protein sequences provided on CD for search purposes				
	Pkey	Gene Name	Accession	UniGene	RATIO	SEQ ID #
	413778	myosin, light polypeptide 2, regulatory	AA090235	Hs.75535	29.6	740 5356
	409601	keratin 1 (epidermolytic hyperkeratosis	AF237621	Hs.80828	24.1	365 366 5064
50	425545	Homo sapiens, clone MGC:12401, mRNA, co	N98529	Hs.158295	21.9	2114 6379
	417153	collagen, type II, alpha 1 (primary ost	X57010	Hs.81343	21.5	1084 1085 5625
	426300	delta-like homolog (Drosophila)	U15979	Hs.169228	20.7	2196 2197 6437
	441134	cellular retinoic acid-binding protein	W29092	Hs.346950	20.6	3500 7475
	439496	Homo sapiens, Similar to RIKEN cDNA 111	BE616501	Hs.32343	19.7	3402 7385
55	431103	pleiotrophin (heparin binding growth fa	M57399	Hs.44	19.3	2748 2749 6840
	426752	titin	X69490	Hs.172004	19.1	2266 2267 6482
	412519	troponin T1, skeletal, slow	AA196241	Hs.73980	18.6	598 5244
	422424	prostate differentiation factor	AI186431	Hs.296638	17.4	1681 6070
	452838	preferentially expressed antigen in mel	U65011	Hs.30743	16.9	4357 4358 8188
60	406704	myosin, heavy polypeptide 7, cardiac mu	M21665	Hs.929	16.9	55 56 4826
	400440	nebulin	X83957	Hs.83870	16.5	24 25 4627
	407013	gb:Human nebulin mRNA, partial cds	U35637	Hs.83870	16.2	94 95 4851
	406687	matrix metalloproteinase 11 (stromelysi	M31126	Hs.352054	15.8	49 50 4823
	424687	matrix metalloproteinase 9 (gelatinase	J05070	Hs.151738	15.7	1986 1987 6289
65	407245	titin	X90568	Hs.172004	15.1	132 133 4881
	422640	troponin C, slow	M37984	Hs.118845	15.0	1718 1719 6099
	432874	melanoma inhibitory activity	W94322	Hs.279651	14.9	2913 6968
	414219	ALL1-fused gene from chromosome 1q	W20010	Hs.75823	14.8	789 5397
	448731	ESTs	AI522273	Hs.173179	14.7	4030 7922
70	453857	Ras-induced senescence 1 (RIS1)	AL080235	Hs.35861	14.5	4449 4450 8266
	420783	lectin, galactoside-binding, soluble, 7	AI659838	Hs.99923	14.4	1478 5924
	417070	titin	Z19077	Hs.172004	14.4	1070 5614
	428305	cartilage linking protein 1	AA446628	Hs.2799	14.3	2426 6607
	429359	matrix metalloproteinase 14 (membrane-l	W00482	Hs.2399	13.9	2551 6702
75	426600	VGF nerve growth factor inducible	NM_003378	Hs.1 71014	13.5	2255 2256 6475
	417389	midkine (neurite growth-promoting facto	BE260964	Hs.82045	13.3	1109 5647
	422069	titin-cap (telethonin)	AJ010063	Hs.343603	12.9	1635 1636 6037
	417866	collagen, type XI, alpha 1	AW067903	Hs.82772	12.8	1162 5685
	419875	proenkephalin	AA853410	Hs.93557	12.7	1391 5859
80	413278	interferon-stimulated protein, 15 kDa	BE563085	Hs.833	12.4	695 5322
	416373	ESTs, Weakly similar to S12658 cysteine	AA195845	Hs.73680	12.4	996 5559
	413031	phosphofructokinase, muscle	BE515051	Hs.75160	12.4	671 5304
	427335	G antigen 7B	AA448542	Hs.278444	12.3	2317 6520
	421773	ESTs	W69233	Hs.112457	12.1	1588 6000
	440274	scrapie responsive protein 1	R24595	Hs.7122	11.9	3464 7443
85	422887	ESTs	AI751848	Hs.49215	11.8	1755 6124
	418678	cancer/testis antigen (NY-ESO-1)	NM_001327	Hs.8 7225	11.8	1269 1270 5765

422106	Fc fragment of IgG binding protein	D84239	Hs.111732	11.8	1646 1647 6044
450098	hypothetical protein FLJ21080	W27249	Hs.8109	11.7	4134 8009
422871	collagen, type XI, alpha 2	AL031228	Hs.121509	11.7	1753 1754 6123
417308	KIAA0101 gene product	H60720	Hs.81892	11.7	1094 5634
438549	trinucleotide repeat containing 3	BE386801	Hs.21858	11.6	3331 7320
448719	trinucleotide repeat containing 3	AA033627	Hs.21858	11.5	4028 7920
405001	interleukin enhancer binding factor 1			11.3	4767
452620	ESTs	AA436504	Hs.119286	11.3	4338 8172
413554	secretogranin II (chromogranin C)	AA319146	Hs.75426	11.2	729 5346
431553	cartilage linking protein 1	X78075	Hs.2799	11.2	2792 6874
418399	hypothetical protein FLJ12442	AF131781	Hs.84753	11.2	1232 1233 5738
417515	ataxia-telangiectasia group D-associate	L24203	Hs.82237	11.1	1129 1130 5659
431211	gap junction protein, beta.2, 26kD (con	M86849	Hs.323733	10.9	2762 2763 6850
422599	non-melanotic cells 1, protein (NM23A)	BE387202	Hs.118638	10.8	1710 6092
428411	ESTs	AW291464	Hs.10338	10.8	2439 6617
425247	matrix metalloproteinase 11 (stromelysin	NM_005940	Hs.1 55324	10.7	2072 2073 6351
420208	silver (mouse homolog) like	BE276055	Hs.95972	10.7	1431 5891
419741	ubiquitin carrier protein E2-C	NM_007019	Hs.9 3002	10.6	1379 1380 5850
431360	loricrin	NM_000427	Hs.2 51680	10.6	2776 2777 6861
425308	receptor tyrosine kinase-like orphan re	M97639	Hs.155585	10.6	2087 2088 6362
425154	collagen, type IX, alpha 1	NM_001851	Hs.1 54850	10.5	2055 2056 6339
404977	Insulin-like growth factor 2 (somatomed			10.4	4766
440099	DKFZP564G202 protein	AL080058	Hs.6909	10.4	3453 3454 7434
428311	tryptophan 2,3-dioxygenase	NM_005651	Hs.1 83671	10.3	2429 2430 6609
434060	hypothetical protein PRO1489	AA744902	Hs.197922	10.3	3025 7058
410621	titin	AA194329	Hs.172004	10.1	481 5149
428398	ESTs	AI249368	Hs.98558	10.1	2435 6614
447377	transcription factor AP-2 alpha	X77343	Hs.334334	10.1	3920 3921 7831
419550	KIAA0128 protein; septin 2	D50918	Hs.90998	10.0	1348 1349 5827
429294	Homo sapiens cDNA: FLJ22463 fis, clone	AA095971	Hs.198793	10.0	2540 6693
412636	desmoplakin (DPI, DPL)	NM_004415	Hs.3 49499	10.0	618 619 5259
427666	calmodulin-like skin protein (CLSP)	AI791495	Hs.180142	9.9	2356 6550
419762	ESTs	AI608647	Hs.32374	9.9	1387 5855
449048	similar to S68401 (cattle) glucose indu	Z45051	Hs.22920	9.8	4061 7945
401781	Target Exon			9.8	4662
405443	Target Exon			9.8	4782
428248	ESTs	AI26772	Hs.40479	9.7	2414 6596
450375	a disintegrin and metalloproteinase dom	AA009647	Hs.352537	9.7	4159 8028
409169	(clone PWHLC2-24) myosin light chain 2	F00991	Hs.50889	9.7	316 5029
416658	fibrillin 2 (congenital contractual ar	U03272	Hs.79432	9.6	1020 1021 5577
439180	v-erb-b2 avian erythroblastic leukemia	AI393742	Hs.199067	9.6	3380 7363
417333	bromodomain and PHD finger containing,	AL157545	Hs.173179	9.6	1096 5636
415166	carboxypeptidase Z	NM_003652	Hs.7 8068	9.6	913 914 5491
403088	NM_003319*:Homo sapiens titin (TTN), mR			9.5	4707
418391	tropoin I, skeletal, slow	NM_003281	Hs.8 4573	9.5	1228 1229 5736
427863	MLL septin-like fusion	AF189712	Hs.181002	9.5	2378 2379 6567
440704	insulin-like growth factor binding prot	M69241	Hs.162	9.4	3482 3483 7459
414024	gbzm79g08.r1 Stratagene neuroepitheliu	AA134712	Hs.22410	9.4	769 5379
417930	Homo sapiens mRNA for KIAA1870 protein, H81136	Hs.334604		9.4	1169 5691
424825	procollagen-lysine, 2-oxoglutarate 5-di	AF207069	Hs.153357	9.4	2005 2006 6302
421733	fibroblast growth factor receptor 3 (ac	AL119671	Hs.1420	9.3	1585 5997
406707	myosin, heavy polypeptide 2, skeletal m	S73840	Hs.931	9.3	61 62 4829
445016	reelin	U79716	Hs.12246	9.3	3738 3739 7684
409125	axonal transport of synaptic vesicles	R17268	Hs.343567	9.3	308 5024
421116	retinol-binding protein 1, cellular	T19132	Hs.101850	9.2	1508 5947
416349	myomesin (M-protein) 2 (165kD)	X69089	Hs.79227	9.2	991 992 5556
417689	KIAA0128 protein; septin 2	AA828347	Hs.90998	9.2	1148 5673
456508	ESTs, Weakly similar to AF208855 1 BM-0	AA502764	Hs.123469	9.1	4521 8325
435968	integral membrane protein 3	AW161481	Hs.111577	9.1	3165 7173
428405	cholinergic receptor, nicotinic, alpha	Y00762	Hs.2266	9.1	2436 2437 6615
415989	ESTs	AI267700	Hs.351201	9.0	962 5530
443426	chromosome 20 open reading frame 1	AF098158	Hs.9329	9.0	3621 3622 7586
453597	myo-inositol 1-phosphate synthase A1	BE281130	Hs.381118	9.0	4429 8249
421815	membrane protein CH1	AW592146	Hs.108636	9.0	1598 6009
434352	small muscle protein, X-linked	AF129505	Hs.86492	8.9	3047 3048 7075
452223	hypothetical protein MGC2827	AA425467	Hs.8035	8.9	4302 8142
409178	kallikrein 5	BE393948	Hs.50915	8.9	319 5032
418140	microfibrillar-associated protein 2	BE613836	Hs.83551	8.8	1196 5713
418113	SRY (sex determining region Y)-box 4	AI272141	Hs.83484	8.8	1194 5711
408915	hepatocellular carcinoma novel gene-3 pr	NM_016651	Hs.4 8950	8.8	274 275 4998
412719	ESTs	AW016610	Hs.816	8.7	633 5270
458079	Homo sapiens similar to RIKEN cDNA 2810	AI796870	Hs.381220	8.7	4566 8363
412276	macrophage migration inhibitory factor	BE262621	Hs.73798	8.6	580 5229
428087	troponin C2, fast	AA100573	Hs.182421	8.6	2396 6582
433447	neuronal pentraxin II	U29195	Hs.3281	8.6	2980 2981 7021
428928	cadherin 1, type 1, E-cadherin (epithel	BE409838	Hs.194657	8.5	2489 6654
416072	growth associated protein 43	AL110370	Hs.79000	8.5	969 5537
414416	hypothetical protein MGC2721	AW409985	Hs.76084	8.5	813 5417
418390	titin immunoglobulin domain protein (my	AF133820	Hs.84665	8.5	1226 1227 5735
442573	branched chain aminotransferase 1, cyto	H93366	Hs.7567	8.5	3570 7541
450447	hypothetical protein P15-2	AF212223	Hs.25010	8.5	4168 4169 8036
417435	carbonic anhydrase III, muscle specific	NM_005181	Hs.8 2129	8.4	1121 1122 5655
402992	Target Exon			8.4	4700
421579	stem cell growth factor; lymphocyte sec	NM_002975	Hs.1 05927	8.4	1567 1568 5987
422633	enolase 3, (beta, muscle)	X56832	Hs.118804	8.4	1716 1717 6098
457411	Iroquois-class homeobox protein IRX2	AW085961	Hs.130093	8.3	4549 8349

	409103	XAGE-1 protein	AF251237	Hs.112208	8.3	304 305 5021
	417409	syndecan 1	BE272506	Hs.82109	8.3	1113 5650
	428484	solute carrier family 7 (cationic amino	AF104032	Hs.184601	8.3	2449 2450 6624
5	412104	Homo sapiens, Similar to RIKEN cDNA 221	AW205197	Hs.240951	8.3	569 5220
	417900	CDC20 (cell division cycle 20, S. cerev	BE250127	Hs.82906	8.3	1165 5688
	449722	cyclin B1	BE280074	Hs.23960	8.2	4112 7990
	425227	ESTs	H84455	Hs.40639	8.2	2069 6348
	414821	Fc fragment of IgG, high affinity Ia, r	M63835	Hs.77424	8.2	876 877 5465
10	407824	Homo sapiens cDNA FLJ14388 fis, clone	H AA147884	Hs.9812	8.2	166 4910
	418067	cystatin E/M	AI127958	Hs.83393	8.2	1189 5706
	457869	Homo sapiens, alpha-1 (VI) collagen	AU077186	Hs.108885	8.2	4561 8359
	409633	ESTs	AW449822	Hs.55200	8.1	371 5068
	412926	macrophage myristoylated alanine-rich C	AI879076	Hs.75061	8.1	655 5290
	426429	myosin-binding protein C, slow-type	X73114	Hs.169849	8.1	2224 2225 6456
15	440042	ESTs	AI073387	Hs.133898	8.1	3448 7430
	441636	Homo sapiens mRNA; cDNA DKFZp566E183	(f AA081846	Hs.7921	8.1	3530 7502
	421458	carbohydrate (keratan sulfate Gal-6) su	NM_003654	Hs.1 04576	8.0	1543 1544 5972
	427239	ubiquitin carrier protein	BE270447	Hs.356512	8.0	2311 6515
20	413511	arginine-rich, mutated in early stage I	AI627178	Hs.75412	8.0	728 5345
	411296	growth suppressor 1	BE207307	Hs.10114	8.0	524 5183
	439979	hypothetical protein FLJ10430	AW600291	Hs.6823	8.0	3442 7424
	423575	Intron of perostin (OSF-2os)	C18863	Hs.163443	7.9	1820 6173
	454140	hypothetical protein FLJ10474	AB040888	Hs.41793	7.9	4493 4494 8301
25	428182	ESTs, Weakly similar to GGC1_HUMAN	G AN BE386042	Hs.293317	7.9	2403 6588
	440087	hypothetical protein FLJ22678	W28969	Hs.7718	7.9	3452 7433
	425234	ESTs, Weakly similar to I38022 hypothet	AW152225	Hs.165909	7.8	2070 6349
	400231	Eos Control		Hs.169476	7.8	4603
	407619	collagen, type IX, alpha 2	AL050341	Hs.37165	7.8	146 147 4892
30	410366	hypothetical protein	AI267589	Hs.302689	7.8	457 5133
	406837	immunoglobulin kappa constant	R70292	Hs.156110	7.8	69 4836
	406782	gb:zw20111.s1 Soares ovary tumor NbHOT	AA430373		7.8	65 4832
	431629	interferon, alpha-inducible protein (cl	AU077025	Hs.265827	7.8	2803 6881
	422867	cartilage oligomeric matrix protein (ps	L32137	Hs.1584	7.8	1751 1752 6122
35	408989	KIAA0746 protein	AW361666	Hs.49500	7.8	290 5010
	420798	keratin 10 (epidermolytic hyperkeratosi	W93774	Hs.99936	7.7	1479 5925
	427378	melanoma antigen, family D, 1	BE515037	Hs.177556	7.7	2322 6523
	409041	Hypothetical protein, XP_051860 (KIAA11	AB033025	Hs.50081	7.7	299 300 5017
	447033	Predicted gene: Eos cloned; secreted w/	AI357412	Hs.157601	7.7	3885 7802
40	423217	collagen, type VII, alpha 1 (epidermoly	NM_000094	Hs.1 640	7.7	1784 1785 6147
	409096	sarcomeric muscle protein	AA194412	Hs.50550	7.7	302 5019
	418506	Unknown protein for MGC:29643 (formerly	AA084248	Hs.372651	7.7	1247 5748
	414152	thrombospondin 4	NM_003248	Hs.7 5774	7.7	782 783 5391
	412140	RAB6 Interacting, kinesin-like (rabkine	AA219691	Hs.73625	7.7	573 5223
45	401780	NM_005557*:Homo sapiens keratin 16 (loc			7.7	4661
	437696	hypothetical protein dJ37E16.5	Z83844	Hs.5790	7.6	3281 7274
	431958	cadherin 3, type 1, P-cadherin (placent	X63629	Hs.2877	7.6	2834 2835 6904
	433075	sortilin 1	NM_002959	Hs.3 51872	7.6	2936 2937 6987
	427747	serine/threonine kinase 12	AW411425	Hs.180655	7.6	2365 6557
50	444006	type I transmembrane protein Fn14	BE395085	Hs.334762	7.6	3668 7627
	416378	ankyrin repeat domain 2 (stretch respon	AW044467	Hs.73708	7.6	997 5560
	409327	collagen, type IX, alpha 3	L41162	Hs.53563	7.6	341 342 5047
	429329	Homo sapiens pannexin 3 (PANX3)	AA456140	Hs.99235	7.5	2547 6699
	432481	Intron of collagen, type XI, alpha 1	AW451645	Hs.151504	7.5	2876 6938
55	427474	aggrecan 1 (chondroitin sulfate proteog	U13192	Hs.2159	7.5	2334 6532
	436481	HSPC150 protein similar to ubiquitin-co	AA379597	Hs.5199	7.5	3192 7197
	426363	transforming growth factor, beta 3	M58524	Hs.2025	7.5	2210 2211 6446
	451099	interleukin 13 receptor, alpha 2	R52795	Hs.25954	7.5	4212 8071
	440650	Human DNA sequence from PAC 75N13 on	ch R44692	Hs.326801	7.5	3477 7455
60	408536	ESTs	AW381532	Hs.135188	7.5	236 4967
	412641	heat shock 90kD protein 1, beta	M16660	Hs.74335	7.5	620 621 5260
	421016	transcription factor 3 (E2A immunoglobu	AA504583	Hs.101047	7.4	1497 5937
	438746	Human melanoma-associated antigen p97	(AI885815	Hs.184727	7.4	3353 7337
	426509	pentaxin-related gene, rapidly induced	M31166	Hs.2050	7.4	2243 2244 6468
65	439755	B7 homolog 3	AW748482	Hs.77873	7.4	3430 7413
	453392	SRY (sex determining region Y)-box 11	U23752	Hs.32964	7.4	4416 4417 8239
	418203	CDC28 protein kinase 2	X54942	Hs.83758	7.4	1202 1203 5719
	412006	ESTs	AW451618	Hs.380683	7.3	565 5217
	414945	lymphocyte antigen 6 complex, locus E	BE076358	Hs.77667	7.3	894 5477
70	407656	Homo sapiens mRNA; cDNA DKFZp434B2119	(AW747986	Hs.37443	7.3	148 4893
	438949	abl-interactor 12 (SH3-containing prote	AA058571	Hs.285728	7.3	3369 7352
	413436	sphingosine kinase 1	AF238083	Hs.68061	7.3	721 722 5339
	410001	kallikrein 11	AB041036	Hs.57771	7.3	403 404 5094
	435793	KIAA1313 protein	AB037734	Hs.4993	7.3	3152 3153 7162
75	446051	ephrin-A3	BE048061	Hs.37054	7.3	3816 7744
	426440	solute carrier family 2 (facilitated gl	BE382756	Hs.169902	7.3	2228 6458
	444371	forkhead box M1	BE540274	Hs.239	7.3	3696 7651
	449294	ESTs	AI651786	Hs.195045	7.3	4079 7961
	401673	C16001416*:gil12743112[ref]XP_010131.2]			7.2	4658
80	401797	Target Exon			7.2	4663
	412755	ESTs, Weakly similar to P4HA_HUMAN	PROL BE144306	Hs.179891	7.2	637 5274
	424415	enolase 2, (gamma, neuronal)	NM_001975	Hs.1 46580	7.2	1947 1948 6263
	401566	NM_005159*:Homo sapiens actin, alpha, ca			7.2	4654
	430713	eukaryotic translation elongation facto	AA351647	Hs.2642	7.2	2726 6824
85	432239	matrix metalloproteinase 13 (collagenas	XB1334	Hs.2936	7.2	2856 2857 6921
	438682	EBP50-PDZ interactor of 64 kD	AA354489	Hs.17719	7.2	3346 7331
	412939	eukaryotic translation elongation facto	AW411491	Hs.75069	7.2	657 5292

	453665	ESTs, Weakly similar to SFRB_HUMAN SPLI AA626250	Hs.326184	7.2	4434 8253	
	428471	stratiffin	X57348	Hs.184510	7.2	2445 2446 6622
	409893	minichromosome maintenance deficient (S AW247090	Hs.57101	7.2	397 5088	
5	425397	topoisomerase (DNA) II alpha (170kD)	J04088	Hs.156346	7.2	2099 2100 6369
	449226	KIAA0367 protein	AB002365	Hs.23311	7.2	4072 4073 7955
	421717	divalent cation tolerant protein CUTA	AF230924	Hs.107187	7.2	1583 1584 5996
	437898	ESTs	W81260	Hs.43410	7.1	3293 7286
	413011	biglycan	AW068115	Hs.821	7.1	669 5302
10	421307	Homo sapiens mRNA; cDNA DKFZp434B0425 (BE539976	Hs.103305	7.1	1528 5963	
	435652	uncharacterized hypothalamus protein HB N32388	Hs.334370	7.1	3142 7154	
	418322	cyclin-dependent kinase inhibitor 3 (CD	AA284166	Hs.84113	7.1	1214 5727
	453876	ESTs, Weakly similar to I38022 hypothet	AW021748	Hs.110406	7.1	4457 8271
	444026	hypothetical protein FLJ14957	AA205759	Hs.10119	7.1	3672 7631
15	421508	absent in melanoma 2	NM_004833	Hs.1 05115	7.1	1551 1552 5977
	426798	ESTs	AA385062	Hs.130260	7.1	2275 6487
	436608	down syndrome critical region protein D	AA628980	Hs.192371	7.0	3205 7207
	436748	collagen, type VI, alpha 2	BE159107	Hs.159263	7.0	3212 7213
	420103	aldehyde dehydrogenase 1 family, member	AA382259	Hs.95197	7.0	1416 5878
	453830	ESTs	AA534296	Hs.20953	7.0	4445 8263
20	422043	retinoic acid induced 1	AL133649	Hs.110953	7.0	1629 1630 6033
	419222	spermine synthase	AD001528	Hs.89718	7.0	1318 1319 5803
	427099	odd Oz/ten-m homolog 2 (Drosophila, mou	AB032953	Hs.173560	7.0	2302 2303 6509
	414346	splicing factor 3b, subunit 2, 145kD	AL035770	Hs.75916	7.0	806 5411
	411089	cell division cycle 2-like 1 (PITSLRE p	AA456454	Hs.214291	7.0	513 5173
25	407811	cysteine knot superfamily 1, BMP antago	AW190902	Hs.40098	7.0	164 4908
	415314	glycoprotein M6B	N88802	Hs.5422	6.9	921 5497
	407792	putative secreted ligand homologous to	AJ077715	Hs.39384	6.9	162 4906
	424001	paternally expressed 10	W67883	Hs.137476	6.9	1882 6217
30	400499	C10001858:gij6679124[ref]NP_032759.1] n			6.9	4628
	446142	ESTs	AJ754693	Hs.145968	6.9	3820 7748
	408988	Homo sapiens clone TUA8 Cri-du-chat reg	AL119844	Hs.49476	6.9	289 5009
	412974	emopamil-binding protein (sterol isomer	R18978	Hs.75105	6.9	664 5297
	411410	laminin, gamma 3	R20693	Hs.69954	6.9	535 5193
35	425256	collapsin response mediator protein 1	BE297611	Hs.155392	6.9	2074 6352
	427171	NIPSNAP, C. elegans, homolog 1	AJ001258	Hs.173878	6.9	2307 2308 6512
	421406	Meis (mouse) homolog 2	AF179897	Hs.104105	6.9	1541 1542 5971
	451934	ESTs	AJ540842	Hs.61082	6.9	4262 8109
	433487	histone deacetylase 2	U31814	Hs.3352	6.9	2983 2984 7023
40	411852	ESTs, Weakly similar to T00329 hypothet	AA528140	Hs.107515	6.8	555 5208
	415752	putative transmembrane protein	BE314524	Hs.78776	6.8	945 5517
	429259	Plakophilin	AA420450	Hs.380088	6.8	2535 6689
	448357	RAB38, member RAS oncogene family	N20169	Hs.108923	6.8	3994 7893
	451766	ephrin-B3	NM_001406	Hs.2 6988	6.8	4255 4256 8104
45	416322	pyrroline-5-carboxylate reductase 1	BE019494	Hs.79217	6.8	989 5554
	447646	Homo sapiens mRNA for KIAA1753 protein,	BE619752	Hs.66053	6.8	3945 7852
	413916	apolipoprotein C-II	N49813	Hs.75615	6.8	753 5367
	414806	phosphatidylserine synthase 1	D14694	Hs.77329	6.8	871 872 5462
	418478	cyclin-dependent kinase inhibitor 2A (m	U38945	Hs.1174	6.8	1245 1246 5747
50	433577	ESTs	AW007080	Hs.284192	6.8	2989 7028
	451811	hypothetical protein MGC1136	AA663485	Hs.8719	6.8	4259 8106
	429345	hypothetical protein	R11141	Hs.199695	6.8	2548 6700
	433101	Homo sapiens mRNA; cDNA DKFZp566L203 (f	AW572317	Hs.12082	6.8	2940 6990
	430413	small inducible cytokine A5 (RANTES)	AW842182	Hs.241392	6.7	2693 6801
55	426457	chimerin (chimaerin) 1	AW894667	Hs.380138	6.7	2229 8459
	418418	ESTs	R61527	Hs.237517	6.7	1238 5742
	426831	S-adenosylhomocysteine hydrolase	BE296216	Hs.172673	6.7	2278 6490
	432179	EphB3	X75208	Hs.2913	6.7	2849 2850 6915
	412709	KIAA0027 protein	AL022327	Hs.74518	6.7	631 632 5269
60	421707	lectormedin-2	NM_014921	Hs.1 07054	6.7	1581 1582 5995
	435066	dyskeratosis congenita 1, dyskerin	BE261750	Hs.4747	6.7	3102 7121
	442577	ESTs	AA292998	Hs.163900	6.6	3571 7542
	442923	ESTs, Weakly similar to unnamed protein	AW248322	Hs.95835	6.6	3590 7558
	427528	minichromosome maintenance deficient (S	AJ077143	Hs.179565	6.6	2341 6537
65	423739	ESTs	AA398155	Hs.97600	6.6	1842 6190
	449780	ribosomal protein L44	AA443241	Hs.75874	6.6	4114 7992
	433972	cisplatin resistance-associated overexp	AJ878910	Hs.278670	6.6	3021 7054
	406868	immunoglobulin heavy constant gamma 3 (AA505445	Hs.300697	6.6	72 4839
	450923	ESTs	AW043951	Hs.38449	6.6	4203 8063
70	454390	KIAA0906 protein	AB020713	Hs.56966	6.6	4497 4498 8304
	409632	serine (or cysteine) proteinase inhibit	W74001	Hs.55279	6.6	370 5067
	409698	short stature homeobox 2	AF022654	Hs.55967	6.6	378 379 5074
	410422	Homo sapiens, clone MGC:15203, mRNA, co	AL042014	Hs.63348	6.6	462 5136
	416078	protein tyrosine phosphatase, receptor	AL034349	Hs.79005	6.6	970 5538
75	417632	glycoprotein M6B	R20855	Hs.379090	6.6	1141 5667
	447499	protocadherin beta 16	AW262580	Hs.147674	6.6	3934 7842
	430200	geminin	BE613337	Hs.234896	6.5	2658 6777
	441094	MYC-associated zinc finger protein (pur	U33819	Hs.7647	6.5	3497 3498 7473
	420197	ESTs, Weakly similar to A57291 cytokine	AW139647	Hs.88134	6.5	1429 5889
	409731	thymosin, beta, identified in neuroblas	AA125985	Hs.56145	6.5	386 5080
80	452046	KIAA0802 protein	AB018345	Hs.27657	6.5	4275 4276 8120
	448672	ESTs	AJ955511	Hs.89582	6.5	4025 7917
	445084	hypothetical protein FLJ14761	H38914	Hs.250848	6.5	3742 7687
	408562	roundabout (axon guidance receptor, Dro	AI436323	Hs.31141	6.5	240 4971
	414438	thioredoxin	AJ879277	Hs.76136	6.5	816 5420
85	420568	protocadherin alpha 10	F09247	Hs.247735	6.5	1462 5913
	452017	prostate cancer associated protein 7	AF109302	Hs.27495	6.5	4270 8117

	416820	glucose-6-phosphate dehydrogenase	NM_000402	Hs.8 0206	6.4	1035 1035 5587
	441020	ESTs	W79283	Hs.35952	6.4	3495 7471
	410361	guanylate binding protein 1, interferon	BE391804	Hs.62661	6.4	456 5132
5	435025	anchor attachment protein 1 (Gaa1p, yea	T08990	Hs.4742	6.4	3098 7117
	410102	ESTs; homologue of PEM-3 (Clona savigny	AW248508	Hs.279727	6.4	422 5107
	431204	cytochrome c oxidase subunit I via polype	F28841	Hs.250760	6.4	2760 6848
	448390	hypothetical protein	AL035414	Hs.21068	6.4	3999 7897
	411102	triadin	AA401295	Hs.23926	6.4	515 5175
10	420028	carbohydrate (N-acetylglucosamine-6-O)	AB014680	Hs.8786	6.4	1408 1409 5872
	434149	hypothetical protein MGC5469	Z43829	Hs.244624	6.4	3030 7063
	447733	MAD2 (mitotic arrest deficient, yeast,	AF157482	Hs.19400	6.4	3955 3956 7860
	423605	cadherin 19, type 2	AF047826	Hs.129887	6.4	1826 1827 6179
	446342	solute carrier family 7 (cationic amino	BE298665	Hs.14846	6.4	3836 7762
15	405516	ENSP00000200457:Thyroid receptor inter			6.4	4785
	430681	ESTs	AW969675	Hs.291232	6.4	2719 6819
	420005	ESTs	AW271106	Hs.133294	6.3	1407 5871
	448595	KIAA0644 gene product	AB014544	Hs.21572	6.3	4015 4016 7910
	414086	aldehyde dehydrogenase 1 family, member	AA114016	Hs.75746	6.3	775 5384
20	417933	thymidylate synthase	X02308	Hs.82962	6.3	1170 1171 5692
	414482	endothelin receptor type A	S57498	Hs.76252	6.3	824 825 5426
	453023	serine protease inhibitor, Kunitz type,	AW028733	Hs.31439	6.3	4380 8208
	423232	leucine-rich neuronal protein	BE244625	Hs.125742	6.3	1787 6149
	451763	hypothetical protein FLJ14220	AW294647	Hs.233634	6.3	4254 8103
25	412182	Splicing factor, arginine/serine-rich,	AA205588	Hs.73737	6.3	577 5226
	452291	CDC7 (cell division cycle 7, S. cerevis	AF015592	Hs.28853	6.3	4310 4311 8150
	438203	ESTs	BE540090	Hs.7345	6.3	3308 7300
	444329	hypothetical protein FLJ12921	W73753	Hs.209637	6.3	3693 7648
30	404030	NM_015669: Homo sapiens protocadherin b			6.3	4735
	431183	KDEL (Lys-Asp-Glu-Leu) endoplasmic reti	NM_006855	Hs.250696	6.3	2756 2757 6845
	428450	KIAA0175 gene product	NM_014791	Hs.1 84339	6.3	2443 2444 6621
	400297	hypothetical protein DKFZp564O1278	AI127076	Hs.288381	6.3	7 4618
	452732	Homo sapiens, clone IMAGE:3535294, mRNA	BE300078	Hs.80449	6.3	4348 8180
	426053	poly(A)-binding protein, cytoplasmic 1	U68105	Hs.172182	6.3	2163 6412
35	412507	EphA4	L36645	Hs.73964	6.3	596 597 5243
	442117	ESTs; hypothetical protein for IMAGE:44	AW664964	Hs.128899	6.3	3551 7523
	443247	c-Myc target JPO1	BE614387	Hs.333893	6.3	3611 7578
	422511	collagen, type XVII, alpha 1	AU076442	Hs.117938	6.3	1692 6078
	429612	pituitary tumor-transforming 1	AF062649	Hs.252587	6.3	2586 2587 6726
40	446334	polymerase (RNA) II (DNA directed) poly	U52427	Hs.75069	6.2	3834 3835 7761
	431567	Homo sapiens cDNA: FLJ21410 fis, clone	N51357	Hs.260855	6.2	2799 6878
	450785	Homo sapiens, alpha-1 (VI) collagen	AA852713	Hs.108885	6.2	4193 8056
	424263	L1 cell adhesion molecule (hydrocephalu	M77640	Hs.1757	6.2	1925 1926 6246
	450835	hypothetical protein FLJ10767	BE262773	Hs.25584	6.2	4199 8060
45	421295	DC2 protein	AW081061	Hs.103180	6.2	1524 5960
	453883	cofactor required for Sp1 transcription	AI638516	Hs.347524	6.2	4459 8273
	442432	hypothetical protein FLJ23468	BE093589	Hs.38178	6.1	3563 7535
	422684	H2A histone family, member Z	BE561617	Hs.119192	6.1	1726 6105
	419833	Homo sapiens tryptophanyl-tRNA syntheta	AA251131	Hs.220697	6.1	1388 5856
50	453331	ESTs	AI240665	Hs.352537	6.1	4413 8236
	432693	ESTs	AW449630	Hs.293790	6.1	2900 6958
	414591	ESTs, Weakly similar to ALU8_HUMAN ALU	AI888490	Hs.248107	6.1	834 6435
	400263	Eos Control		Hs.75309	6.1	4613
	438915	Williams-Beuren syndrome chromosome reg	AA280174	Hs.355711	6.1	3365 7348
55	406672	major histocompatibility complex, class	M26041	Hs.198253	6.1	43 44 4820
	435099	flap structure-specific endonuclease 1	AC004770	Hs.4756	6.1	3104 3105 7123
	422100	ADP-ribosylation factor-like 7	AI096988	Hs.111554	6.1	1644 6042
	415702	gb:HSPD18414 HM3 Homo sapiens cDNA clon	F28877	Hs.73680	6.1	942 5515
	408901	hypothetical protein FLJ10468	AK001330	Hs.48855	6.1	272 273 4997
60	402810	NM_004930: Homo sapiens capping protein			6.1	4692
	421335	ARS component B	X99977	Hs.103505	6.1	1529 1530 5964
	425272	ESTs, Weakly similar to C35826 hypothet	AA354138	Hs.47209	6.1	2078 6355
	438944	KIAA1444 protein	AA302517	Hs.92732	6.1	3368 7351
	430044	ESTs	AA464510	Hs.152812	6.1	2642 6765
65	416640	neuron-specific protein	BE262478	Hs.13406	6.1	1019 5576
	424440	ESTs	AA340743	Hs.133208	6.1	1951 6266
	403857	Target Exon			6.1	4730
	406836	immunoglobulin kappa constant 1	AW514501	Hs.156110	6.0	68 4835
	421878	Homo sapiens cDNA FLJ11643 fis, clone H	AA299652	Hs.111496	6.0	1607 6017
70	419452	PTK7 protein tyrosine kinase 7	U33635	Hs.90572	6.0	1340 1341 5821
	407688	Human D9 splice variant B mRNA, complet	W25317	Hs.37616	6.0	149 4894
	430686	desmoglein 1	NM_001942	Hs.2 633	6.0	2721 2722 6821
	427375	metallocarboxypeptidase CPX-1	AL035460	Hs.177536	6.0	2320 2321 6522
	451698	endothelin converting enzyme-like 1	Y16187	Hs.26880	6.0	4249 4250 8100
75	419956	cadherin 19, type 2	AL137939	Hs.40096	6.0	1398 5865
	430439	DKFZP434B061 protein	AL133561	Hs.380155	6.0	2695 2696 6803
	425292	37 kDa leucine-rich repeat (LRR) protei	NM_005824	Hs.1 55545	6.0	2083 2084 6359
	400244	Eos Control		Hs.7957	6.0	4606
	407788	S100 calcium-binding protein A2	BE514982	Hs.38991	6.0	161 4905
80	406663	immunoglobulin heavy constant mu	U24683		6.0	39 40 4818
	429903	cyclin-dependent kinase 5, regulatory su	AL134197	Hs.93597	6.0	2616 6748
	426158	v-erb-b2 avian erythroblastic leukemia	NM_001982	Hs.1 99067	6.0	2184 2185 6428
	408829	heparan sulfate (glucosamine) 3-O-sulfo	NM_006042	Hs.4 8384	6.0	264 265 4991
	424326	ADAM-like disintegrin protease, decysin	NM_014479	Hs.1 45296	6.0	1934 1935 6252
	410240	synaptotagmin 2	AL157424	Hs.61289	6.0	437 5117
85	408938	ESTs	AA059013	Hs.22607	6.0	279 5002
	409028	Z-band alternatively spliced PDZ-motif	AB014513	Hs.49998	6.0	296 297 5015

	411372	low density lipoprotein receptor (famil	AI147861	Hs.213289	6.0	530 5188
	420303	KIAA1474 protein	AA258282	Hs.278436	6.0	1443 5900
	407844	ESTs	AW073716	Hs.8037	6.0	168 4912
5	431448	hypothetical protein DKFZp564O1278	AL137517	Hs.306201	6.0	2785 2786 6869
	415701	gamma-glutamyl hydrolase (conjugase, fo	NM_003878	Hs.78619	6.0	940 941 5514
	428834	ESTs	AW899713	Hs.10338	6.0	2479 6647
	425930	ribosomal protein L18a	H93691	Hs.163593	6.0	2154 6406
	421506	thymidine kinase 1, soluble	BE302796	Hs.105097	6.0	1550 5976
10	451149	RNA binding motif protein 8B	AL047586	Hs.10283	5.9	4214 8073
	448493	ESTs	AI524124	Hs.270307	5.9	4006 7903
	437330	Homo sapiens mRNA; cDNA DKFZp761J1112 (AL353944	Hs.50115	5.9	3253 7250
	416297	solute carrier family 25 (mitochondrial	AA157634	Hs.79172	5.9	988 5553
	424049	KIAA0624 protein	AB014524	Hs.136380	5.9	1889 1890 6222
15	433124	hypothetical protein SMAP31	U51712	Hs.13775	5.9	2942 6992
	422809	hypothetical protein FLJ10549	AK001379	Hs.121028	5.9	1741 1742 6115
	414522	immunoglobulin J chain	AW518944	Hs.76325	5.9	827 5428
	451598	ESTs	N29102	Hs.79658	5.9	4241 8093
	414732	minichromosome maintenance deficient (S	AW410976	Hs.77152	5.9	859 5453
	408122	hypothetical protein FLJ10718	AI432652	Hs.42824	5.9	193 4935
20	433001	clone HQ0310 PRO0310p1	AF217513	Hs.279905	5.9	2923 2924 6977
	414763	quiescin Q6	U97276	Hs.77266	5.9	866 867 5459
	434449	hypothetical protein FLJ22041 similar t	AW953484	Hs.3849	5.9	3057 7083
	418394	Kruppel-like factor 5 (intestinal)	AF132818	Hs.84728	5.9	1230 1231 5737
	417891	protein phosphatase 1, regulatory (inhi	W79410	Hs.82887	5.9	1164 5687
25	434203	hypothetical protein PRO1855	BE262677	Hs.283558	5.9	3033 7066
	443780	activating transcription factor 5	NM_012068	Hs.9 754	5.9	3643 3644 7606
	439963	platelet-activating factor acetylhydrol	AW247529	Hs.6793	5.9	3441 7423
	431243	syndecan 4 (amphiglycan, ryudocan)	U46455	Hs.252189	5.9	2767 6854
30	427400	hypothetical protein FLJ11939	AW245084	Hs.94229	5.9	2325 6525
	429207	ESTs	AA447941	Hs.123423	5.9	2532 6686
	417675	similar to murine leucine-rich repeat p	AI808607	Hs.3781	5.9	1144 5670
	410929	ESTs	H47233	Hs.30643	5.8	504 5166
	408716	Homo sapiens mRNA for KIAA1769 protein,	AI567839	Hs.151714	5.8	251 4981
35	432691	mitogen-activated protein kinase 7	U29725	Hs.3080	5.8	2897 2898 6956
	432247	ESTs	AA531287	Hs.105805	5.8	2859 6923
	434629	glioma-amplified sequence-41	AA789081	Hs.4029	5.8	3064 7090
	431070	transcription factor 19 (SC1)	AW408164	Hs.249184	5.8	2744 6837
	426991	Homo sapiens cDNA FLJ10674 fis, clone N	AK001536	Hs.214410	5.8	2294 6502
40	436895	carbonic anhydrase XII	AF037335	Hs.5338	5.8	3224 3225 7224
	413313	glycyl-LRNA synthetase	NM_002047	Hs.2 93885	5.8	699 700 5325
	428342	Homo sapiens cDNA FLJ13458 fis, clone P	AI739168	Hs.349283	5.8	2432 6611
	424441	H2A histone family, member X	X14850	Hs.147097	5.8	1952 1953 6267
	445930	Homo sapiens clone 24747 mRNA sequence	AF055009	Hs.13456	5.8	3804 7734
45	402260	NM_001436*:Homo sapiens fibrillarin (FB			5.8	4676
	422386	heparan sulfate (glucosamine) 3-O-sulfo	AF105374	Hs.115830	5.8	1676 1677 6067
	406621	immunoglobulin lambda locus	X57809	Hs.181125	5.8	26 27 4810
	414638	stress-associated endoplasmic reticulum	W03516	Hs.76698	5.8	840 5440
	437597	SCG10-like-protein	AA730767	Hs.285753	5.8	3273 7267
50	418110	hypothetical protein FLJ22202	R43523	Hs.217754	5.8	1193 5710
	422268	maternal G10 transcript	N25485	Hs.330310	5.8	1667 6060
	413566	sprouty (Drosophila) homolog 4	AW604451	Hs.381153	5.8	730 5347
	414695	proteasome (prosome, macropain) subunit	BE439915	Hs.76913	5.8	850 5446
	415200	SWI/SNF related, matrix associated, act	AL040328	Hs.78202	5.8	920 5496
55	422627	transforming growth factor, beta-induce	BE336857	Hs.118787	5.8	1715 6097
	415672	ESTs	N53097	Hs.193579	5.8	937 5511
	419437	neogenin (chicken) homolog 1	U61262	Hs.90408	5.8	1338 1339 5820
	420531	ribosome binding protein 1 (dog 180kD h	AI652069	Hs.98614	5.8	1459 5911
	433058	Homo sapiens, Similar to CG8405 gene pr	H86865	Hs.380962	5.7	2933 6985
60	430285	ESTs	AI917602	Hs.106440	5.7	2675 6789
	400252	NM_004651*:Homo sapiens ubiquitin speci		Hs.171501	5.7	4609
	409637	Homo sapiens mRNA; cDNA DKFZp434K0621 (AA323948	Hs.55407	5.7	372 5069
	445515	Homo sapiens, clone IMAGE:3457003, mRNA	BE388665	Hs.179999	5.7	3776 7713
	450847	stanniocalcin 1	NM_003155	Hs.2 5590	5.7	4201 4202 8062
65	415444	solute carrier family 20 (phosphate tra	BE247295	Hs.78452	5.7	926 5502
	425863	Human unidentified mRNA, partial sequen	U43604	Hs.159901	5.7	2152 6404
	448386	KIAA1329 protein	AB037750	Hs.21061	5.7	3997 3998 7896
	408482	adenosine A2b receptor	NM_000676	Hs.4 5743	5.7	226 227 4959
	429921	collagen, type XI, alpha 1	AA526911	Hs.82772	5.7	2620 6749
70	426968	amphiphysin (Stiff-Mann syndrome with b	U07616	Hs.173034	5.7	2290 2291 6499
	440516	cadherin 2, type 1, N-cadherin (neurona	S42303	Hs.161	5.7	3472 3473 7451
	444783	anillin (Drosophila Scraps homolog), ec	AK001468	Hs.62180	5.7	3722 3723 7672
	424223	putative DNA/chromatin binding motif	AJ243706	Hs.143323	5.7	1915 1916 6240
	450087	MUM2 protein	BE293180	Hs.24379	5.7	4133 8008
75	427550	nuclear RNA helicase, DECD variant of D	BE242818	Hs.311609	5.7	2342 6538
	428977	cyclin B2	AK001404	Hs.194698	5.7	2496 6659
	428171	ribosomal protein L35	AA489323	Hs.182825	5.7	2402 6587
	422311	cytokine receptor-like factor 1	AF073515	Hs.114948	5.7	1669 1670 6062
	418533	myosin-binding protein C, fast-type	NM_004533	Hs.8 5937	5.7	1253 1254 5754
80	436396	wingless-type MMTV Integration site fam	AI683487	Hs.152213	5.7	3184 7189
	431457	integrin, alpha 11	NM_012211	Hs.2 56297	5.7	2787 2788 6870
	417920	adenosine monophosphate deaminase 2 (is	S47833	Hs.82927	5.7	1167 1168 5690
	428520	hypothetical protein FLJ10097	AA331901	Hs.184736	5.7	2452 6626
	441544	ESTs	AW300043	Hs.127137	5.7	3523 7496
	429002	junction plakoglobin	AW248439	Hs.2340	5.6	2498 6661
85	420190	hypothetical protein EST00098	AI816209	Hs.95867	5.6	1428 5888
	419745	slug (chicken homolog), zinc finger pro	AF042001	Hs.93005	5.6	1381 1382 5851

	419517	Homo sapiens clone 23620 mRNA sequence	AF052107	Hs.90797	5.6	1346 5825
	419073	transmembrane receptor Unc5H2 mRNA	AW372170	Hs.183918	5.6	1286 5786
	425071	deiodinase, iodothyronine, type II	NM_013989	Hs.1 54424	5.6	2043 2044 6330
5	407366	gb:Homo sapiens c133 mRNA, partial seq	AF026942	Hs.17518	5.6	137 4885
	428862	SRY (sex determining region Y)-box 9 (c	NM_000346	Hs.2 316	5.6	2483 2484 6650
	430281	CGI-69 protein	AJ878842	Hs.237924	5.6	2674 6788
	437188	KIAA1814 protein	AL080221	Hs.375566	5.6	3240 7238
	442549	TNF receptor-associated factor 4	AJ751601	Hs.8375	5.6	3567 7538
10	413076	wee1 (S. pombe) homolog	U10564	Hs.75188	5.6	678 679 5310
	442700	hypothetical protein MGC5576	AA377618	Hs.103834	5.6	3578 7548
	408958	signal recognition particle 54kD	T99607	Hs.49346	5.6	283 5005
	457458	ESTs	AW972881	Hs.276507	5.6	4552 8352
	416406	lipoma HMGIC fusion partner-like 2	D86961	Hs.79299-	5.6	1001 1002 5564
	432559	ESTs	AW452948	Hs.257631	5.6	2886 6947
15	453582	hypothetical protein FLJ11937	AW854339	Hs.33476	5.6	4427 8247
	445363	tubulin-specific chaperone d	NM_005993	Hs.1 2570	5.6	3762 3763 7702
	447343	ESTs, Highly similar to S02392 alpha-2-	AA256641	Hs.236894	5.6	3916 7828
	427498	methyl-CpG binding domain protein 3	NM_003926	Hs.1 78728	5.6	2336 2337 6534
	433212	ESTs	BE218049	Hs.121820	5.6	2956 7001
20	414561	Homo sapiens amino acid transport syste	AJ064813	Hs.195155	5.6	831 5432
	407103	hypothetical protein MGC13170	AA424881	Hs.256301	5.6	110 4862
	428976	ras homolog gene family, member I	AL037824	Hs.194695	5.6	2495 6658
	440848	ATPase, H transporting, lysosomal (vacu	BE314650	Hs.7476	5.6	3488 7464
25	427052	CK2 Interacting protein 1; HQ0024c prot	AF168676	Hs.173380	5.5	2298 2299 6506
	405058	Target Exon			5.5	4769
	428028	Interleukin-1 receptor-associated kinas	U52112	Hs.182018	5.5	2392 6578
	447712	kinesin family member C3	BE622873	Hs.23131	5.5	3951 7857
	420842	hypothetical protein MGC10986	AJ083668	Hs.50601	5.5	1485 5929
30	411789	Adlcan	AF245505	Hs.72157	5.5	553 554 5207
	410581	tumor endothelial marker 7/precursor	AA018982	Hs.125036	5.5	478 5146
	420376	protocadherin 18	AL137471	Hs.97266	5.5	1447 1448 5903
	418336	glutathione peroxidase 3 (plasma)	BE179882	Hs.353196	5.5	1219 5730
	424688	myosin, light polypeptide 3, alkali; ve	AA216287	Hs.1815	5.5	1988 6290
	424481	proteolipid protein 1 (Pelizaeus-Merzba	R19453	Hs.1787	5.5	1960 6272
35	411021	tiitin	F00055	Hs.172004	5.5	508 5169
	432994	ESTs	AA573452	Hs.150941	5.5	2922 6976
	418004	aldehyde dehydrogenase 3 family, member	U37519	Hs.87539	5.5	1174 1175 5695
	438937	ESTs	AW952654	Hs.73964	5.5	3367 7350
40	413199	ELAV (embryonic lethal, abnormal vision	M62843	Hs.75236	5.5	687 688 5317
	432406	KIAA0969 protein	AJ340571	Hs.343666	5.5	2871 6933
	425262	GS3955 protein	D87119	Hs.155418	5.5	2076 2077 6354
	454071	ESTs	AJ041793	Hs.42502	5.5	4487 8295
	422515	multifunctional polypeptide similar to	AW500470	Hs.117950	5.5	1693 6079
45	452281	Homo sapiens cDNA FLJ11041 fis, clone P	T93500	Hs.28792	5.5	4309 8149
	418526	solute carrier family 16 (monocarboxyli	BE019020	Hs.85838	5.5	1251 5752
	434078	chromosome 8 open reading frame 4	AW880709	Hs.283683	5.5	3027 7060
	428748	Ksp37 protein	AW593206	Hs.98785	5.5	2468 6638
	422765	baculoviral IAP repeat-containing 5 (su	AW409701	Hs.1578	5.5	1734 6110
50	423915	alpha-actinin-2-associated LIM protein	AF039018	Hs.135281	5.5	1869 1870 6209
	428291	interferon stimulated gene (20kD)	AA534009	Hs.183487	5.5	2423 6604
	439999	ras homolog gene family, member E	AA115811	Hs.6838	5.5	3444 7426
	419488	nucleophosmin/nucleoplasmin 3	AA316241	Hs.90691	5.5	1342 5822
	439688	hypothetical protein FLJ12921	AW445181	Hs.209637	5.5	3418 7401
55	434175	ESTs	AW979081	Hs.165469	5.5	3032 7065
	429441	lipophilin B (uteroglobin family member	AJ224172	Hs.204096	5.5	2560 2561 6708
	443572	cleavage and polyadenylation specific f	AA025610	Hs.9605	5.5	3625 7589
	424078	paternally expressed 3	AB006625	Hs.139033	5.5	1893 1894 6225
	450998	splicing factor 3b, subunit 4, 49kD	BE387614	Hs.25797	5.4	4205 8065
60	400259	NM_017432::Homo sapiens prostate tumor		Hs.19555	5.4	4610
	407785	ESTs, Weakly similar to A43932 mucin 2	AW207285	Hs.98279	5.4	160 4904
	435854	putative ankyrin-repeat containing prot	AJ278120	Hs.4996	5.4	3157 3158 7166
	457211	ESTs, Weakly similar to S51797 vasodila	AW972565	Hs.32399	5.4	4543 8344
	419682	paired-like homeodomain transcription f	H13139	Hs.92282	5.4	1368 5841
65	407178	AP-2 beta transcription factor	AA195651	Hs.352312	5.4	118 4870
	416065	proliferating cell nuclear antigen	BE267931	Hs.78996	5.4	968 5536
	418532	neurotrophic tyrosine kinase, receptor,	F00797	Hs.374321	5.4	1252 5753
	427337	Fc fragment of IgG, low affinity IIb,	Z46223	Hs.176663	5.4	2318 2319 6521
	448517	hypothetical protein FLJ22649 similar t	AA082750	Hs.42194	5.4	4009 7906
70	452401	tumor necrosis factor, alpha-induced pr	NM_007115	Hs.2 9352	5.4	4325 4326 8161
	450414	KIAA1716 protein	AJ907735	Hs.21446	5.4	4165 8033
	445932	Homo sapiens clone 24859 mRNA sequence	BE046441	Hs.333555	5.4	3805 7735
	427923	FGENESH predicted 11 TM protein	AW274357	Hs.301406	5.4	2385 6572
	430130	Homo sapiens mRNA; cDNA DKFZp761G02121	AL137311	Hs.234074	5.4	2650 2651 6772
75	428121	KIAA0284 protein	AB006622	Hs.182536	5.4	2398 2399 6584
	408660	ESTs, Moderately similar to PC4259 ferr	AA525775	Hs.89040	5.4	247 4977
	410011	PFTAIRE protein kinase 1	AB020641	Hs.57856	5.4	406 407 5096
	425616	nuclear matrix protein NMP200 related t	BE561911	Hs.173980	5.4	2121 6384
	442578	hypothetical protein FLJ10781	AK001643	Hs.8395	5.4	3572 3573 7543
80	414751	choline kinase	AL120829	Hs.77221	5.4	863 5456
	437763	tissue inhibitor of metalloproteinase 1	AA469369	Hs.5831	5.4	3285 7278
	427674	H2B histone family, member Q	NM_003528	Hs.2 178	5.4	2359 2360 6553
	404458	CX000877::gil11877268[emb]CAC18893.1[(5.4	4749
	450296	hepatocyte growth factor-regulated tyro	AL041949	Hs.24756	5.4	4153 8023
85	419236	Homo sapiens cDNA FLJ11481 fis, clone H	AA330447	Hs.135159	5.3	1321 5805
	435256	cytokine-like protein C17	AF193766	Hs.13872	5.3	3116 3117 7133
	447436	Homo sapiens cDNA: FLJ21449 fis, clone	AI932971	Hs.18593	5.3	3928 7837

	400235	NM_005336: Homo sapiens high density lip	Hs.177516	5.3	4604
	435593	DKFZP586J1624 protein	R88872	Hs.4964	5.3
	441362	RAD51 (S. cerevisiae) homolog (E coli R	BE614410	Hs.23044	5.3
5	424971	tumor suppressing subtransferable candi	AA479005	Hs.154036	5.3
	426514	bone morphogenetic protein 7 (osteogeni	BE616633	Hs.170195	5.3
	451681	ESTs, Weakly similar to AA64_HUMAN 64 K	Z28564	Hs.255950	5.3
	445302	hypothetical protein FLJ10675	AK001537	Hs.12488	5.3
	432504	oxygen regulated protein (150kD)	AL121015	Hs.277704	5.3
10	413762	FK506-binding protein 4 (59kD)	AW411479	Hs.848	5.3
	453905	LIM domain kinase 1	NM_002314	Hs.3 6566	5.3
	419693	FXD domain-containing ion transport re	AA133749	Hs.301350	5.3
	421778	actin related protein 2/3 complex, subu	AA428000	Hs.283072	5.3
	449129	ESTs	AI631602	Hs.258949	5.3
15	432647	fibroblast growth factor receptor 2 (ba	AI807481	Hs.278581	5.3
	406830	peptidylprolyl isomerase A (cyclophilin	AI829848	Hs.342389	5.3
	452410	Homo sapiens mRNA; cDNA DKFZp434E2321 (AL133619	Hs.29383	5.3
	418045	ESTs	AI972919	Hs.118837	5.3
	430326	DKFZP727051 protein	BE251590	Hs.239370	5.3
20	419088	integrin, beta 8	AI538323	Hs.380684	5.3
	416860	actin filament associated protein	D25248	Hs.80306	5.3
	456181	ras inhibitor	L36463	Hs.1030	5.3
	430838	hypothetical protein FLJ12015	N46664	Hs.169395	5.3
	439053	chaperonin containing TCP1, subunit 2 (BE244588	Hs.6456	5.3
25	444354	hypothetical protein R33729_1	AA847582	Hs.10927	5.3
	421846	protein kinase C substrate 80K-H	AA017707	Hs.1432	5.3
	425703	collagen, type VI, alpha 2	X06195	Hs.159263	5.3
	433180	K562 cell-derived leucine-zipper-like p	AB038651	Hs.31854	5.3
	408826	Homo sapiens clone HB-2 mRNA sequence	AF216077	Hs.48376	5.3
30	428227	small inducible cytokine subfamily B (C	AA321649	Hs.2248	5.3
	431565	butyrate-induced transcript 1	AF161470	Hs.260622	5.3
	422363	replication factor C (activator 1) 3 (3	T55979	Hs.115474	5.3
	418870	chemokine (C-X-C motif), receptor 4 (fu	AF147204	Hs.89414	5.3
	417089	Homo sapiens cDNA: FLJ21909 fis, clone	H52280	Hs.18612	5.3
35	406885	gb:Human mRNA for pre-mRNA splicing fac	D28423		5.3
	446157	Homo sapiens cDNA: FLJ22562 fis, clone	BE270828	Hs.131740	5.3
	404208	C6001282:gi 4504223 ref NP_000172.1 g			5.3
	404854	Target Exon			5.3
	445875	Homo sapiens clone 24453 mRNA sequence	AF070524	Hs.13410	5.3
40	448603	DNA segment on chromosome X and Y (unig	L03426	Hs.21595	5.3
	417079	interleukin 1 receptor antagonist	U65590	Hs.81134	5.3
	438393	Homo sapiens cDNA: FLJ22272 fis, clone	AA351815	Hs.50740	5.3
	426613	hydroxyacyl-Coenzyme A dehydrogenase, t	U96132	Hs.171280	5.3
	412564	cardiac ankyrin repeat protein	X83703	Hs.355934	5.3
45	441389	endocytic receptor (macrophage mannose	AF134838	Hs.7835	5.3
	403171	C2001472:gi 5809678 gb AA81484.2 (U6			5.2
	410223	calsequestrin 1 (fast-twitch, skeletal	S73775	Hs.60708	5.2
	425848	valyl-tRNA synthetase 2	BE242709	Hs.159637	5.2
	415697	DKFZP566I1024 protein	AI365603	Hs.279696	5.2
50	449644	ESTs	AW960707	Hs.8935	5.2
	447519	ESTs	U46258	Hs.339665	5.2
	421920	gamma-aminobutyric acid (GABA) receptor	BE551245	Hs.1438	5.2
	435060	ESTs, Weakly similar to fork head like	AI422719	Hs.120873	5.2
	449139	phenylalanine-tRNA synthetase-like	BE268315	Hs.23111	5.2
55	428046	ESTs, Moderately similar to 138022 hypo	AW812795	Hs.337534	5.2
	414267	dimethylarginine dimethylaminohydrolase	AL078459	Hs.303180	5.2
	424291	ephrin-B1	AL120051	Hs.144700	5.2
	425712	ESTs, Moderately similar to ALU1_HUMAN	AA412548	Hs.21423	5.2
	419285	KIAA0062 protein	D31887	Hs.89868	5.2
60	406636	gb:Homo sapiens (clone WR4.12VL) anti-t	L12064		5.2
	408212	hypothetical protein	AA297567	Hs.43728	5.2
	433320	ESTs, Highly similar to CTXN RAT CORTEX	D60647	Hs.250879	5.2
	440700	guanine nucleotide binding protein (G p	AW952281	Hs.296184	5.2
	402855	NM_001839: Homo sapiens calponin 3, aci			5.2
65	414175	hypothetical protein DKFZp761D112	AI308876	Hs.103849	5.2
	413815	discoidin domain receptor family, membe	AL046341	Hs.75562	5.2
	428865	BarH-like homeobox 1	BE544095	Hs.164960	5.2
	450701	hypothetical protein XP_098151 (leucine	H39960	Hs.288467	5.2
	424442	ESTs, Weakly similar to ZN91_HUMAN ZINC	AW051949	Hs.90035	5.2
70	450680	Homo sapiens clone 25194 mRNA sequence	AF131784	Hs.25318	5.2
	438619	TU12B1-TY protein	AB032773	Hs.374350	5.2
	428727	general transcription factor IIH, polyp	AF078847	Hs.78452	5.2
	422175	ESTs, Highly similar to T00391 hypothet	N79885	Hs.6382	5.2
	408604	ESTs	D51408	Hs.21925	5.1
75	404815	ENSP00000251989:DJ100N22.1 (NOVEL EGF-			5.1
	416700	cathepsin D (lysosomal aspartyl proteas	AW498958	Hs.343475	5.1
	442285	uncharacterized hypothalamus protein HT	W28729	Hs.374989	5.1
	430333	TIA1 cytotoxic granule-associated RNA-b	S70114	Hs.239489	5.1
	433882	procollagen-proline, 2-oxoglutarate 4-d	U90441	Hs.3622	5.1
80	415705	collin	U06632	Hs.966	5.1
	450983	ERO1 (S. cerevisiae)-like	AA305384	Hs.25740	5.1
	426138	Homo sapiens clone 23798 and 23825 mRNA	D81871	Hs.167036	5.1
	418607	KIAA1402 protein	AL137426	Hs.86392	5.1
	421857	hypothetical protein FLJ23322	AW601852	Hs.285932	5.1
85	424375	Homo sapiens clone 24820 mRNA sequence	AF070547	Hs.146312	5.1
	449475	hypothetical protein PP1057	AI348027	Hs.129826	5.1
	408196	SRY (sex determining region Y)-box 22	AL034548	Hs.43627	5.1

5	437044	differentially expressed in Fancon's a	AL035864	Hs.69517	5.1	3233 7232
	436291	protein regulator of cytokinesis 1	BE568452	Hs.344037	5.1	3180 7185
	429150	smoothened (Drosophila) homolog	AF120103	Hs.197366	5.1	2519 2520 6577
	441954	Fancon anemia, complementation group G	AI744935	Hs.8047	5.1	3542 7514
	414465	ribosomal protein S5	AW270645	Hs.76194	5.1	820 5423
	421140	signal sequence receptor, delta (transl	AA298741	Hs.102135	5.1	1509 5948
	432731	fibronectin 1	R31178	Hs.287820	5.1	2904 6961
	427157	thymine-DNA glycosylase	U51166	Hs.173824	5.1	2305 2306 6511
	437191	serine protease inhibitor, Kazal type,	NM_006846	Hs.3 31555	5.1	3241 3242 7239
10	442173	KIAA0144 gene product	N76101	Hs.8127	5.1	3552 7524
	418059	gbzn55d05.s1 Stratagene muscle 937209	AA211586		5.1	1186 5703
	424005	vang (van gogh, Drosophila)-like 2	AB033041	Hs.137507	5.1	1883 1884 6218
	434659	core histone macroH2A2.2	AF151534	Hs.92023	5.1	3068 3069 7093
	433819	ESTs	AW511097	Hs.110069	5.1	3007 7042
15	435056	glycoprotein M6B	AW023337	Hs.5422	5.1	3100 7119
	431205	tropomodulin 4 (muscle)	AA194560	Hs.250763	5.1	2761 6849
	418867	msh (Drosophila) homeo box homolog 2	D31771	Hs.89404	5.1	1277 1278 5772
	406851	major histocompatibility complex, class	AA609784	Hs.352392	5.1	71 4838
	410687	lysyl oxidase-like 1	U24389	Hs.65436	5.1	485 486 5153
20	412490	Homo sapiens cDNA: FLJ22528 fis, clone	AW803564	Hs.288850	5.1	595 5242
	408056	ephrin-A4	AA312329	Hs.42331	5.1	188 4930
	412446	ESTs	AI768015	Hs.352375	5.1	586 5235
	432370	N-acetylneuraminic acid phosphate synth	AA308334	Hs.274424	5.1	2867 6930
25	448140	BCM-like membrane protein precursor	AF145761	Hs.20450	5.1	3980 3981 7882
	427584	v-myb avian myeloblastosis viral oncoge	BE410293	Hs.179718	5.1	2348 6542
	442051	abl-interactor 12 (SH3-containing prote	AA774284	Hs.285728	5.1	3547 7519
	417709	KIAA0247 gene product	D87434	Hs.82426	5.1	1149 1150 5674
	444019	putative nucleolar RNA helicase	BE173977	Hs.10098	5.1	3670 7629
	433012	ATX1 (antioxidant protein 1, yeast) hom	NM_004045	Hs.2 79910	5.1	2925 2926 6978
30	449353	ESTs	AA001220	Hs.242947	5.1	4084 7966
	438866	tissue inhibitor of metalloproteinase 2	U44385	Hs.6441	5.1	3360 3361 7344
	434355	ESTs	AA630865	Hs.186556	5.1	3049 7076
	417796	ESTs	AA206141	Hs.367818	5.1	1159 5582
35	410279	hypothetical protein FLJ14117	BE271977	Hs.61809	5.1	447 5124
	440028	ESTs, Weakly similar to T17227 hypothet	AW473675	Hs.367649	5.1	3446 7428
	407241	gb:Human omega light chain protein 14.1	M34516		5.1	130 131 4880
	421566	early growth response 2 (Krox-20 (Droso	NM_000399	Hs.1 395	5.1	1563 1564 5984
	400220	Eos Control		Hs.155560	5.0	4600
40	448425	ESTs	AI500359	Hs.371249	5.0	4004 7901
	428013	hypothetical protein	AF151020	Hs.181444	5.0	2390 2391 6577
	405387	NM_022170: Homo sapiens Williams-Beuren			5.0	4779
	439070	ESTs	AI733278	Hs.7621	5.0	3375 7358
	436543	integrin beta 4 binding protein	NM_002212	Hs.5 215	5.0	3198 3199 7201
45	450065	transcriptional co-activator with PDZ-b	AL050107	Hs.24341	5.0	4130 4131 8006
	433043	lymphoid nuclear protein (LAF-4) mRNA	W57554	Hs.125019	5.0	2930 6982
	417166	Paired box protein Pax-3	AA431323	Hs.42146	5.0	1088 5628
	444984	fatty acid desaturase 1	H15474	Hs.132898	5.0	3737 7683
	422066	malate dehydrogenase 2, NAD (mitochondr	AW249275	Hs.343521	5.0	1634 6036
50	417437	interferon regulatory factor 4	U52682	Hs.82132	5.0	1123 1124 5656
	403081	NM_003319: Homo sapiens titin (TTN), mR			5.0	4704
	439453	thyroid hormone receptor interactor 13	BE264974	Hs.6566	5.0	3399 7382
	425322	protein kinase, DNA-activated, catalyti	U63630	Hs.155637	5.0	2089 2090 6363
	434837	lysophosphatidic acid acyltransferase-d	AF156776	Hs.353175	5.0	3080 3081 7102
55	414420	immediate early response 3	AA043424	Hs.76095	5.0	814 5418
	400300	HER2 receptor tyrosine kinase (c-erb-b2	X03363	Hs.323910	5.0	8 9 4619
	447898	6.2 kd protein	AW969638	Hs.380920	5.0	3966 7868
	412819	FK506 binding protein precursor	T25829	Hs.24048	5.0	651 5286
	452110	Homo sapiens cDNA FLJ11309 fis, clone P	T47667	Hs.28005	5.0	4290 8132
60	432211	hypothetical protein FLJ10986	BE274530	Hs.273333	5.0	2852 6917
	457060	beta tubulin 1, class VI	AA402364	Hs.303023	5.0	4538 8339
	430152	aquaporin 3	AB001325	Hs.234642	5.0	2653 2654 6774
	409299	small nuclear ribonucleoprotein D2 poly	AA045650	Hs.53125	5.0	339 5045
	443802	KIAA1291 protein	AW504924	Hs.9805	5.0	3647 7609
65	445162	piccolo (presynaptic cytomatrix protein	AB011131	Hs.12376	5.0	3749 3750 7693
	417115	small nuclear ribonucleoprotein polypep	AW952792	Hs.334612	5.0	1081 5622
	409944	four and a half LIM domains 3	BE297925	Hs.57687	5.0	399 5090
	416801	sal (Drosophila)-like 2	X98834	Hs.79971	5.0	1032 5585
	445160	sine oculis homeobox (Drosophila) homol	AI299144	Hs.101937	5.0	3748 7692
70	429139	ESTs	F09092	Hs.66087	5.0	2517 6675
	445462	hypothetical protein MGC3077	AA378776	Hs.288649	5.0	3771 7709

TABLE 8B:

75	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

80	Pkey	CAT Number	Accession
	406782	0_0	AA430373 AA968771
	406636	0_0	L12064 L12083 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080
	418059	1164438_1	AA211586 F35799 F29720 AW937408 AW937387 AA211641

TABLE 8C:

85	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA

sequence of human chromosome 22.* Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

5	Pkey	Ref	Strand	NL_position
	405001	6015406	Minus	104646-104819
	404977	3738341	Minus	43081-43229
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
	405443	7408143	Plus	90716-90887,101420-101577
10	403088	8954241	Plus	169894-170193,170504-170806
	402992	7767907	Minus	42137-42515
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	401673	7689903	Minus	122587-122705,122765-123047
	401797	6730720	Plus	6973-7118
15	401566	8469090	Minus	96277-96420,96979-97160
	400499	9796071	Minus	148495-148806
	405516	9454624	Plus	112707-112876,113676-113854
	404030	7671252	Plus	149362-151749
	402810	6010110	Plus	12715-12856,13527-13643
20	403857	7708910	Minus	2524-3408
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	405058	7655685	Plus	150740-151556
	404458	7770571	Minus	35710-36276
	404208	3080468	Minus	105346-105573
25	404854	7143420	Plus	14260-14537
	403171	9838164	Minus	74502-74703
	402855	9662953	Minus	59763-59909
	404815	5911819	Minus	64494-64691
30	405387	6587915	Minus	3769-3833,5708-5895
	403081	8954241	Plus	155749-156048,156142-156459

TABLE 9A

35	Pkey:	Unique Eos probeset Identifier number				
	Gene name:	Unigene gene title				
	Accession:	Exemplar Accession number, Genbank accession number				
	UniGene:	Unigene number				
40	RATIO:	95th percentile of malignant fibrous histiocytoma AIs divided by the 50th percentile of normal body tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator				
	SEQ ID #:	nucleic acid and protein sequences provided on CD for search purposes				
	Pkey	Gene Name	Accession	UniGene	RATIO	SEQ ID #
45	426300	delta-like homolog (Drosophila)	U15979	Hs.169228	22.5	2196 2197 6437
	404977	Insulin-like growth factor 2 (somatomed			21.4	4766
	422487	mucin 4, tracheobronchial	AJ010901	Hs.198267	19.9	1689 1690 6076
	406687	matrix metalloproteinase 11 (stromelys	M31126	Hs.352054	18.3	49 50 4823
	418338	neuronal pentraxin I	NM_002522	Hs.8 4154	16.5	1220 1221 5731
	409633	ESTs	AW449822	Hs.55200	16.4	371 5068
50	429359	matrix metalloproteinase 14 (membrane-	W00482	Hs.2399	16.2	2551 6702
	450701	hypothetical protein XP_098151 (leucine	H39960	Hs.288467	15.8	4183 8048
	425247	matrix metalloproteinase 11 (stromelys	NM_005940	Hs.1 55324	15.1	2072 2073 6351
	444670	hypothetical protein MGC5370	H58373	Hs.332938	14.4	3714 7666
	422867	cartilage oligomeric matrix protein (ps	L32137	Hs.1584	13.6	1751 1752 6122
55	420162	cyclin-dependent kinase 4	BE378432	Hs.95577	13.5	1422 5883
	453857	Ras-induced senescence 1 (RIS1)	AL080235	Hs.35861	13.3	4449 4450 8266
	422887	ESTs	AI751848	Hs.49215	13.3	1755 6124
	412709	KIAA0027 protein	AL022327	Hs.74518	13.2	631 632 5269
	430044	ESTs	AA464510	Hs.152812	13.0	2642 6765
60	408202	DKFZP586L151 protein	AA227710	Hs.43658	12.7	202 4942
	413554	secretogranin II (chromogranin C)	AA319146	Hs.75426	12.6	729 5346
	415166	carboxypeptidase Z	NM_003652	Hs.7 8068	12.3	913 914 5491
	422386	heparan sulfate (glucosamine) 3-O-sulfo	AF105374	Hs.115830	11.8	1676 1677 6067
	424687	matrix metalloproteinase 9 (gelatinase	J05070	Hs.151738	11.8	1986 1987 6289
65	444381	hypothetical protein BC014245	BE387335	Hs.283713	11.7	3697 7652
	442426	hypothetical protein MGC5370	AI373062	Hs.332938	11.7	3562 7534
	452620	ESTs	AA436504	Hs.119286	11.5	4338 8172
	446619	secreted phosphoprotein 1 (osteopontin,	AU076643	Hs.313	11.5	3861 7782
	418140	microfibrillar-associated protein 2	BE613836	Hs.83551	11.4	1196 5713
70	414477	amplified in osteosarcoma	U41635	Hs.76228	11.4	822 823 5425
	423575	Intron of perostin (OSF-2os)	C18863	Hs.163443	11.3	1820 6173
	453331	ESTs	AI240665	Hs.352537	11.3	4413 8236
	422424	prostate differentiation factor	AI186431	Hs.296638	11.2	1681 6070
	418399	hypothetical protein FLJ12442	AF131781	Hs.84753	11.2	1232 1233 5738
75	425292	37 kDa leucine-rich repeat (LRR) protei	NM_005824	Hs.1 55545	11.2	2083 2084 6359
	426559	paired basic amino acid cleaving system	AB001914	Hs.170414	11.2	2253 2254 6474
	423961	perostin (OSF-2os)	D13666	Hs.136348	11.1	1878 1879 6215
	409132	protein kinase, AMP-activated, beta 2 n	AJ224538	Hs.50732	11.1	309 310 5025
	418054	lysyl oxidase-like 2	NM_002318	Hs.8 3354	11.1	1184 1185 5702
80	421458	carbohydrate (keratan sulfate Gal-6) su	NM_003654	Hs.1 04576	11.1	1543 1544 5972
	452401	tumor necrosis factor, alpha-induced pr	NM_007115	Hs.2 9352	11.0	4325 4326 8161
	415989	ESTs	AI267700	Hs.351201	10.8	962 5530
	439755	B7 homolog 3	AW748482	Hs.77873	10.8	3430 7413
	419762	ESTs	AI608647	Hs.32374	10.6	1387 5855
85	451934	ESTs	AI540842	Hs.61082	10.5	4262 8109
	428311	tryptophan 2,3-dioxygenase	NM_005651	Hs.1 83671	10.5	2429 2430 6609

	417308	KIAA0101 gene product	H60720	Hs.81892	10.4	1094 5634
	442700	hypothetical protein MGC5576	AA377618	Hs.103834	10.2	3578 7548
	404550	Target Exon			10.1	4750
5	437330	Homo sapiens mRNA; cDNA DKFZp761J1112 (AL353944	Hs.50115		10.0	3253 7250
	442285	uncharacterized hypothalamus protein HT W28729	Hs.374989		10.0	3554 7526
	413004	Interleukin enhancer binding factor 2, T35901	Hs.75117		9.9	667 5300
	434449	hypothetical protein FLJ22041 similar t	AW953484	Hs.3849	9.9	3057 7083
	423472	breast carcinoma amplified sequence 1	AF041260	Hs.129057	9.9	1812 1813 6167
10	426156	natriuretic peptide receptor A/guanylat	BE244537	Hs.167382	9.9	2183 6427
	419741	ubiquitin carrier protein E2-C	NM_007019	Hs.9 3002	9.8	1379 1380 5850
	449784	ESTs	AW161319	Hs.12915	9.8	4115 7993
	406964	FGENES predicted novel secreted protein	M21305		9.8	87 88 4847
	439053	chaperonin containing TCP1, subunit 2 (BE244588	Hs.6456	9.8	3374 7357
15	408972	DKFZP586D0919 protein	AL050100	Hs.49378	9.8	287 288 5008
	410687	lysyl oxidase-like 1	U24389	Hs.65436	9.8	485 486 5153
	448386	KIAA1329 protein	AB037750	Hs.21061	9.8	3997 3998 7896
	407656	Homo sapiens mRNA; cDNA DKFZp434B2119 (AW747986	Hs.37443	9.7	148 4893	
	424086	lysyl oxidase	AJ351010	Hs.102267	9.6	1896 6227
20	431211	gap junction protein, beta 2, 26kD (con	M86849	Hs.323733	9.6	2762 2763 6850
	412755	ESTs, Weakly similar to P4HA_HUMAN PROL BE144306	Hs.179891	9.5	637 5274	
	426991	Homo sapiens cDNA FLJ10674 fis, clone N AK001536	Hs.214410	9.5	2294 6502	
	450098	hypothetical protein FLJ21080	W27249	Hs.8109	9.4	4134 8009
	411296	growth suppressor 1	BE207307	Hs.10114	9.4	524 5183
25	409012	DKFZP434I216 protein	AL117435	Hs.49725	9.4	293 294 5013
	413211	hypothetical protein MGC4365	AW967107	Hs.109274	9.4	689 5318
	449077	ESTs	AW262836	Hs.252844	9.4	4063 7947
	425130	ESTs	AA448208	Hs.99163	9.3	2050 6335
	440502	regulator of G-protein signalling 12	AJ824113	Hs.78281	9.3	3470 7449
30	449717	cerebral cell adhesion molecule	AB040935	Hs.23954	9.3	4110 4111 7989
	422961	B-cell CLL/lymphoma 9	Y13620	Hs.122607	9.3	1763 1764 6131
	421508	absent in melanoma 2	NM_004833	Hs.1 05115	9.3	1551 1552 5977
	421155	lysyl oxidase	H87879	Hs.102267	9.3	1512 5950
	434096	pleiomorphic adenoma gene-like 1	AW662958	Hs.75825	9.3	3029 7062
35	433612	Homo sapiens Ku70-binding protein (KUB3 AF078164	Hs.61188	9.2	2991 2992 7030	
	450375	a disintegrin and metalloproteinase dom	AA009647	Hs.352537	9.2	4159 8028
	443780	activating transcription factor 5	NM_012068	Hs.9 754	9.2	3643 3644 7606
	445417	a disintegrin-like and metalloprotease	AK001058	Hs.12680	9.1	3766 7705
	447500	ESTs	AJ381900	Hs.159212	9.1	3935 7843
40	451292	KIAA1295 protein	AB037716	Hs.26204	9.1	4221 4222 8079
	417900	CDC20 (cell division cycle 20, S. cerev	BE250127	Hs.82906	9.0	1165 5688
	413011	biglycan	AW068115	Hs.821	8.9	669 5302
	408989	KIAA0746 protein	AW361666	Hs.49500	8.9	290 5010
	449722	cyclin B1	BE280074	Hs.23960	8.9	4112 7990
45	431750	ESTs	AA514986	Hs.283705	8.8	2816-6891
	431089	ESTs, Weakly similar to unknown protein	BE041395	Hs.374629	8.8	2745 6838
	415701	gamma-glutamyl hydrolase (conjugase, fo	NM_003878	Hs.78619	8.8	940 941 5514
	452701	glutamine-fructose-6-phosphate transami	NM_005110	Hs.3 0332	8.7	4345 4346 8178
	426369	Kreisler (mouse) mal-related leucine zi	AF134157	Hs.169487	8.6	2213 2214 6448
50	431103	pleiotrophin (heparin binding growth fa	M57399	Hs.44	8.6	2748 2749 6840
	422567	glypican 6	AF111178	Hs.118407	8.6	1702 1703 6087
	408692	dipeptidylpeptidase VI	AL040127	Hs.34074	8.5	248 4978
	412140	RAB6 interacting, kinesin-like (rakine	AA219691	Hs.73625	8.5	573 5223
	440099	DKFZP564G202 protein	AL080058	Hs.6909	8.5	3453 3454 7434
55	423600	ESTs	AI633559	Hs.310359	8.5	1824 6177
	444931	general transcription factor IIIA	AV652066	Hs.75113	8.5	3735 7681
	422087	matrix metalloproteinase 2 (gelatinase	X58968	Hs.111301	8.5	1641 6040
	421143	immunoglobulin superfamily containing i	AB024536	Hs.102171	8.5	1510 1511 5949
	445302	hypothetical protein FLJ10675	AK001537	Hs.12488	8.4	3757 3758 7699
60	427099	odd Oz/ten-m homolog 2 (Drosophila, mou	AB032953	Hs.173560	8.4	2302 2303 6509
	439223	UL16 binding protein 2	AW238299	Hs.250618	8.4	3383 7366
	452862	ADAMTS2 (a disintegrin-like and metall	AW378065	Hs.8687	8.3	4360 8190
	452683	progesterone membrane binding protein	AJ089575	Hs.374574	8.3	4341 8175
	454140	hypothetical protein FLJ10474	AB040888	Hs.41793	8.3	4493 4494 8301
65	452017	prostate cancer associated protein 7	AF109302	Hs.27495	8.3	4270 8117
	453018	ESTs, Weakly similar to Trad [H.sapiens	AA054522	Hs.61581	8.3	4379 8207
	430055	ESTs	BE539658	Hs.283705	8.3	2644 6767
	423217	collagen, type VII, alpha 1 (epidermol	NM_000094	Hs.1 640	8.3	1784 1785 6147
	431866	angiopoietin-like 2	NM_012098	Hs.8 025	8.2	2830 2831 6902
70	418932	cadherin 4, type 1, R-cadherin (retinal	L34059	Hs.89484	8.2	1285 1286 5777
	439070	ESTs	AJ733278	Hs.7621	8.2	3375 7358
	457869	Homo sapiens, alpha-1 (VI) collagen	AU077186	Hs.108885	8.2	4561 8359
	424126	ESTs	AA335635	Hs.96917	8.1	1902 6231
	422627	transforming growth factor, beta-induce	BE336857	Hs.118787	8.1	1715 6097
75	417866	collagen, type XI, alpha 1	AW067903	Hs.82772	8.1	1162 5685
	445900	Homo sapiens clone 24787 mRNA sequence	AF070526	Hs.125036	8.1	3803 7733
	407756	ubiquitin specific protease 18	AA116021	Hs.38260	8.1	159 4903
	459702	gb:an03c03.x1 Stralagene schizo brain S	AJ204995		8.1	4596 8393
	443426	chromosome 20 open reading frame 1	AF098158	Hs.9329	8.1	3621 3622 7586
80	423739	ESTs	AA398155	Hs.97600	8.1	1842 6190
	417059	extracellular matrix protein 1	AL037672	Hs.81071	8.0	1067 5611
	445537	EGF-like-domain, multiple 6	AJ245671	Hs.12844	8.0	3780 3781 7716
	438451	ESTs	AJ081972	Hs.220261	8.0	3323 7313
	424916	ESTs	AW887440	Hs.23096	8.0	2028 6319
85	416349	myomesin (M-protein) 2 (165kD)	X69089	Hs.79227	7.9	991 992 5556
	400242	Eos Control		Hs.144700	7.9	4605
	428289	complement component 2	M26301	Hs.2253	7.9	2421 2422 6603

	447198	ESTs	D61523	Hs.283435	7.9	3898 7814
	428182	ESTs, Weakly similar to GGC1_HUMAN	AN BE386042	Hs.293317	7.9	2403 6588
	409041	Hypothetical protein, XP_051860 (KIAA11	AB033025	Hs.50081	7.9	299 300 5017
	417849	nkfogen 2	AW291587	Hs.82733	7.9	1161 5684
5	444371	forkhead box M1	BE540274	Hs.239	7.9	3696 7651
	437898	ESTs	W81260	Hs.43410	7.8	3293 7286
	408349	homeo box C10	BE546947	Hs.44276	7.8	213 4949
	417675	similar to murine leucine-rich repeat p	AI808607	Hs.3781	7.8	1144 5670
	449353	ESTs	AA001220	Hs.242947	7.7	4084 7966
10	427315	Homo sapiens mRNA; cDNA DKFZp564N0763	AA179949	Hs.175563	7.7	2316 6519
	435080	hypothetical protein FLJ14428	AI831760	Hs.155111	7.7	3103 7122
	444784	ecdonucleotide pyrophosphatase/phosphod	D12485	Hs.11951	7.7	3724 3725 7673
	429500	hexabrachion (tenascin C, cytactin)	X78565	Hs.289114	7.7	2574 2575 6718
	403171	C2001472:gil5809678[gb]AAB41848.2[U6		7.7	4710
15	421778	actin related protein 2/3 complex, subu	AA428000	Hs.283072	7.6	1591 6003
	440594	ESTs	AW445167	Hs.126036	7.6	3475 7453
	425397	topoisomerase (DNA) II alpha (170kD)	J04088	Hs.156346	7.6	2099 2100 6369
	416700	cathepsin D (lysosomal aspartyl proteas	AW498958	Hs.343475	7.6	1023 5579
	425234	ESTs, Weakly similar to I38022 hypothel	AW152225	Hs.165909	7.6	2070 6349
20	417930	Homo sapiens mRNA for KIAA1870 protein,	H81136	Hs.334604	7.6	1169 5691
	427747	serine/threonine kinase 12	AW411425	Hs.180655	7.6	2365 6557
	433447	neuronal pentraxin II	U29195	Hs.3281	7.6	2980 2981 7021
	409178	kallikrein 5	BE393948	Hs.50915	7.5	319 5032
	452828	ESTs, Weakly similar to KIAA1528 protei	W30807	Hs.32374	7.5	4354 8185
25	421743	DKFZP564I1171 protein	T35958	Hs.107614	7.5	1586 5998
	416561	holocarboxylase synthetase (biotin-[pro	D87328	Hs.79375	7.5	1013 1014 5572
	429990	DKFZP547E1010 protein	AL050260	Hs.323817	7.5	2634 2635 6760
	435767	ESTs	H73505	Hs.117874	7.5	3151 7161
	409103	XAGE-1 protein	AF251237	Hs.112208	7.5	304 305 5021
30	419682	paired-like homeodomain transcription f	H13139	Hs.92282	7.5	1368 5841
	410581	tumor endothelial marker 7 precursor	AA018982	Hs.125036	7.5	478 5146
	413595	ESTs	AW235215	Hs.16145	7.5	731 5348
	407896	Zic family member 1 (odd-paired Drosoph	D76435	Hs.41154	7.4	176 177 4919
	425588	ESTs	F07396	Hs.46627	7.4	2120 6383
35	421570	hypothetical protein FLJ21919	AL080172	Hs.105894	7.4	1566 5986
	406673	major histocompatibility complex, class	M34996	Hs.198253	7.4	90 91 4821
	428189	ESTs	AA424030	Hs.46627	7.4	2404 6589
	429609	cell adhesion molecule with homology to	AF002246	Hs.210863	7.4	2584 2585 6725
	447070	ESTs	AI871458	Hs.200022	7.4	3886 7803
40	425308	receptor tyrosine kinase-like orphan re	M97639	Hs.155585	7.4	2087 2088 6362
	448961	ESTs	AI610643	Hs.187285	7.4	4052 7937
	428834	ESTs	AW899713	Hs.10338	7.4	2479 6647
	403907	Autosomal Highly Conserved Protein			7.3	4732
	407824	Homo sapiens cDNA FLJ14388 fis, clone	RI AA147884	Hs.9812	7.3	166 4910
45	422048	spondin 2, extracellular matrix protein	NM_012445	Hs.2 88126	7.3	1631 1632 6034
	427335	G antigen 7B	AA448542	Hs.278444	7.3	2317 6520
	414219	ALL1-fused gene from chromosome 1q	W20010	Hs.75823	7.3	789 5397
	412978	homeo box C6	AI431708	Hs.820	7.3	665 5298
	410001	kallikrein 11	AB041036	Hs.57771	7.3	403 404 5094
50	450704	ESTs	H85157	Hs.40696	7.3	4184 8049
	452281	Homo sapiens cDNA FLJ11041 fis, clone	P T93500	Hs.28792	7.3	4309 8149
	436869	KIAA0711 gene product	NM_014867	Hs.5 333	7.3	3221 3222 7222
	433435	Ts translation elongation factor, mitoc	BE545277	Hs.340959	7.3	2978 7019
	420059	RAB23, member RAS oncogene family	AF161486	Hs.94769	7.3	1412 1413 5875
55	404815	ENSP00000251989:DJ100N22.1 (NOVEL	EGF-		7.3	4761
	414443	platelet-derived growth factor receptor	AU077268	Hs.76144	7.3	817 5421
	442040	UDP-N-acetyl-alpha-D-galactosamine:poly	AW294162	Hs.301062	7.3	3545 7517
	408135	methyltransferase-like 1	AA317248	Hs.42957	7.3	194 4936
	432691	mitogen-activated protein kinase 7	U29725	Hs.3080	7.3	2897 2898 6956
60	412006	ESTs	AW451618	Hs.380683	7.3	565 5217
	433001	clone HQ0310 PRO0310p1	AF217513	Hs.279905	7.2	2923 2924 6977
	457411	trovols-class homeobox protein IRX2	AW085961	Hs.130093	7.2	4549 8349
	446921	small inducible cytokine subfamily A (C	AB012113	Hs.16530	7.2	3878 3879 7797
	424408	collagen, type V, alpha 1	AI754813	Hs.146428	7.2	1943 6260
65	442573	branched chain aminotransferase 1, cyto	H93366	Hs.7567	7.2	3570 7541
	444301	asporin (LRR class 1)	AK000136	Hs.10760	7.2	3691 3692 7647
	409142	SMC4 (structural maintenance of chromos	AL136877	Hs.50758	7.2	312 313 5027
	423225	Thy-1 cell surface antigen	AA852604	Hs.125359	7.2	1786 6148
	436252	Homo sapiens cDNA FLJ11562 fis, clone	H AI539519	Hs.142827	7.1	3179 7184
70	457211	ESTs, Weakly similar to S51797 vasodila	AW972565	Hs.32399	7.1	4543 8344
	449929	ESTs	AA004786	Hs.163792	7.1	4121 7999
	410270	tumor endothelial marker 1 precursor	AF279142	Hs.195727	7.1	442 443 5121
	450506	fibroblast activation protein, alpha	NM_004460	Hs.4 18	7.1	4170 4171 8037
	413472	solute carrier family 1 (glial high aff	BE242870	Hs.75379	7.1	725 5342
75	438866	tissue inhibitor of metalloproteinase 2	U44385	Hs.6441	7.1	3360 3361 7344
	419703	ESTs	AI793257	Hs.128151	7.1	1375 5847
	419745	slug (chicken homolog), zinc finger pro	AF042001	Hs.93005	7.1	1381 1382 5851
	409637	Homo sapiens mRNA; cDNA DKFZp434K0621	AA323948	Hs.55407	7.0	372 5069
	410611	KIAA1628 protein	AW954134	Hs.20924	7.0	480 5148
80	429415	procollagen C-endopeptidase enhancer	NM_002593	Hs.2 02097	7.0	2557 2558 6706
	452083	ESTs	AA022668	Hs.349970	7.0	4284 8127
	411704	hypothetical protein FLJ10074	AI499220	Hs.71573	7.0	547 5202
	408829	heparan sulfate (glucosamine) 3-O-sulfo	NM_006042	Hs.4 8384	7.0	264 265 4991
	416322	pymofine-5-carboxylate reductase 1	BE019494	Hs.79217	6.9	989 5554
85	454033	homeo box HB9	AF107457	Hs.37035	6.9	4483 8292
	445784	ESTs	AI253155	Hs.146065	6.9	3798 7728

	436748	collagen, type VI, alpha 2	BE159107	Hs.159263	6.9	3212 7213
	451304	collagen, type XVI, alpha 1	M92642	Hs.26208	6.9	4224 4225 8081
	422901	ribosomal protein L44	R81936	Hs.75874	6.9	1757 6126
5	417389	midkine (neurite growth-promoting facto	BE260964	Hs.82045	6.9	1109 5647
	429294	Homo sapiens cDNA: FLJ22463 fis, clone	AA095971	Hs.198793	6.9	2540 6693
	421913	osteoglycin (osteainductive factor, mhm	AI934365	Hs.109439	6.8	1611 6020
	429973	ESTs	AI423317	Hs.164680	6.8	2628 6756
	453642	dipeptidylpeptidase VI	AI370936	Hs.34074	6.8	4431 8251
10	415885	KIAA0161 gene product	D79983	Hs.78894	6.8	953 954 5524
	449780	ribosomal protein L44	AA443241	Hs.75874	6.8	4114 7992
	426600	VEF nerve growth factor inducible	NM_003378	Hs.171014	6.8	2255 2256 6475
	437574	hypothetical protein FLJ21195 similar t	AI797592	Hs.207407	6.8	3272 7266
	429441	lipophilin B (uteroglobin family member	AJ224172	Hs.204096	6.8	2560 2561 6708
	418203	CDC28 protein kinase 2	X54942	Hs.83758	6.8	1202 1203 5719
15	416658	fibrillin 2 (congenital contractural ar	U03272	Hs.79432	6.8	1020 1021 5577
	422562	AE-binding protein 1	AI962060	Hs.118397	6.8	1700 6085
	452973	ESTs	H88409	Hs.40527	6.8	4375 8203
	414172	phosphatidylinositol glycan, class C	AW954324	Hs.75790	6.8	785 5393
20	428248	ESTs	AI126772	Hs.40479	6.7	2414 6596
	443883	serine (or cysteine) proteinase inhibit	AA114212	Hs.9930	6.7	3653 7614
	422007	ESTs	AI739435	Hs.39168	6.7	1624 6029
	417944	collagen, type V, alpha 2	AU077196	Hs.82985	6.7	1172 5693
	424915	ESTs	R42755	Hs.23096	6.7	2027 6318
25	453175	RAB32, member RAS oncogene family	NM_006834	Hs.32217	6.7	4400 4401 8225
	421552	secreted frizzled-related protein 4	AF026692	Hs.105700	6.7	1559 1560 5982
	452106	ESTs	AI141031	Hs.21342	6.6	4289 8131
	422890	ankyrin 3, node of Ranvier (ankyrin G)	Z43784	Hs.351357	6.6	1756 6125
	425708	hypothetical protein FLJ22530	AK001342	Hs.14570	6.6	2128 2129 6388
30	407811	cysteine knot superfamily 1, BMP antago	AW190902	Hs.40098	6.6	164 4908
	418478	cyclin-dependent kinase inhibitor 2A (m	U38945	Hs.1174	6.6	1245 1246 5747
	420888	dihydropyrimidinase-like 4	AB006713	Hs.100058	6.6	1486 1487 5930
	429451	heme oxygenase (decycling) 1	BE409861	Hs.202833	6.6	2562 6709
	422105	Fc fragment of IgG binding protein	D84239	Hs.111732	6.5	1646 1647 6044
35	450785	Homo sapiens, alpha-1 (VI) collagen	AA852713	Hs.108885	6.5	4193 8056
	428317	ESTs	AW022609	Hs.50745	6.5	2431 6610
	421823	ESTs	N40850	Hs.28625	6.5	1600 6011
	418322	cyclin-dependent kinase inhibitor 3 (CD	AA284166	Hs.84113	6.5	1214 5727
	426968	amphiphysin (Stiff-Mann syndrome with b	U07616	Hs.173034	6.5	2290 2291 6499
40	442295	Homo sapiens cDNA FLJ11469 fis, clone	H AI827248	Hs.224398	6.5	3555 7527
	400419	Target	AF084545		6.5	22 23 4626
	407604	collagen, type VIII, alpha 2	AW191962	Hs.353001	6.5	145 4891
	450847	stanniocalcin 1	NM_003155	Hs.25590	6.5	4201 4202 8062
	416391	mesoderm specific transcript (mouse) ho	AI878927	Hs.79284	6.5	999 5562
45	422765	baculoviral IAP repeat-containing 5 (su	AW409701	Hs.1578	6.5	1734 6110
	420576	KIAA1858 protein	AA297634	Hs.54925	6.5	1463 5914
	441020	ESTs	W79283	Hs.35962	6.4	3495 7471
	408118	calcium binding protein Cab45 precursor	T23064	Hs.42806	6.4	192 4934
	409433	ESTs	AA074382	Hs.135255	6.4	349 5053
50	432239	matrix metalloproteinase 13 (collagenas	X81334	Hs.2936	6.4	2856 2857 6921
	434652	bladder cancer overexpressed protein	AF148713	Hs.125830	6.4	3066 3067 7092
	438459	Homo sapiens cDNA FLJ13655 fis, clone P	T49300	Hs.35304	6.4	3325 7315
	417605	regulator of G-protein signalling 3	AF006609	Hs.82294	6.4	1138 1139 5665
	424420	prostaglandin E synthase	BE614743	Hs.146688	6.4	1949 6264
55	425964	progesterone membrane binding protein	AW889928	Hs.9071	6.4	2157 6408
	433078	Homo sapiens cDNA FLJ12231 fis, clone M	AW015188	Hs.121575	6.4	2938 6988
	442432	hypothetical protein FLJ23468	BE093589	Hs.38178	6.3	3563 7535
	452046	KIAA0802 protein	AB018345	Hs.27657	6.3	4275 4276 8120
	402992	Target Exon			6.3	4700
60	426363	transforming growth factor, beta 3	M58524	Hs.2025	6.3	2210 2211 6446
	451253	claudin 10	H48299	Hs.26126	6.3	4220 8078
	412104	Homo sapiens, Similar to RIKEN cDNA 221	AW205197	Hs.240951	6.3	569 5220
	418110	hypothetical protein FLJ22202	R43523	Hs.217754	6.3	1193 5710
	451763	hypothetical protein FLJ14220	AW294647	Hs.233634	6.3	4254 8103
65	419750	Homo sapiens cDNA FLJ14236 fis, clone N	AL079741	Hs.183114	6.3	1385 5853
	408212	hypothetical protein	AA297567	Hs.43728	6.3	206 4945
	427751	conserved gene amplified in osteosarcom	AF000152	Hs.355816	6.3	2366 2367 6558
	431124	doublesex and mab-3 related transcript	AF284221	Hs.59506	6.3	2753 2754 6843
	434377	intron of periostin (OSF-2os)	AW137148	Hs.306593	6.2	3051 7078
70	413438	sphingosine kinase 1	AF238083	Hs.68061	6.2	721 722 5339
	439285	hypothetical protein FLJ20093	AL133916	Hs.47860	6.2	3389 7372
	431183	KDEL (Lys-Asp-Glu-Leu) endoplasmic ret	NM_006855	Hs.250696	6.2	2756 2757 6845
	431347	insulin-like growth factor 2 (somatomed	AI133461	Hs.251664	6.2	2774 6859
	426855	Homo sapiens mRNA; cDNA DKFZp566P013	AL117427	Hs.172778	6.2	2279 6491
75	438085	ESTs	R52518	Hs.7967	6.2	3299 7292
	452063	ESTs, Weakly similar to TWST_HUMAN TWIS	R53185	Hs.32366	6.2	4281 8124
	447359	adenylate kinase 5	NM_012093	Hs.18268	6.2	3918 3919 7830
	419156	amelogenin (X chromosome, amelogenesis	AC002366	Hs.1238	6.2	1311 1312 5797
	420005	ESTs	AW271106	Hs.133294	6.2	1407 5871
80	410867	fibrillin 1 (Marfan syndrome)	X63556	Hs.750	6.2	498 499 5162
	452199	hypothetical protein MGC3133	BE255643	Hs.110695	6.2	4297 8139
	410240	synaptotagmin 2	AL157424	Hs.61289	6.1	437 5117
	447733	MAD2 (mitotic arrest deficient, yeast,	AF157482	Hs.19400	6.1	3955 3956 7860
	424162	ESTs, Weakly similar to ALU2_HUMAN ALU	AA336229	Hs.93135	6.1	1907 6235
85	418283	cathepsin K (pycnodystosis)	S79895	Hs.83942	6.1	1210 1211 5724
	426935	collagen, type I, alpha 1	NM_000088	Hs.172928	6.1	2288 2289 6498
	450447	hypothetical protein P15-2	AF212223	Hs.25010	6.1	4168 4169 8036

	417437	interferon regulatory factor 4	U52682	Hs.82132	6.1	1123 1124 5656
	401797	Target Exon			6.1	4663
	421251	enigma (LIM domain protein)	Z28913	Hs.102948	6.1	1521 5957
5	427060	ESTs	AW378993	Hs.90286	6.1	2300 6507
	436311	ESTs	AA708958	Hs.168732	6.1	3181 7186
	434629	glioma-amplified sequence-41	AA789081	Hs.4029	6.1	3064 7090
	410295	nidogen (enactin)	AA741357	Hs.356624	6.1	450 5127
	401131	NM_001651*:Homo sapiens aquaporin 5 (AQ			6.1	4644
10	421579	stem cell growth factor; lymphocyte sec	NM_002975	Hs.1 05927	6.0	1567 1568 5987
	429707	matrix metalloproteinase 23B	W76631	Hs.211819	6.0	2606 6738
	428046	ESTs, Moderately similar to I38022 hypo	AW812795	Hs.337534	6.0	2393 6579
	444734	7-dehydrocholesterol reductase	NM_001360	Hs.1 1806	6.0	3718 3719 7669
	451766	ephrin-B3.	NM_001406	Hs.2 6988	6.0	4255 4256 8104
15	449294	ESTs	A1651786	Hs.195045	6.0	4079 7961
	410361	guanylate binding protein 1, interferon	BE391804	Hs.62661	6.0	456 5132
	451149	RNA binding motif protein 8B	AL047586	Hs.10283	6.0	4214 8073
	453164	SNARE associated protein snapin	F33692	Hs.32018	6.0	4396 8222
	446211	S100 calcium-binding protein A13	AI021993	Hs.14331	6.0	3824 7752
20	407083	H.sapiens XG mRNA (clone PEP11)	Z48511		6.0	107 4859
	456508	ESTs, Weakly similar to AF208855 1 BM-O	AA502764	Hs.123469	6.0	4521 8325
	452291	CDC7 (cell division cycle 7, S. cerevis	AF015592	Hs.28853	6.0	4310 4311 8150
	452160	cysteine sulfinic acid decarboxylase-re	BE378541	Hs.355568	6.0	4292 8134
	449318	Homo sapiens, Similar to RIKEN cDNA 573	AW236021	Hs.78531	6.0	4080 7962
25	442743	ESTs, Weakly similar to MUC2_HUMAN	MUC1 A1801351	Hs.302110	6.0	3583 7551
	419169	ESTs, Weakly similar to S72482 hypothe	AW851980	Hs.262346	5.9	1314 5799
	445363	tubulin-specific chaperone d	NM_005993	Hs.1 2570	5.9	3762 3763 7702
	432731	fibronectin 1	R31178	Hs.287820	5.9	2904 6961
	425760	galactosamine (N-acetyl)-6-sulfate sulf	D17629	Hs.159479	5.9	2134 2135 6392
30	402855	NM_001839*:Homo sapiens calponin 3, aci			5.9	4694
	438203	ESTs	BE540090	Hs.7345	5.9	3308 7300
	428450	KIAA0175 gene product	NM_014791	Hs.1 84339	5.9	2443 2444 6621
	434879	collagen, type VI, alpha 2	M34572	Hs.159263	5.9	3086 3087 7107
	422809	hypothetical protein FLJ10549	AK001379	Hs.121028	5.9	1741 1742 6115
35	423905	lung type-I cell membrane-associated gl	AW579960	Hs.135150	5.9	1867 6207
	415758	protein kinase C, zeta	BE270465	Hs.78793	5.9	946 5518
	427871	Homo sapiens, clone IMAGE:3507281, mRNA	AW992405	Hs.352406	5.9	2380 6568
	458956	gb:ht98f11.x1 NCI_CGAP_Lu24 Homo sapien	BE220675		5.9	4587 8383
	426798	ESTs	AA385062	Hs.130260	5.8	2275 6487
40	424440	ESTs	AA340743	Hs.133208	5.8	1951 6266
	445875	Homo sapiens clone 24453 mRNA sequence	AF070524	Hs.13410	5.8	3801 7731
	420139	lipase, hormone-sensitive	NM_005357	Hs.9 5351	5.8	1419 1420 5881
	439897	KIAA0942 protein	NM_015310	Hs.6 763	5.8	3437 3438 7420
	432527	ESTs	AW975028	Hs.102754	5.8	2883 6944
45	428398	ESTs	AI249368	Hs.98558	5.8	2435 6614
	432576	ESTs, Weakly similar to I38022 hypothe	AW157424	Hs.165954	5.8	2888 6949
	421848	collagen, type VI, alpha 1	X15880	Hs.108885	5.8	1602 1603 6013
	404245	NM_007116*:			5.8	4743
	408901	hypothetical protein FLJ10468	AK001330	Hs.48855	5.8	272 273 4997
50	439979	hypothetical protein FLJ10430	AW600291	Hs.6823	5.8	3442 7424
	452436	ESTs, Moderately similar to A46010 X-li	BE077546	Hs.31447	5.8	4330 8164
	432211	hypothetical protein FLJ10986	BE274530	Hs.273333	5.8	2852 6917
	425398	hypothetical protein similar to tenasci	AL049689	Hs.156369	5.8	2101 2102 6370
	447757	KIAA0859 protein	AA071276	Hs.19469	5.8	3960 7863
55	434775	ESTs	AA648983	Hs.370514	5.8	3074 7098
	422586	hypothetical protein FLJ22127	AA312704	Hs.59457	5.8	1709 6091
	441669	Homo sapiens cDNA FLJ11436 fis, clone	H R78195	Hs.29692	5.8	3532 7504
	424066	ESTs, Weakly similar to I38022 hypothe	Z99348	Hs.112461	5.8	1891 6223
	422201	G protein-coupled receptor 30	NM_001505	Hs.1 13207	5.7	1658 1659 6054
60	449378	ESTs	AW664026	Hs.59892	5.7	4085 7967
	421815	membrane protein CH1	AW592146	Hs.108636	5.7	1598 6009
	408792	coagulation factor X	L29433	Hs.47913	5.7	260 261 4988
	409190	sarcoma amplified sequence	AU076536	Hs.50984	5.7	321 5034
	435232	cyclin-dependent kinase inhibitor 2C (p	NM_001262	Hs.4 864	5.7	3114 3115 7132
65	411893	ESTs	R82845	Hs.273789	5.7	558 5211
	428959	WNT1 Inducible signaling pathway protei	AF100779	Hs.194680	5.7	2493 2494 6657
	421686	KIAA0584 protein	AB011166	Hs.106794	5.7	1578 1579 5993
	418113	SRY (sex determining region Y)-box 4	AI272141	Hs.83484	5.7	1194 5711
	433842	ESTs	A1652156	Hs.26346	5.7	3009 7044
70	409664	ESTs	AA076743	Hs.129770	5.7	374 5071
	427855	KIAA1877 protein	R61253	Hs.98265	5.7	2376 6565
	453880	ESTs, Weakly similar to I38022 hypothe	AI803166	Hs.135121	5.7	4458 8272
	410169	hypothetical protein MGC3047	AI373741	Hs.59384	5.7	428 5112
	409731	thymosin, beta, identified in neuroblas	AA125985	Hs.56145	5.7	386 5080
75	414001	ESTs, Moderately similar to ALU1_HUMAN	AI610347	Hs.103812	5.7	762 5374
	409125	axonal transport of synaptic vesicles	R17268	Hs.343567	5.7	308 5024
	421991	KIAA0990 protein	NM_014918	Hs.1 10488	5.6	1622 1623 6028
	414359	cadherin 11, type 2, OB-cadherin (osteo	M62194	Hs.75929	5.6	808 5413
	412446	ESTs	AI768015	Hs.352375	5.6	586 5235
80	419511	general transcription factor IIIA	AA429750	Hs.75113	5.6	1345 5824
	428981	ESTs, Weakly similar to ALU2_HUMAN	ALU BE313077	Hs.93135	5.6	2497 6660
	407862	Homo sapiens cDNA FLJ10934 fis, clone	O BE548267	Hs.337986	5.6	171 4915
	410711	KIAA0318 protein	AB002316	Hs.65746	5.6	489 490 5155
	446102	ESTs	AW168067	Hs.317694	5.6	3819 7747
85	411756	discoïdin domain receptor family, membe	BE294350	Hs.71891	5.6	550 5205
	410929	ESTs	H47233	Hs.30643	5.6	504 5166
	431789	mitogen-activated protein kinase 4	H19500	Hs.269222	5.6	2821 6895

418986	ESTs	AI123555	Hs.293821	5.6	1288 5779
401130	Target Exon			5.6	4643
425131	ESTs	BE252230	Hs.99163	5.6	2051 6336
433430	ESTs	AI863735	Hs.369982	5.6	2977 7018
408296	DKFZP586G1517 protein	AL117452	Hs.44155	5.6	209 210 4947
429299	hypothetical protein MGC13102	AI620463	Hs.347408	5.6	2541 6694
435460	ESTs	AA682439	Hs.118380	5.6	3126 7142
411789	Adican	AF245505	Hs.72157	5.6	553 554 5207
417933	thymidylate synthetase	X02308	Hs.82962	5.6	1170 1171 5692
411335	KIAA1096 protein	AA132813	Hs.69559	5.6	526 5185
431070	transcription factor 19 (SC1)	AW408164	Hs.249184	5.5	2744 6837
434837	lysophosphatidic acid acyltransferase-d	AF156776	Hs.353175	5.5	3080 3081 7102
400245	Eos Control		Hs.7957	5.5	4607
423633	ESTs	N39053	Hs.164146	5.5	1830 6182
418097	ESTs	R45137	Hs.279789	5.5	1191 5708
410096	hypothetical protein MGC5540	AW245200	Hs.267400	5.5	420 5105
429965	Homo sapiens cDNA FLJ11789 fis, clone	H AL040379	Hs.99551	5.5	2627 6755
452839	ribosomal protein L44	R96290	Hs.75874	5.5	4359 8189
426386	bladder cancer overexpressed protein	AA748850	Hs.125830	5.5	2216 6450
439999	ras homolog gene family, member E	AA115811	Hs.6838	5.5	3444 7426
426013	ESTs	AI818098	Hs.4779	5.5	2160 6410
426509	pentaxin-related gene, rapidly induced	M31166	Hs.2050	5.5	2243 2244 6468
407874	Homo sapiens cDNA FLJ14059 fis, clone	H AI766311	Hs.289047	5.5	175 4918
427378	melanoma antigen, family D, 1	BE515037	Hs.177556	5.5	2322 6523
414053	transgelin 2	BE391635	Hs.75725	5.5	774 5383
411894	GLI-Kruppel family member GLI3 (Greig c	M57609	Hs.72916	5.5	559 560 5212
432692	ESTs	AW974944	Hs.285814	5.5	2899 6957
426155	ESTs	AA370953	Hs.163553	5.5	2182 6426
411358	KIAA1691 protein	R47479	Hs.94761	5.5	527 5186
449129	ESTs	AI631602	Hs.258949	5.5	4066 7950
432503	ESTs	AA551196	Hs.188952	5.5	2878 6940
439130	ESTs	AA306090	Hs.345588	5.5	3378 7361
448848	hypothetical protein	AF131851	Hs.22241	5.5	4042 4043 7931
413053	ESTs, Moderately similar to KIAA1399 pr	AW963263	Hs.65377	5.5	674 5306
432693	ESTs	AW449630	Hs.293790	5.5	2900 6958
425428	DKFZP586B0621 protein	AL110261	Hs.157211	5.5	2104 2105 6372
451952	ESTs	AL120173	Hs.301663	5.5	4264 8111
408562	roundabout (axon guidance receptor, Dro	AI436323	Hs.31141	5.5	240 4971
441607	neuronal cell adhesion molecule	NM_005010	Hs.7 912	5.5	3526 3527 7499
427596	extracellular glycoprotein EMILIN-2 pre	AA449506	Hs.270143	5.5	2350 6544
422532	protective protein for beta-galactosida	AL008726	Hs.118126	5.5	1697 1698 6083
457500	protein kinase, interferon-inducible do	NM_002759	Hs.2 74382	5.5	4555 4556 8354
435538	low density lipoprotein receptor-relate	AB011540	Hs.4930	5.5	3132 3133 7148
448520	doublecortin and CaM kinase-like 1	AB002367	Hs.21355	5.5	4010 4011 7907
415689	ESTs	AW959615	Hs.111045	5.5	938 5512
409248	KIAA1209 protein	AB033035	Hs.51965	5.5	330 331 5040
408660	ESTs, Moderately similar to PC4259 ferr	AA525775	Hs.89040	5.5	247 4977
445162	piccolo (presynaptic cytomatrix protein	AB011131	Hs.12376	5.5	3749 3750 7693
449029	solute carrier family 7 (cationic amino	N28989	Hs.22891	5.5	4058 7942
400288	Integrin, alpha 5 (fibronectin receptor	X06256	Hs.149609	5.4	1 2 4614
400295	AI905687:IL-BT095-190199-019 BT095 Homo	W72838	Hs.348419	5.4	6 4617
445439	regulator of nonsense transcripts 1	BE243084	Hs.12719	5.4	3770 7708
419726	bone morphogenetic protein 1	U50330	Hs.1274	5.4	1376 1377 5848
431457	Integrin, alpha 11	NM_012211	Hs.2 56297	5.4	2787 2788 6870
417412	Interleukin 1 receptor, type I	X16896	Hs.82112	5.4	1116 1117 5652
417259	chondroitin sulfate proteoglycan 2 (ver	AW903838	Hs.81800	5.4	1092 5632
418867	msh (Drosophila) homeo box homolog 2	D31771	Hs.89404	5.4	1277 1278 5772
447709	GDNF family receptor alpha 2	U97145	Hs.19317	5.4	3949 3950 7856
430439	DKFZP434B061 protein	AL133561	Hs.380155	5.4	2695 2696 6803
429207	ESTs	AA447941	Hs.123423	5.4	2532 6686
444006	type I transmembrane protein Fn14	BE395085	Hs.334762	5.4	3668 7627
410889	twist (Drosophila) homolog (acrocephalo	X91662	Hs.66744	5.4	501 502 5164
427585	collagen, type X, alpha 1 (Schmid metap	D31152	Hs.179729	5.4	2349 6543
429101	uterine-derived 14 kDa protein	AW452174	Hs.173780	5.4	2513 6672
447197	gb:yh88b01.a1 Soares placenta Nb2HP Hom	R36075	Hs.358552	5.4	3897 7813
422648	Melanoma associated gene	D86983	Hs.118893	5.4	1720 1721 6100
426485	platelet-derived growth factor receptor	NM_006207	Hs.1 70040	5.4	2238 2239 6465
421787	nuclear receptor subfamily 2, group C,	AA227068	Hs.108301	5.4	1594 6006
408741	carboxypeptidase A3 (mast cell)	M73720	Hs.646	5.4	252 253 4982
443184	ESTs	AI638728	Hs.135159	5.4	3607 7574
433895	mitogen-activated protein kinase kinase	AI287912	Hs.3628	5.4	3014 7048
453596	hypothetical protein FLJ14834	AA441838	Hs.62905	5.4	4428 8248
424001	paternally expressed 10	W67883	Hs.137476	5.4	1882 6217
411263	kinesin-like 6 (mitotic centromere-asso	BE297802	Hs.69360	5.3	523 5182
447414	neuroblastoma (nerve tissue) protein	D82343	Hs.74376	5.3	3924 3925 7834
450296	hepatocyte growth factor-regulated tyro	AL041949	Hs.24756	5.3	4153 8023
421506	thymidine kinase 1, soluble	BE302796	Hs.105097	5.3	1550 5976
424192	P311 protein	U30521	Hs.142827	5.3	1911 1912 6238
416140	roundabout (axon guidance receptor, Dro	AI918035	Hs.301198	5.3	978 5545
452877	ESTs	AI250789	Hs.32478	5.3	4364 8193
433819	ESTs	AW511097	Hs.110069	5.3	3007 7042
440856	ESTs	AW993377	Hs.130390	5.3	3489 7465
432101	EphA3	AI918950	Hs.123642	5.3	2841 6909
432988	ESTs, Weakly similar to IDN4-GGTR14 [H	R39234	Hs.251699	5.3	2921 6975
426514	bone morphogenetic protein 7 (osteogeni	BE616633	Hs.170195	5.3	2246 6470
431117	delta (Drosophila)-like 1	AF003522	Hs.250500	5.3	2751 2752 6842

434269	similar to murine leucine-rich repeat p	AK001991	Hs.3781	5.3	3037 3038 7069
420255	membrane metallo-endopeptidase (neutral	NM_007289	Hs.1298	5.3	1438 1439 5896
438828	hypothetical protein DKFZp761F2014	AL134275	Hs.6434	5.3	3356 7340
400297	hypothetical protein DKFZp564O1278	AI127076	Hs.288381	5.3	7 4618
422100	ADP-ribosylation factor-like 7	AI096988	Hs.111554	5.3	1644 6042
441944	Homo sapiens clone 23767 and 23782 mRNA	AW855861	Hs.8025	5.3	3541 7513
407603	Homo sapiens, clone IMAGE:4299322, mRNA	AW955705	Hs.62604	5.3	144 4890
453830	ESTs	AA534296	Hs.20953	5.3	4445 8263
456181	ras inhibitor	L36463	Hs.1030	5.3	4516 4517 8321
412773	similar to vaccinia virus HindIII K4L O	H15785	Hs.74573	5.3	639 5276
419405	ESTs	AI377043	Hs.42189	5.3	1333 5816
432791	sentrin/SUMO-specific protease	NM_014554	Hs.6 6450	5.3	2907 2908 6963
419999	ESTs	AI760942	Hs.191754	5.3	1406 5870
420238	ESTs, Weakly similar to 2109260A B cell	AA256783	Hs.12549	5.3	1436 5894
456063	retinol-binding protein 4, interstitial	NM_006744	Hs.7 6461	5.3	4511 4512 8317
437342	hypothetical protein DKFZp761K1423	AW903297	Hs.236438	5.3	3254 7251
423057	ESTs, Moderately similar to 138022 hypo	AW961597	Hs.130816	5.3	1773 6139
426148	Homo sapiens cDNA FLJ10728 fis, clone	AI751071	Hs.167135	5.3	2179 6424
417153	collagen, type II, alpha 1 (primary ost	X57010	Hs.81343	5.3	1084 1085 5625
419987	osteomodulin	NM_005014	Hs.9 4070	5.3	1402 1403 5868
409170	ESTs	W91994	Hs.16145	5.3	317 5030
414312	ESTs	AA155694	Hs.191060	5.3	800 5407
418452	C-type (calcium dependent, carbohydrate	BE379749	Hs.85201	5.3	1241 5744
426471	transforming growth factor, alpha	M22440	Hs.170009	5.2	2233 2234 6462
428342	Homo sapiens cDNA FLJ13458 fis, clone	AI739168	Hs.349283	5.2	2432 6611
444829	ubiquitin specific protease 22	AB028986	Hs.12064	5.2	3726 3727 7674
443191	a disintegrin-like and metalloprotease	N93301	Hs.155824	5.2	3608 7575
448197	KIAA1303 protein	AB037724	Hs.20677	5.2	3984 3985 7885
414919	ESTs	AW087337	Hs.194461	5.2	890 5474
439319	ESTs	AW016401	Hs.2549	5.2	3392 7375
424898	ESTs	H17954	Hs.6664	5.2	2021 6314
412577	CD163 antigen	Z22968	Hs.74076	5.2	608 609 5252
419437	neogenin (chicken) homolog 1	U61262	Hs.90408	5.2	1338 1339 5820
408161	hypothetical protein MGC3032	AW952912	Hs.300383	5.2	195 4937
421485	hypothetical protein FLJ10134	AA243499	Hs.104800	5.2	1547 5974
422550	microfibrillar-associated protein 4	BE297626	Hs.296049	5.2	1699 6084
426716	sera domain, immunoglobulin domain (Ig)	NM_006379	Hs.171921	5.2	2264 2265 6481
417079	interleukin 1 receptor antagonist	U65590	Hs.81134	5.2	1073 1074 5616
439668	frizzled (Drosophila) homolog 8	AI091277	Hs.302634	5.2	3414 7397
452682	progesterone membrane binding protein	AA456193	Hs.374574	5.2	4340 8174
422170	anti-Mullerian hormone	AI791949	Hs.112432	5.2	1655 6051
407216	lysyl oxidase	N91773	Hs.348385	5.2	123 4875
421233	tetraspan NET-6 protein	AA209534	Hs.284243	5.2	1518 5955
436608	down syndrome critical region protein D	AA628980	Hs.192371	5.2	3205 7207
426698	KIAA1866 protein	AA852773	Hs.334838	5.2	2463 6635
414821	Fc fragment of IgG, high affinity Ia, r	M63835	Hs.77424	5.2	876 877 5465
426304	Homo sapiens cDNA FLJ11477 fis, clone	H AA374532	Hs.124673	5.1	2198 6438
449679	toll-like 1	AI823951	Hs.129700	5.1	4106 7986
410108	OSBP-related protein 6	AA081659	Hs.318775	5.1	423 5108
409509	ESTs	AL036923	Hs.322710	5.1	353 5056
434868	collagen, type VI, alpha 2	R50032	Hs.159263	5.1	3085 7106
449897	transmembrane protein vezatin; hypothet	AW819642	Hs.24135	5.1	4120 7998
414024	gb:zm79g08.r1 Stratagene neuroepitheliu	AA134712	Hs.22410	5.1	759 5379
418506	Unknown protein for MGC:29643 (formerly	AA084248	Hs.372651	5.1	1247 5748
433513	ESTs	AI566356	Hs.171437	5.1	2985 7024
416406	lipoma HMGIC fusion partner-like 2	D86961	Hs.79299	5.1	1001 1002 5564
452078	ESTs	AA022620	Hs.52170	5.1	4283 8126
416986	ESTs	AI471952	Hs.148676	5.1	1057 5603
429480	elastin (supravalvular aortic stenosis,	M36860	Hs.9295	5.1	2565 2566 6712
439703	ESTs	AF086538	Hs.196245	5.1	3420 7403
414117	proteolipid protein 1 (Pellizaeus-Merzba	W88559	Hs.355807	5.1	777 5386
408996	glycoprotein (transmembrane) nmb	AI979168	Hs.82226	5.1	291 5011
434431	ESTs	AW131454	Hs.168571	5.1	3056 7082
440676	LIM and senescent cell antigen-like dom	NM_004987	Hs.1 12378	5.1	3479 3480 7457
447217	neuropilin 2	BE465754	Hs.17778	5.1	3904 7819
421362	hypothetical protein FLJ20043	AK000050	Hs.103853	5.1	1531 1532 5965
441389	endocytic receptor (macrophage mannose	AF134838	Hs.7835	5.1	3514 3515 7488
423857	Homo sapiens mRNA; cDNA DKFZp564O0862	N48902	Hs.133481	5.1	1857 6200
410132	Microfibril-associated glycoprotein-2	NM_003480	Hs.3 00946	5.1	425 426 5110
452410	Homo sapiens mRNA; cDNA DKFZp434E2321	(AL133619	Hs.29383	5.1	4328 4329 8163
423989	OLF-1/EBF associated zinc finger gene	AF221712	Hs.137168	5.1	1880 1881 6216
441362	RAD51 (S. cerevisiae) homolog (E. coli R	BE614410	Hs.23044	5.1	3512 7486
426283	kynureninase (L-kynurenine hydrolase)	NM_003937	Hs.1 69139	5.0	2192 2193 6435
435854	putative ankyrin-repeat containing prot	AJ278120	Hs.4996	5.0	3157 3158 7166
448425	ESTs	AI500359	Hs.371249	5.0	4004 7901
439332	Homo sapiens mRNA; cDNA DKFZp547M072	(f AW842747	Hs.378821	5.0	3393 7376
422565	singed (Drosophila)-like (sea urchin la	BE259035	Hs.118400	5.0	1701 6086
450746	general transcription factor II, i	D82673	Hs.278589	5.0	4187 8051
421822	coagulation factor XI (plasma thrombopl	AV650066	Hs.1430	5.0	1599 6010
452958	ESTs	AA883929	Hs.40527	5.0	4372 8200
448410	hypothetical protein FLJ20220	AK000227	Hs.21126	5.0	4000 4001 7898
437829	ESTs	AI358522	Hs.103834	5.0	3289 7282
426479	mouse double minute 2, human homolog of	Z12020	Hs.170027	5.0	2235 2236 6463
446512	ESTs	H30351	Hs.207982	5.0	3848 7771
437139	ESTs, Weakly similar to RTA RAT PROBABL	W73685	Hs.118513	5.0	3238 7236
442657	ESTs	BE502631	Hs.130645	5.0	3576 7546

	436291	protein regulator of cytokinesis 1	BE568452	Hs.344037	5.0	3180 7185
	408988	Homo sapiens clone TUA8 Cri-du-chat reg	AL119844	Hs.49476	5.0	289 5009
	408968	hypothetical protein FLJ20644	AI652236	Hs.49376	5.0	286 5007
	441368	ESTs	AA931532	Hs.126836	5.0	3513 7487
5	420737	CD70 ; tumor necrosis factor (ligand)	L08096	Hs.99899	5.0	1473 1474 5920
	420173	ESTs	AA256151	Hs.22999	5.0	1426 5886
	443920	Homo sapiens cDNA FLJ13655 fis, clone	P AL037764	Hs.35304	5.0	3659 7620
	435370	ESTs	AI964074	Hs.225838	5.0	3120 7136
10	453935	ESTs	AI633770	Hs.42572	5.0	4470 8281
	412942	mitogen-activated protein kinase-activa	AL120344	Hs.75074	5.0	658 5293
	456534	phospholipase C, beta 3, neighbor pseud	X91195	Hs.100623	5.0	4522 8326
	413094	TOLLIP protein	H24184	Hs.25413	5.0	680 5311
	415014	ESTs	AW954054	Hs.24951	5.0	900 5481
	412992	protease, serine, 11 (IGF binding)	AI423369	Hs.75111	5.0	666 5299
15	424512	integrin, beta 5	X53002	Hs.149846	5.0	1968 1969 6277
	449969	Homo sapiens cDNA FLJ14337 fis, clone	P AW295142	Hs.180187	5.0	4123 8001
	448498	ESTs	AA418276	Hs.375003	5.0	4007 7904
	418423	KIAA0513 gene product	NM_014732	Hs.3 01658	5.0	1239 1240 5743
20	416051	mannosidase, alpha, class 1A, member 1	AA835868	Hs.25253	5.0	966 5534
	431448	hypothetical protein DKFZp564O1278	AL137517	Hs.306201	5.0	2785 2786 6869
	423400	Homo sapiens mRNA; cDNA DKFZp434M038 (f	AL122123	Hs.127958	5.0	1802 6159
	408374	forkhead box F1	AW025430	Hs.155591	5.0	216 4951
	425525	ESTs	AA358883	Hs.23871	5.0	2111 6377
25	425703	collagen, type VI, alpha 2	X06195	Hs.159263	5.0	2126 2127 6387
	457464	ESTs	AW972234	Hs.126680	4.9	4554 8353
	419452	PTK7 protein tyrosine kinase 7	U33635	Hs.90572	4.9	1340 1341 5821
	412708	ESTs, Weakly similar to CGHU7L collagen	R26830	Hs.106137	4.9	630 5268
	425818	matrix metalloproteinase 17 (membrane-i	AB021225	Hs.159581	4.9	2145 2146 6398
	424876	Homo sapiens clone IMAGE:297403, mRNA s	AI056991	Hs.269873	4.9	2016 6310
30	426075	ESTs, Weakly similar to 2109260A B cell	AW513691	Hs.270149	4.9	2170 6417
	413401	ESTs	AI361861	Hs.118659	4.9	712 6332
	421680	Human DNA sequence from clone CTA-984G1	AL031186	Hs.289106	4.9	1576 1577 5992
	402233	NM_030760*:Homo sapiens endothelial dif			4.9	4674
	414945	lymphocyte antigen 6 complex, locus E	BE076358	Hs.77667	4.9	894 5477
35	427254	ESTs	AL121523	Hs.97774	4.9	2312 6516
	432290	Homo sapiens cDNA FLJ10237 fis, clone	H AK001099	Hs.274273	4.9	2862 6926
	448888	caspase recruitment domain protein 6	AW196663	Hs.200242	4.9	4049 7935
	451333	hypothetical protein FLJ10052	AK000914	Hs.26244	4.9	4226 4227 8082
40	447436	Homo sapiens cDNA: FLJ21449 fis, clone	AI932971	Hs.18593	4.9	3928 7837
	402507	Target Exon			4.9	4683
	427557	plasminogen activator, urokinase recept	NM_002659	Hs.1 79657	4.9	2343 2344 6539
	428411	ESTs	AW291464	Hs.10338	4.9	2439 6617
	418216	AF15q14 protein	AA662240	Hs.283099	4.9	1206 5721
45	440952	ESTs	AI291804	Hs.118101	4.9	3490 7466
	422684	H2A histone family, member Z	BE561617	Hs.119192	4.9	1726 6105
	442173	KIAA0144 gene product	N76101	Hs.8127	4.9	3552 7524
	451743	ESTs	AW074266	Hs.336428	4.9	4251 8101
	438545	KIAA1151 protein	AB032977	Hs.6298	4.9	3329 3330 7319
50	424242	hypothetical protein MGC13102	AA337476	Hs.347408	4.9	1921 6243
	453392	SRY (sex determining region Y)-box 11	U23752	Hs.32964	4.9	4416 4417 8239
	447270	general transcription factor IIIC, poly	AC002551	Hs.331	4.9	3910 3911 7824
	424765	hypothetical protein FLJ14033 similar t	AA428211	Hs.371383	4.9	1998 6297
	403909	Autosomal Highly Conserved Protein			4.9	4734
55	423464	CSR1 protein	NM_016240	Hs.1 28856	4.8	1809 1810 6165
	439456	hypothetical protein FLJ20980	AI752409	Hs.109314	4.8	3400 7383
	429612	pituitary tumor-transforming 1	AF062649	Hs.252587	4.8	2586 2587 6726
	452526	hypothetical protein MGC3040	W38537	Hs.280740	4.8	4336 8170
	411975	ESTs	AI916058	Hs.144583	4.8	564 5216
60	412359	gb:QV3-LT0048-140200-083-e05 LT0048	Hom AW837985	Hs.56729	4.8	583 5232
	450812	MCF.2 cell line derived transforming se	AB002360	Hs.25515	4.8	4196 4197 8058
	417534	myosin IE	NM_004998	Hs.8 2251	4.8	1131 1132 5660
	426400	Homo sapiens clone 25121 neuronal olfac	M78361	Hs.169743	4.8	2218 6452
	453874	collagen, type XIV, alpha 1 (undulin)	AW591783	Hs.36131	4.8	4456 8270
65	434924	hypothetical protein FLJ13433	AA443164	Hs.23259	4.8	3093 7112
	421483	hypothetical protein MGC11333	NM_003388	Hs.1 04717	4.8	1545 1546 5973
	418007	matrix metalloproteinase 1 (interstitia	M13509	Hs.83169	4.8	1177 1178 5697
	420261	fibroblast growth factor receptor 1 (fm	AW206093	Hs.748	4.8	1440 5897
	451957	Homo sapiens cDNA FLJ13545 fis, clone	P AI796320	Hs.10299	4.8	4265 8112
70	452055	hypothetical protein MGC10858	AI377431	Hs.141693	4.8	4279 8122
	444783	enitlin (Drosophila Scraps homolog), ac	AK001468	Hs.62180	4.8	3722 3723 7672
	456346	ESTs	AW974998	Hs.222430	4.8	4519 8323
	448140	BCM-like membrane protein precursor	AF146761	Hs.20450	4.8	3980 3981 7882
	427474	aggreCAN 1 (chondroitin sulfate proteog	U13192	Hs.2159	4.8	2334 6532
75	418672	ESTs	L44284	Hs.12915	4.8	1266 5763
	426064	Homer, neuronal immediate early gene, 3	BE387014	Hs.166146	4.8	2168 6415
	418327	paired-like homeodomain transcription f	U70370	Hs.84136	4.8	1217 1218 5729
	429351	hypothetical protein FLJ10628	AK001490	Hs.200016	4.8	2549 2550 6701
	431429	reticulan 3	AF072813	Hs.252831	4.8	2783 6867
80	437623	chromosome condensation-related SMC-ass	D63880	Hs.5719	4.8	3275 3276 7269
	409361	sine oculis homeobox (Drosophila) homol	NM_005982	Hs.5 4416	4.8	344 345 5049
	442572	hypothetical protein FLJ22415	AI001922	Hs.135121	4.8	3569 7540
	433797	ESTs	AA609579	Hs.112724	4.8	3003 7039
	451052	Homo sapiens cDNA: FLJ22165 fis, clone	AA281504	Hs.24444	4.8	4208 8068
85	421535	phosphorylformylglycinamide synth	AB002359	Hs.105478	4.8	1557 1558 5981
	442619	ESTs, Weakly similar to AF164793 1 prot	AA447492	Hs.20183	4.8	3575 7545
	428648	potassium voltage-gated channel, subfam	AF052728	Hs.188021	4.7	2459 2460 6632

	400615	Target Exon		4.7	4634
	446497	ESTs	AV656647	Hs.34226	3841 7766
	410422	Homo sapiens, clone MGC:15203, mRNA, co	AL042014	Hs.63348	462 5136
5	432842	hypothetical protein MGC4485	AW674093	Hs.334822	2911 6966
	435021	ESTs	AA922192	Hs.73962	3097 7116
	450755	ESTs	AA010984	Hs.159464	4190 8054
	441266	Homo sapiens, clone IMAGE:3502329, mRNA	H15968	Hs.293845	3505 7480
	425573	serine (or cysteine) proteinase inhibitor	AB006423	Hs.158308	2116 2117 6381
10	415179	gb:HUM091D02B Human fetal brain (TFujw	D80630		916 5493
	422033	claudin 5 (transmembrane protein delete	AW245805	Hs.110903	1626 6031
	447343	ESTs, Highly similar to S02392 alpha-2-	AA256641	Hs.236894	3916 7828
	433209	KIAA1474 protein	AB040907	Hs.278436	2953 2954 6999
	415115	hypothetical protein	AA214228	Hs.127751	910 5489
15	414577	hypothetical protein FLJ20992 similar t	AI056548	Hs.378938	832 5433
	418156	nuclear receptor subfamily 1, group I,	W17056	Hs.83623	1198 5715
	435149	KIAA1150 protein	AW401809	Hs.4779	3110 7128
	416680	brain abundant, membrane attached signa	AW245540	Hs.79516	1022 5578
	434577	Homo sapiens cDNA: FLJ22487 fis, clone	R37316	Hs.179769	3062 7088
20	459674	gb:zp53f03.r1 Stratagene NT2 neuronal p	AA180511		4595 8392
	405267	NM_007116*			4775
	413031	phosphofructokinase, muscle	BE515051	Hs.75160	671 5304
	450065	transcriptional co-activator with PDZ-b	AL050107	Hs.24341	4130 4131 8006
	441440	ESTs	AI807981	Hs.30495	3519 7492
25	433935	13kDa differentiation-associated protei	AF112208	Hs.44163	3018 3019 7052
	447101	ESTs	N72185	Hs.44189	3890 7807
	438089	nuclear receptor subfamily 1, group I,	W05391	Hs.351546	3301 7294
	440086	v-rat simian leukemia viral oncogene ho	NM_005402	Hs.6 906	3450 3451 7432
	434558	ESTs	AW264102	Hs.39168	3061 7087
30	451032	Homo sapiens mRNA; cDNA DKFZp564P116	W03692	Hs.323079	4206 8066
	439579	gb:Homo sapiens full length insert cDNA	AF086400		3408 7391
	434423	LIM domain only 4	NM_006769	Hs.3 844	3054 3055 7081
	409829	lymphocyte-specific protein 1	M33552	Hs.56729	389 390 5083
	439734	cAMP response element-binding protein C	AC005013	Hs.149	3426 7409
35	429305	myelin protein zero-like 1	AF095727	Hs.287832	2542 2543 6695
	408049	desmoplakin (DPI, DPII)	AW076098	Hs.345588	187 4929
	435099	flap structure-specific endonuclease 1	AC004770	Hs.4756	3104 3105 7123
	422110	secreted protein, acidic, cysteine-rich	AI376736	Hs.121555	1648 6045
	433556	calcium/calmodulin-dependent protein ki	W56321	Hs.111460	2987 7026
40	435937	ESTs	AA830893	Hs.119769	3164 7172
	445936	hypothetical protein FLJ22329	BE543594	Hs.367653	3806 7736
	414706	KIAA0097 gene product	AW340125	Hs.76989	854 5449
	441834	KIAA0736 gene product	AL138034	Hs.7979	3539 7511
	445745	KIAA0455 gene product	AB007924	Hs.13245	3796 3797 7727
45	433028	AD-017 protein	AI199144	Hs.283737	2928 6980
	428283	Homo sapiens mRNA; cDNA DKFZp564P116	(f AI439096	Hs.323079	2420 6602
	446142	ESTs	AI754693	Hs.145968	3820 7748
	447598	ESTs	AI799968	Hs.199630	3941 7848
	402812	NM_004930*:Homo sapiens capping protein			4693
50	406672	major histocompatibility complex, class	M26041	Hs.198253	43 44 4820
	441859	interleukin-4 induced gene-1 protein (F	AW194364	Hs.380444	3540 7512
	437188	KIAA1814 protein	AL080221	Hs.375566	3240 7238
	416389	integrin, beta 5	AA180072	Hs.149846	998 5561
	424503	integrin, alpha 5 (fibronectin receptor	NM_002205	Hs.1 49609	1965 1966 6275
55	452242	glycosyltransferase	R50956	Hs.159993	4305 8145
	453280	Homo sapiens mRNA; cDNA DKFZp761C082	(f AL157476	Hs.32913	4410 8233
	421631	Homo sapiens mRNA; cDNA DKFZp434D0720	(f AL137551	Hs.106254	1571 5989
	453884	KIAA0186 gene product	AA355925	Hs.36232	4460 8274
	451050	ESTs	AW937420	Hs.351869	4588 8067
60	428645	ESTs, Weakly similar to 2017205A dihydr	AA431400	Hs.98729	2458 6631
	419983	Homo sapiens mRNA; cDNA DKFZp586E1624	W55956	Hs.94030	1401 5867
	408503	ESTs, Weakly similar to T12552 hypothet	AW119059	Hs.348603	233 4964
	410600	ESTs, Moderately similar to S65657 alph	AW575742	Hs.351676	479 5147
	433882	procollagen-proline, 2-oxoglutarate 4-d	U90441	Hs.3622	3012 3013 7047
65	416914	brain and reproductive organ-expressed	AA344481	Hs.80426	1045 5595
	438411	gb:ys81c10.r1 Soares retina N2b4HR Homo	H91928	Hs.169370	3321 7311
	425082	Inositol 1,4,5-trisphosphate receptor, I	N44238	Hs.102991	2048 6333
	445930	Homo sapiens clone 24747 mRNA sequence	AF055009	Hs.13456	3804 7734
	402794	Target Exon			4691
70	408393	ESTs	AW015318	Hs.143509	219 4953
	425274	minichromosome maintenance deficient (m	BE281191	Hs.155462	2079 6356
	427933	ESTs	AW974643	Hs.190571	2386 6573
	437664	ESTs, Moderately similar to ALU1_HUMAN	AW977714	Hs.380667	3277 7270
	402888	Target Exon			4698
75	439195	gb:yyw28d08.s1 Morton Fetal Cochlea Homo	H89360		3381 7364
	408920	fibronectin leucine rich transmembrane	AL120071	Hs.48998	276 4999
	439593	ESTs	BE073597	Hs.124863	3410 7393
	446659	ESTs	AI335361	Hs.226376	3865 7786
	428513	plexin C1	BE220806	Hs.184697	2451 6625
80	429047	ciliary neurotrophic factor receptor	NM_001842	Hs.1 94774	2507 2508 6668
	421292	ESTs, Weakly similar to ALU1_HUMAN ALU	AI620485	Hs.136753	1523 5959
	453828	ESTs	AW970960	Hs.293821	4444 8262
	407112	ESTs, Weakly similar to ALU7_HUMAN ALU	AA070801	Hs.51615	111 4863
	439737	Homo sapiens mRNA full length insert cD	AI751438	Hs.41271	3427 7410
85	403857	Target Exon			4730
	448595	KIAA0644 gene product	AB014544	Hs.21572	4015 4016 7910
	451678	DKFZP564D0764 protein	AA374181	Hs.26799	4244 8095

	430410	trypsin beta 1	AF099144	Hs.347933	4.5	2689 2690 6799
	400289	matrix metalloproteinase 10 (stromelysin)	X07820	Hs.2258	4.5	3 4 4615
	417640	protein C receptor, endothelial (EPCR)	D30857	Hs.82353	4.5	1143 5669
	429903	cyclin-dependent kinase 5, regulatory subunit	AL134197	Hs.93597	4.5	2616 6746
5	452110	Homo sapiens cDNA FLJ11309 fis, clone P	T47667	Hs.28005	4.5	4290 8132
	445133	ESTs	AW157646	Hs.198689	4.5	3745 7690
	448202	Rho guanine nucleotide exchange factor	AB002292	Hs.20695	4.5	3986 3987 7886
	436808	ESTs	AA731602	Hs.120266	4.5	3217 7218
10	406646	major histocompatibility complex, class	M33600	Hs.375570	4.5	35 37 4816
	440087	hypothetical protein FLJ22678	W28969	Hs.7718	4.5	3452 7433
	442577	ESTs	AA292998	Hs.163900	4.5	3571 7542
	436962	DKFZP5641052 protein	AW377314	Hs.5364	4.5	3229 7228
	424265	hair/enhancer-of-split related with YR	AF173901	Hs.144287	4.5	1927 1928 6247
15	451399	ESTs	AL042110	Hs.10432	4.5	4228 8083
	430209	collagen, type V, alpha 3	AF177941	Hs.235368	4.5	2659 2660 6778
	418526	soluble carrier family 16 (monocarboxylate)	BE019020	Hs.85838	4.5	1251 6752
	425074	Homo sapiens cDNA: FLJ22165 fis, clone	AA495930	Hs.351869	4.5	2045 6331
	435575	triggering receptor expressed on myeloid	AF213457	Hs.44234	4.5	3139 3140 7152
20	402408	NM_030920: Homo sapiens hypothetical pr			4.5	4681
	424308	minichromosome maintenance deficient (S	AW975531	Hs.154443	4.5	1932 6250
	428926	brain-specific angiogenesis inhibitor 1	NM_001702	Hs.1 94654	4.5	2487 2488 6653
	410059	a disintegrin-like and metalloprotease	NM_007038	Hs.5 8324	4.5	416 417 5103
	425272	ESTs, Weakly similar to C35826 hypothet	AA354138	Hs.47209	4.5	2078 6355
25	448786	Homo sapiens cDNA FLJ11881 fis, clone H	BE048842	Hs.179075	4.5	4040 7929
	424909	cell division cycle 25B	S78187	Hs.153752	4.5	2024 2025 6316
	448438	Homo sapiens cDNA FLJ11640 fis, clone H	BE613081	Hs.24654	4.5	4005 7902
	433180	X562 cell-derived leucine zipper-like p	AB038651	Hs.31854	4.5	2949 2950 6997
	437470	hypothetical protein DKFZp547D065	AL390147	Hs.134742	4.5	3267 3268 7262
30	443164	ESTs, Weakly similar to ALU1_HUMAN ALU	AI038503	Hs.55780	4.5	3606 7573
	450254	neuropeptide G protein-coupled receptor	NM_004885	Hs.9 9231	4.5	4147 4148 8018
	417160	proteolipid protein 1 (Pelizaeus-Merzba	N76497	Hs.355807	4.5	1086 5626
	428977	cyclin B2	AK001404	Hs.194698	4.5	2496 6659
	436895	carbonic anhydrase XII	AF037335	Hs.5338	4.5	3224 3225 7224
35	429163	gb:am20a10.s1 Soares_NFL_T_GBC_S1	Homo AA884766		4.5	2521 6678
	440516	cadherin 2, type 1, N-cadherin (neurona	S42303	Hs.161	4.5	3472 3473 7451
	422737	collagen, type III, alpha 1 (Ehlers-Dan	M26939	Hs.119571	4.5	1730 1731 6108
	446388	NP0007 protein	AA292979	Hs.7788	4.5	3837 7763
	412896	major histocompatibility complex, class	AW804157	Hs.375570	4.5	653 6288
40	451938	down-regulator of transcription 1, TBP-	AI354355	Hs.16697	4.5	4263 8110
	411962	gb:zk85d12.r1 Soares_pregnant uterus_Nb	AA099050		4.5	563 5215
	426618	smg GDS-ASSOCIATED PROTEIN	AL036456	Hs.171374	4.5	2259 6477
	421389	Homo sapiens cDNA FLJ12777 fis, clone N	AA531291	Hs.101064	4.5	1537 5968
	407721	dual-specificity tyrosine-(Y)-phosphory	Y12735	Hs.38018	4.5	153 154 4898
45	424330	Homo sapiens cDNA FLJ13596 fis, clone P	AW073953	Hs.34054	4.5	1936 6253
	438855	Homo sapiens mRNA: cDNA DKFZp586J021	(f AW946276	Hs.6441	4.5	3359 7343
	437446	ESTs, Moderately similar to CA1C RAT CO	AA788946	Hs.101302	4.5	3264 7259
	445424	coractin SH3 domain-binding protein	AB028945	Hs.12696	4.5	3767 3768 7706
	433859	ESTs	AW896758	Hs.273789	4.5	3010 7045
50	417512	glycoprotein (transmembrane) nmb	X76534	Hs.82226	4.5	1127 1128 5658
	436159	ESTs	AI056637	Hs.369849	4.5	3172 7178
	404913	NM_024408: Homo sapiens Notch (Drosophi			4.5	4763
	428269	ESTs, Moderately similar to ZN91_HUMAN	W35195	Hs.95659	4.5	2416 6598
	431674	G-protein coupled receptor	AA098901	Hs.301642	4.5	2809 6885
55	446219	ESTs	AI287344	Hs.369078	4.4	3826 7754
	434175	ESTs	AW979081	Hs.165469	4.4	3032 7065
	419733	Homo sapiens cDNA FLJ14415 fis, clone H	AW362955	Hs.356547	4.4	1378 5849
	423872	uronyl 2-sulfotransferase	AB020316	Hs.134015	4.4	1859 1860 6202
	424874	Homo sapiens cDNA FLJ20812 fis, clone A	AA347951	Hs.326413	4.4	2015 6309
60	451460	ESTs	AI797550	Hs.209652	4.4	4232 8087
	411573	KIAA1077 protein	AB029000	Hs.70823	4.4	542 543 5199
	446673	LPAP for lysophosphatidic acid phosphat	NM_016361	Hs.1 5871	4.4	3866 3867 7787
	450835	hypothetical protein FLJ10767	BE262773	Hs.25584	4.4	4199 8060
	450087	MUM2 protein	BE293180	Hs.24379	4.4	4133 8008
65	446522	putative receptor protein	NM_003876	Hs.1 5196	4.4	3850 3851 7773
	409799	phosphoserine phosphatase-like	D11928	Hs.76845	4.4	387 5081
	416737	LIM domain protein	AF154335	Hs.79691	4.4	1028 1029 5582
	422949	gb:EST21657 Adrenal gland tumor Homo	sa AA319435	Hs.283435	4.4	1761 6129
	443114	ESTs	AI033377	Hs.368631	4.4	3602 7569
70	458629	Homo sapiens cDNA FLJ13565 fis, clone P	AW373104	Hs.25094	4.4	4577 8374
	436396	wingless-type MMTV integration site fam	AI683487	Hs.152213	4.4	3184 7189
	415906	Homo sapiens cDNA: FLJ22256 fis, clone	AI751357	Hs.288741	4.4	956 5526
	414931	Homo sapiens mRNA: cDNA DKFZp761M0223	AK000342	Hs.77646	4.4	891 892 5475
	418836	ESTs	AI655499	Hs.161712	4.4	1276 5771
75	413278	interferon-stimulated protein, 15 kDa	BE563085	Hs.833	4.4	695 5322
	400292	NAME OMITTED ... receptor kinase	AA250737	Hs.72472	4.4	5 4616
	425139	protease, serine, 23	AW630488	Hs.25338	4.4	2054 6338
	423332	sorting nexin 7	AI091466	Hs.127241	4.4	1795 6155
	443105	chondroitin sulfate proteoglycan 4 (mel	X96753	Hs.9004	4.4	3600 3601 7568
80	441297	ubiquitin-conjugating enzyme E2E 1 (hom	AW403084	Hs.7766	4.4	3508 7483
	424834	Homo sapiens cDNA FLJ10570 fis, clone N	AK001432	Hs.153408	4.4	2009 6304
	422573	Integrin, alpha V (vitronectin recepto	AW297985	Hs.295726	4.4	1704 6088
	447200	Homo sapiens cDNA FLJ14028 fis, clone H	BE543146	Hs.281434	4.4	3899 7815
	438540	low density lipoprotein receptor-relate	AB017498	Hs.6347	4.4	3343 3344 7329
	454024	hypothetical protein FLJ23403	AA993527	Hs.293907	4.4	4481 8290
85	456940	ESTs	H46986	Hs.31861	4.4	4534 8336
	409124	N-acetylglucosaminidase, alpha- (Sanfil	AW292809	Hs.50727	4.4	307 5023

438274	ESTs	AI918906	Hs.55080	4.4	3313 7304
417819	ESTs	AI253112	Hs.133540	4.4	1160 5683
413020	gb:yr31h09.r1 Soares fetal liver spleen	R98736		4.4	670 5303
419086	Kallmann syndrome 1 sequence	NM_000216	Hs.8 9591	4.4	1300 1301 5789
433075	sortilin 1	NM_002959	Hs.3 51872	4.4	2936 2937 6987
452461	transcription factor	N78223	Hs.108106	4.4	4333 8167
445547	galactosylceramidase (Krabbe disease)	D86181	Hs.273	4.3	3782 3783 7717
444838	ESTs	AV651680	Hs.208558	4.3	3728 7675
414416	hypothetical protein MGC2721	AW409985	Hs.76084	4.3	813 5417
408449	dynamitin 1	NM_004408	Hs.1 66161	4.3	224 225 4958
425289	interferon, gamma-inducible protein 16	AW139342	Hs.155530	4.3	2082 6358
426265	ESTs	AA421069	Hs.97896	4.3	2189 6432
450222	FATA box binding protein (TBP)-associat	U75308	Hs.24644	4.3	4143 4144 8016
450385	synuclein, alpha interacting protein (s	AI631024	Hs.24948	4.3	4162 8030
416498	potassium channel, subfamily K, member	U33632	Hs.79351	4.3	1007 1008 5568
410268	six transmembrane epithelial antigen of	AA316181	Hs.61635	4.3	441 5120
438913	ESTs	AI380429	Hs.172445	4.3	3364 7347
410055	gene for serine/threonine protein kinas	AJ250839	Hs.58241	4.3	414 415 5102
430547	diacylglycerol kinase, iota	NM_004717	Hs.2 42947	4.3	2707 2708 6811
430030	lectin, galactoside-binding, soluble, 1	BE300094	Hs.227751	4.3	2641 6764
406627	ESTs	T64904	Hs.163780	4.3	30 4812
450001	solute carrier family 6 (neurotransmitt	NM_001044	Hs.4 06	4.3	4127 4128 8004
427578	ESTs, Highly similar to TUL3_HUMAN TUBB	AI591305	Hs.169084	4.3	2347 6541
417791	ESTs	AW965339	Hs.44269	4.3	1158 5681
426250	Homo sapiens cDNA FLJ11752 fis, clone H	BE243154	Hs.183702	4.3	2188 6431
409893	minichromosome maintenance deficient (S	AW247090	Hs.57101	4.3	397 5088
403908	Autosomal Highly Conserved Protein			4.3	4733
426316	meningioma (disrupted in balanced trans	NM_002430	Hs.2 68515	4.3	2203 2204 6441
439402	ESTs	W02753	Hs.103002	4.3	3395 7378
410275	transcription factor AP-2 gamma (activa	U85658	Hs.61796	4.3	445 446 5123
421802	Homo sapiens, Similar to CGI-78 protein	BE261458	Hs.108408	4.3	1595 6007
426365	RNA binding motif protein 8B	AA376667	Hs.380056	4.3	2212 6447
426207	HSPC182 protein	BE390657	Hs.30026	4.3	2186 6429
433036	ESTs	AA574091	Hs.105964	4.3	2929 6981
416640	neuron-specific protein	BE262478	Hs.13406	4.3	1019 5576
412723	hypothetical protein AF301222	AA648459	Hs.335951	4.3	634 5271
446548	ESTs	AI769392	Hs.200215	4.3	3856 7777
422526	ESTs	AA311763	Hs.131056	4.3	1695 6081
422656	UIM homeobox protein 2	AI870435	Hs.1569	4.3	1722 6101
452223	hypothetical protein MGC2827	AA425467	Hs.8035	4.3	4302 8142
433800	lung type-I cell membrane-associated gl	AI034361	Hs.135150	4.3	3004 7040
408447	Homo sapiens cDNA FLJ11227 fis, clone P	AK002089	Hs.45080	4.3	223 4957
411408	calcium channel, voltage-dependent, L t	U76666	Hs.69949	4.3	534 535 5192
416072	growth associated protein 43	AL110370	Hs.79000	4.3	969 5537
425580	galanin	L11144	Hs.1907	4.3	2118 2119 6382
443907	TYRO protein tyrosine kinase binding pr	AU076484	Hs.9963	4.3	3656 7617
424084	hypothetical protein FLJ23056	AI940675	Hs.20914	4.3	1895 6226
422828	prion protein 2 (doublet)	AL133396	Hs.348821	4.3	1744 1745 6117
435523	membrane-spanning 4-domains, subfamily	T62849	Hs.11090	4.3	3131 7147
409956	inhibin, beta A (activin A, activin AB	AW103364	Hs.727	4.3	400 5091
432787	HSPC054 protein	NM_014152	Hs.2 78946	4.3	2905 2906 6962
422168	S100 calcium-binding protein A7 (psoria	AA586894	Hs.112408	4.3	1654 6050
439165	KCNQ1 overlapping transcript 1	AA029517	Hs.95162	4.3	3379 7362
406431	NM_024867*Homo sapiens hypothetical pr			4.3	4806
422609	sialidase 1 (lysosomal sialidase)	Z46023	Hs.118721	4.3	1711 6093
435256	cytokine-like protein C17	AF193766	Hs.13872	4.3	3116 3117 7133
435520	HNOEL-iso protein	AA297990	Hs.9315	4.3	3130 7146
453876	ESTs, Weakly similar to I38022 hypothet	AW021748	Hs.110406	4.3	4457 8271
451752	KIAA1171 protein	AB032997	Hs.353087	4.3	4252 4253 8102
410188	hypothetical protein DKFZp586H0623	AL096739	Hs.107260	4.3	429 430 5113
416283	vascular endothelial growth factor C	NM_005429	Hs.7 9141	4.3	985 986 5551
416065	proliferating cell nuclear antigen	BE267931	Hs.78996	4.3	968 5536
408331	dual specificity phosphatase 12	NM_007240	Hs.4 4229	4.3	211 212 4948
438337	hypothetical protein FLJ11196	AK002058	Hs.6166	4.3	3317 3318 7308
429687	nucleoporin 153kD	AI675749	Hs.211608	4.3	2605 6737
453085	KIAA0251 protein	AW954243	Hs.351573	4.3	4390 8216
411943	ESTs, Weakly similar to S44608 C02F5.6	BE502436	Hs.7962	4.3	562 5214
430299	serine carboxypeptidase 1 precursor pro	W28673	Hs.106747	4.3	2678 6792
435461	ESTs	AI075846	Hs.133996	4.3	3127 7143
423032	RAS p21 protein activator (GTPase activ	AI684746	Hs.119274	4.3	1771 6137
421079	NCK adaptor protein 2	AW404994	Hs.101695	4.3	1504 5943
412652	ESTs	AI801777	Hs.352554	4.3	626 5264
418102	hypothetical protein MGC15880	R58958	Hs.26608	4.3	1192 5709
422938	centromere protein A (17kD)	NM_001809	Hs.1594	4.3	1759 1760 6128
428305	cartilage linking protein 1	AA446628	Hs.2799	4.3	2426 6607
432241	KIAA1151 protein	AI937060	Hs.6298	4.3	2858 6922
433969	ESTs, Weakly similar to PC4395 mucin 3	AW207279	Hs.271786	4.3	3020 7053
441224	calumenin	AU076964	Hs.7753	4.3	3504 7479
435472	triggering receptor expressed on myeloid	AW972330	Hs.283022	4.3	3129 7145
413672	gb:QV0-HT0368-310100-091-h10 HT0368	Hom BE156536	Hs.353632	4.3	737 5353
410552	fibroblast growth factor receptor 1 (fm	X66945	Hs.748	4.3	474 475 5144
448775	nudix (nucleoside diphosphate linked mo	AB025237	Hs.388	4.3	4036 4037 7927
435837	Homo sapiens cDNA FLJ11431 fis, clone H	AI689210	Hs.187276	4.2	3156 7165
452698	chemokine (C-C motif) receptor 1	NM_001295	Hs.3 01921	4.2	4343 4344 8177
431825	ESTs	AI983564	Hs.292917	4.2	2826 6899
409021	fatty acid binding protein 3, muscle an	AA156640	Hs.49881	4.2	295 5014

	453905	LIM domain kinase 1	NM_002314	Hs.3 6566	4.2	4462 4463 8276
	450414	KIAA1716 protein	AI907735	Hs.21446	4.2	4165 8033
	440105	Homo sapiens clone 23809 mRNA sequence	AA694010	Hs.6932	4.2	3455 7435
	435142	ESTs	AI051957	Hs.110122	4.2	3109 7127
5	446006	deafness, autosomal dominant 5	NM_004403	Hs.1 3530	4.2	3808 3809 7738
	447674	cyclin-dependent kinase 2	BE270640	Hs.19192	4.2	3947 7854
	413821	ESTs, Weakly similar to C4HU complement	AA844126	Hs.55964	4.2	746 5361
	453910	Kruppel-like zinc finger protein GLS2	AL133794	Hs.16313	4.2	4464 8277
	416137	ubiquitin activating enzyme E1-like pro	BE279513	Hs.278607	4.2	977 5544
10	407116	ESTs	AA130986	Hs.271627	4.2	112 4864
	417387	ESTs	AW021102	Hs.21509	4.2	1108 5646
	412719	ESTs	AW016610	Hs.816	4.2	633 5270
	444001	ESTs, Moderately similar to S65657 alph	AI095087	Hs.152299	4.2	3667 7626
	443351	Homo sapiens cDNA FLJ13471 fis, clone P	AW016783	Hs.30799	4.2	3617 7583
15	432235	ESTs	AA531129	Hs.190297	4.2	2855 6920
	429978	ribosomal protein S6	AA249027	Hs.353161	4.2	2629 6757
	401621	NM_025193:Homo sapiens 3 beta-hydroxy-d			4.2	4656
	415321	ESTs, Weakly similar to A47582 B-cell g	R54203	Hs.268723	4.2	922 5498
	436449	ESTs	AI418027	Hs.120361	4.2	3189 7194
20	416860	actin filament associated protein	D25248	Hs.80306	4.2	1043 5593
	411089	cell division cycle 2-like 1 (PITSLRE p	AA456454	Hs.214291	4.2	513 5173
	403903	C5001632:gij10645308jgbAAG21430.1jAC0			4.2	4731
	420834	ESTs	AA837124	Hs.88780	4.2	1484 5928
	453754	ESTs	AW972580	Hs.172753	4.2	4438 8257
25	431350	ESTs	AI192528	Hs.164537	4.2	2775 6860
	452056	Homo sapiens, clone IMAGE:4054156, mRNA	AW955055	Hs.101150	4.2	4280 8123
	412014	ESTs, Weakly similar to A46010 X-linked	AI620650	Hs.43761	4.2	566 5218
	438867	oplate receptor-like 1	AW451157	Hs.2859	4.2	3362 7345
	448684	hypothetical protein FLJ13390 similar t	AA923142	Hs.24884	4.2	4026 7918
30	450066	ESTs, Weakly similar to I38022 hypothet	H56499	Hs.252692	4.2	4132 8007
	407792	putative secreted ligand homologous to	AI077715	Hs.39384	4.2	162 4906
	448103	hypothetical protein FLJ11362	AA968672	Hs.8929	4.2	3976 7878
	414152	thrombospondin 4	NM_003248	Hs.7 5774	4.2	782 783 5391
	422766	heparan sulfate (glucosamine) 3-O-sulfo	AA334108	Hs.159572	4.2	1735 6111
35	414178	ESTs, Weakly similar to I38022 hypothet	AW957372	Hs.46791	4.2	788 5396
	426890	ESTs	AA393167	Hs.41294	4.2	2283 6494
	421814	thrombospondin 2	L12350	Hs.108623	4.2	1596 1597 6008
	435906	SAR1 protein	AI686379	Hs.110796	4.2	3161 7169
	438461	phosphoserine aminotransferase	AW075485	Hs.286049	4.2	3326 7316
40	439706	ESTs, Weakly similar to DAP1_HUMAN	DEAT AW872527	Hs.59761	4.2	3421 7404
	418117	linker for activation of T cells	AI922013	Hs.83496	4.2	1195 5712
	439815	hypothetical protein FLJ20420	AA206079	Hs.6693	4.2	3433 7416
	419271	ESTs	N34901	Hs.348603	4.2	1324 5808
45	451691	ESTs	AI809278	Hs.208152	4.2	4248 8099
	420900	ESTs	AL045633	Hs.44269	4.2	1490 5933
	440524	ESTs	R71264	Hs.16798	4.2	3474 7452
	431988	protein kinase C, beta 1	AC002302	Hs.349845	4.2	2837 6906
	412580	similar to CABLES [Homo sapiens]	AA113262	Hs.17901	4.2	610 5253
50	457313	transcriptional coactivator	AF047002	Hs.241520	4.2	4544 4545 8345
	416361	ESTs, Weakly similar to CA13_HUMAN	COLL AW204907	Hs.6872	4.2	995 5558
	425077	synovial sarcoma translocation gene on	AB014593	Hs.154429	4.2	2046 2047 6332
	413945	CD14 antigen	NM_000591	Hs.7 5627	4.2	758 759 5371
	427790	hypothetical protein MGC8641	NM_002687	Hs.1 80832	4.2	2369 2370 6560
55	453931	ESTs	AL121278	Hs.25144	4.2	4469 8280
	431410	ESTs	AW299534	Hs.105739	4.2	2781 6865
	410512	hypothetical protein MGC3180	AA085603	Hs.250570	4.2	468 5140
	447726	maltrin 2	AL137638	Hs.19368	4.1	3953 3954 7859
	434826	pyruvate dehydrogenase phosphatase	AF155661	Hs.22265	4.1	3078 3079 7101
	402685	Target Exon			4.1	4687
60	440028	ESTs, Weakly similar to T17227 hypothet	AW473675	Hs.367649	4.1	3446 7428
	428418	ESTs	AI368826	Hs.8768	4.1	2441 6619
	416404	ESTs	AA180138	Hs.107924	4.1	1000 5563
	435181	KIAA1571 protein	AA669339	Hs.28838	4.1	3112 7130
65	442767	ESTs	AI017208	Hs.131149	4.1	3584 7552
	427528	minichromosome maintenance deficient (S	AU077143	Hs.179565	4.1	2341 6537
	456327	ESTs	H68741	Hs.38774	4.1	4518 8322
	437763	tissue inhibitor of metalloproteinase 1	AA469369	Hs.5831	4.1	3285 7278
	458823	ESTs	AW207574	Hs.179501	4.1	4581 8378
70	458997	ESTs	AW937420	Hs.351869	4.1	4588 8384
	444207	cathepsin D (lysosomal aspartyl proteas	AI565004	Hs.374415	4.1	3686 7643
	415812	TATA box binding protein (TBP)-associat	AA077268	Hs.78865	4.1	949 5521
	416823	ESTs	N68454	Hs.16222	4.1	1037 5588
	414907	polo (Drosophila)-like kinase	X90725	Hs.77597	4.1	886 887 5472
75	438454	ESTs	AI377324	Hs.136888	4.1	3324 7314
	432435	ESTs	BE218886	Hs.282070	4.1	2874 6936
	428344	Homo sapiens cDNA FLJ12425 fis, clone M	AW449466	Hs.9299	4.1	2433 6612
	432106	ESTs, Weakly similar to RETROVIRUS-RELA	N58323	Hs.269098	4.1	2842 6910
	408705	HSPCO34 protein	AA312135	Hs.46967	4.1	250 4980
80	409702	eukaryotic translation elongation facto	AI752244	Hs.351558	4.1	380 5075
	412802	aquaporin 1 (channel-forming integral p	U41518	Hs.74602	4.1	645 646 5282
	434095	milk fat globule-EGF factor 8 protein (AA011117	Hs.3745	4.1	3028 7061
	420303	KIAA1474 protein	AA258282	Hs.278436	4.1	1443 5900
	425207	Homo sapiens, clone MGC:3182, mRNA,	com AB014551	Hs.337774	4.1	2065 2066 6346
	448569	signal transducer and activator of tran	BE382657	Hs.21486	4.1	4014 7909
85	431882	engrailed homolog 1	NM_001426	Hs.2 71977	4.1	2832 2833 6903
	437673	ESTs	AW665685	Hs.153034	4.1	3279 7272

405203	NM_002086*:Homo sapiens growth factor r		4.1	4772	
428825	ESTs, Weakly similar to I38022 hypothet	AI084336	Hs.128783	2478 6646	
425966	cyclin F	NM_001761	Hs.1 973	2158 2159 6409	
439496	Homo sapiens, Similar to RIKEN cDNA 111	BE616501	Hs.32343	3402 7385	
443715	cyclin E1	AI583187	Hs.9700	3638 7601	
417426	laminin, beta 1	NM_002291	Hs.8 2124	1119 1120 5654	
416292	nasopharyngeal carcinoma susceptibility	AA179233	Hs.42390	987 5552	
415107	gb:HUM089A11B Clontech human fetal brai	D60154		909 5488	
443950	epithelial membrane protein 3	NM_001425	Hs.9 999	3660 3661 7621	
426413	gb:EST80805 Synovial sarcoma Homo sapie	AA377823		2219 6453	
418514	TOLLIP protein	AW068487	Hs.25413	1248 5749	
414110	gb:601112444F1 NIH_MGC_16 Homo sapiens	BE251752		776 5385	
444024	ESTs	AW205686	Hs.348603	3671 7630	
457396	DKFZP547E1010 protein	Z20964	Hs.323817	4546 8346	
408932	TP53TG3 protein	AW594172	Hs.278513	277 5000	
458806	Homo sapiens PNAS-13 mRNA, complete cds	BE514753	Hs.292057	4580 8377	
447898	6.2 kd protein	AW969638	Hs.380920	3966 7868	
412530	hypothetical protein FLJ13346	AA766268	Hs.266273	600 5246	
439452	B-cell CLL/lymphoma 11B (zinc finger pr	AA918317	Hs.57987	3398 7381	
442328	ESTs, Weakly similar to ALU4_HUMAN ALU	AI952430	Hs.150614	3556 7528	
425133	3-phosphoinositide dependent protein ki	NM_002613	Hs.1 54729	2052 2053 6337	
432539	karyopherin beta 2b, transportin	AL138169	Hs.278378	2885 6946	
433446	ESTs	AW469546	Hs.122116	2979 7020	
449611	ESTs	AI970394	Hs.197075	4100 7981	
425354	complement component 3a receptor 1	U62027	Hs.155935	2093 2094 6365	
439453	thyroid hormone receptor interactor 13	BE264974	Hs.6566	3399 7382	
422320	ESTs, Weakly similar to AAB47496 NG5 [H	AI745249	Hs.23650	1671 6063	
449475	hypothetical protein PP1057	AI348027	Hs.129826	4091 7973	
413950	ESTs	NB B	AA249096	Hs.32793	760 5372
430071	transcription factor 8 (represses inter	AA355986	Hs.380991	2648 6770	
453708	ESTs	AI191811	Hs.54629	4435 8254	
400263	Eos Control		Hs.75309	4613	
443402	elastin (supravalvular aortic stenosis,	U77846	Hs.9295	3619 3620 7585	
407065	gb:H.sapiens DAT1 gene, partial, VNTR	Y10141		103 104 4857	
404063	Target Exon			4737	
433932	neuronal protein	AW954599	Hs.169330	3017 7051	
419081	ESTs	AI798863	Hs.87191	1299 5788	
447072	tyrosylprotein sulfotransferase 1	D61594	Hs.17279	3887 7804	
445413	CGI-147 protein	AA151342	Hs.12677	3765 7704	
439727	Homo sapiens clone 23645 mRNA sequence	R25060	Hs.6651	3424 7407	
432222	gb:an03c03.x1 Stralagene schizo brain S	AI204995		4596 6919	
408915	heptacellular carcinoma novel gene-3 pr	NM_016651	Hs.4 8950	274 275 4998	
417687	ESTs	AI828596	Hs.250691	1147 5672	
453271	ESTs	AA903424	Hs.6786	4409 8232	
443595	PPAR(gamma) angiotensin related protei	AF169312	Hs.9613	3626 3627 7590	
413658	A kinase (PRKA) anchor protein 10	AA055369	Hs.372446	734 5351	
401176	Target Exon			4646	
428976	ras homolog gene family, member I	AL037824	Hs.194695	2495 6658	
441831	PR domain containing 16	AA992586	Hs.302022	3538 7510	
414280	zyxin	BE410769	Hs.75873	796 5403	
404632	NM_022490:Homo sapiens hypothetical pro			4754	
449263	NICE-5 protein	BE560779	Hs.337078	4076 7958	
407688	Human D9 splice variant B mRNA, complet	W25317	Hs.37616	149 4894	
408513	ESTs	AW206468	Hs.103118	234 4965	
437980	KIAA1474 protein	R50393	Hs.278436	3295 7288	
412326	small inducible cytokine A3 (homologous	R07566	Hs.73817	582 5231	
410577	glioma pathogenesis-related protein	X91911	Hs.64639	476 477 5145	
428206	KIAA0836 protein	AB020643	Hs.183006	2405 2406 6590	
448743	KIAA1136 protein	AB032952	Hs.21896	4032 4033 7924	
416062	Homo sapiens cDNA FLJ14609 fis, clone N	AA724811	Hs.334791	967 5535	
445252	Homo sapiens clone 23927 mRNA sequence	AF052109	Hs.12473	3752 7695	
428579	G protein-coupled receptor 64	NM_005756	Hs.1 84942	2454 2455 6628	
433221	KIAA1484 protein	AB040917	Hs.97860	2958 2959 7003	
427584	v-myb avian myeloblastosis viral oncoge	BE410293	Hs.179718	2348 6542	
441648	ESTs	H05734	Hs.30559	3531 7503	
407907	procollagen-lysine, 2-oxoglutarate 5-di	AI752235	Hs.41270	179 4921	
414175	hypothetical protein DKFZp761D112	AI308876	Hs.103849	786 5394	
419326	ESTs	W94915	Hs.42419	1329 5812	
459247	ESTs, Highly similar to T42626 secreted	N46243	Hs.110373	4590 8386	
438685	ESTs	AA814034	Hs.146065	3347 7332	
440080	ESTs	AW051597	Hs.143707	3449 7431	
419222	spermine synthase	AD001528	Hs.89718	1318 1319 5803	
426340	FYN oncogene related to SRC, FGR, YES	Z97989	Hs.169370	2208 6444	
424365	ESTs, Moderately similar to I54374 gene	AI653164	Hs.128665	1938 6255	
428412	ESTs	AA428240	Hs.126083	2440 6618	
407566	Homo sapiens cDNA FLJ12280 fis, clone M	AW068805	Hs.288467	142 4888	
419574	hypothetical protein	AK001989	Hs.91165	1353 1354 5830	
445893	ESTs, Weakly similar to TRHY_HUMAN TRIC	AI610702	Hs.202813	3802 7732	
423811	homeo box C4	AW299598	Hs.50895	1854 6198	
447818	Homo sapiens clone 24670 mRNA sequence	W79940	Hs.355279	3965 7867	
400231	Eos Control		Hs.169476	4603	
451598	ESTs	N29102	Hs.79658	4241 8093	
408482	adenosine A2b receptor	NM_000676	Hs.4 5743	226 227 4959	
425741	Homo sapiens clone 24628 mRNA sequence	AF052152	Hs.129997	2133 6391	
446254	Homo sapiens cDNA FLJ12832 fis, clone N	BE179829	Hs.179852	3830 7757	
442410	ESTs	AW996503	Hs.197680	3559 7531	

408433	ras-related C3 botulinum toxin substrat	AW162931	Hs.45002	4.0	221 4955
445809	phosphoribosyl pyrophosphate synthetase	AA295298	Hs.13339	4.0	3799 7729
409698	short stature homeobox 2	AF022654	Hs.55967	4.0	378 379 5074

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TABLE 9B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

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Pkey	CAT Number	Accession
459702	539529_1	BG207209 BE166299 AJ204995 BG199355 AW969908 AA528756 AW440776 BI044354
458956	81880_1	BE873716 BE907282 AA009992 BE220675 AA345621
415179	1863582_1	D80630 D80896 D80895
459674	118159_1	AW974566 AA649022 BF740489 BF930101 BF930097 BF930102 AA180511
439579	24302_1	AF086400 W73990 W79232
439195	21979_1	AF086037 H89360 H89546
429163	1238297_1	AW974271 AA592975 AA447312 AA884766
411962	2307710_1	AA099050 AA099526 T47733
413020	1485885_1	BE048113 R98736 Z42904
415107	1856205_1	D61323 D60154 D81503 D81360 D60938 D60422 D60251 D81628 D60135
426413	372468_1	AW954494 AA377823 BG219617 BG195685 BG618269 AJ022688
414110	1634167_1	BE253764 BE250764 BE255757 BE251752 BE251925
432222	539529_1	BG207209 BE166299 AJ204995 BG199355 AW969908 AA528756 AW440776 BI044354

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TABLE 9C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

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TABLE 10A

Pkey:	Unique Eos probeset identifier number
Gene name:	UniGene gene title
Accession:	Exemplar Accession number, Genbank accession number
UniGene:	UniGene number
RATIO:	95th percentile of soft tissue sarcoma AIs divided by the 50th percentile of normal soft tissue AIs, where the 10th percentile of normal tissue AIs was subtracted from both the numerator and denominator
SEQ ID #:	nucleic acid and protein sequences provided on CD for search purposes

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Pkey	Gene Name	Accession	UniGene	RATIO	SEQ ID #
426752	titin	X69490	Hs.172004	20.8	2266 2267 6482
400440	nebulin	X83957	Hs.83870	17.8	24 25 4627
417070	titin	Z19077	Hs.172004	16.6	1070 5614
407013	gb:Human nebulin mRNA, partial cds	U35637	Hs.83870	16.2	94 95 4851
406704	myosin, heavy polypeptide 7, cardiac mu	M21665	Hs.929	14.6	55 56 4826
417866	collagen, type XI, alpha 1	AW067903	Hs.82772	13.8	1162 5685
417389	midkine (neurile growth-promoting facto	BE260964	Hs.82045	13.0	1109 5647
410621	titin	AA194329	Hs.172004	12.3	481 5149

	444381	hypothetical protein BC014245	BE387335	Hs.283713	12.0	3697 7652
	432874	melanoma inhibitory activity	W94322	Hs.279651	11.3	2913 6968
	418054	lysyl oxidase-like 2	NM_002318	Hs.8 3354	11.3	1184 1185 5702
5	405001	interleukin enhancer binding factor 1			11.3	4767
	428405	cholinergic receptor, nicotinic, alpha	Y00762	Hs.2266	11.1	2436 2437 6615
	414482	endothelin receptor type A	S57498	Hs.76252	11.0	824 825 5426
	410687	lysyl oxidase-like 1	U24389	Hs.65436	10.4	485 486 5153
	413011	biglycan	AW068115	Hs.821	10.3	669 5302
10	422311	cytokine receptor-like factor 1	AF073515	Hs.114948	10.0	1669 1670 6062
	409633	ESTs	AW449822	Hs.55200	9.9	371 5068
	411296	growth suppressor 1	BE207307	Hs.10114	9.4	524 5183
	438089	nuclear receptor subfamily 1, group I,	W05391	Hs.351546	8.8	3301 7294
	403088	NM_003319: Homo sapiens titin (TTN), mR			8.7	4707-
	422069	titin-cap (teletthin)	AJ010063	Hs.343603	8.7	1635 1636 6037
15	443426	chromosome 20 open reading frame 1	AF098158	Hs.9329	8.4	3621 3622 7586
	438091	nuclear receptor subfamily 1, group I,	AW373062	Hs.351546	8.3	3302 7295
	413666	sprouty (Drosophila) homolog 4	AW604451	Hs.381153	8.3	730 5347
	413278	interferon-stimulated protein, 15 kDa	BE563085	Hs.833	8.2	695 5322
20	414821	Fc fragment of IgG, high affinity Ia, r	M63835	Hs.77424	8.2	876 877 5465
	425397	topoisomerase (DNA) II alpha (170kD)	J04088	Hs.156346	8.2	2099 2100 6369
	423778	flavin containing monooxygenase 2	Y09267	Hs.132821	8.2	1846 1847 6193
	418506	Unknown protein for MGC:29643 (formerly	AA084248	Hs.372651	8.1	1247 5748
	429259	Plakophilin	AA420450	Hs.380088	8.0	2535 6689
25	438746	Human melanoma-associated antigen p97	AJ885815	Hs.184727	7.9	3353 7337
	435523	membrane-spanning 4-domains, subfamily	T62849	Hs.11090	7.8	3131 7147
	422627	transforming growth factor, beta-induce	BE336857	Hs.118787	7.7	1715 6097
	414812	monokine induced by gamma interferon	X72755	Hs.77367	7.6	874 875 5464
	427747	serine/threonine kinase 12	AW411425	Hs.180655	7.6	2365 6557
30	444006	type I transmembrane protein Fn14	BE395085	Hs.334762	7.6	3668 7627
	432481	Intron 1 of collagen, type XI, alpha 1	AW451645	Hs.151504	7.5	2876 6938
	421143	immunoglobulin superfamily containing I	AB024536	Hs.102171	7.5	1510 1511 5949
	452701	glutamine-fructose-6-phosphate transami	NM_005110	Hs.3 0332	7.5	4345 4346 8178
	451099	interleukin 13 receptor, alpha 2	R52795	Hs.25954	7.5	4212 8071
35	425308	receptor tyrosine kinase-like orphan re	M97639	Hs.155585	7.5	2087 2088 6362
	409142	SMC4 (structural maintenance of chromos	AL136877	Hs.50758	7.4	312 313 5027
	428981	ESTs, Weakly similar to ALU2_HUMAN ALU	BE313077	Hs.93135	7.3	2497 6660
	415166	carboxypeptidase Z	NM_003652	Hs.7 8068	7.3	913 914 5491
	452683	progesterone membrane binding protein	AJ089575	Hs.374574	7.3	4341 8175
40	414443	platelet-derived growth factor receptor	AU077268	Hs.76144	7.3	817 5421
	423217	collagen, type VII, alpha 1 (epidermoly	NM_000094	Hs.1 640	7.2	1784 1785 6147
	421508	absent in melanoma 2	NM_004833	Hs.1 05115	7.1	1551 1552 5977
	450447	hypothetical protein P15-2	AF212223	Hs.25010	7.0	4168 4169 8036
	424162	ESTs, Weakly similar to ALU2_HUMAN ALU	AA336229	Hs.93135	7.0	1907 6235
45	446051	ephrin-A3	BE048061	Hs.37054	7.0	3816 7744
	407792	putative secreted ligand homologous to	AJ077715	Hs.39384	6.9	162 4906
	400499	C10001858:g[6679124]ref NP_032759.1 n			6.9	4628
	437206	ESTs, Weakly similar to I38344 titin, c	AW975934	Hs.172004	6.8	3245 7242
	451766	ephrin-B3	NM_001406	Hs.2 6988	6.8	4255 4256 8104
50	418478	cyclin-dependent kinase inhibitor 2A (m	U38945	Hs.1174	6.8	1245 1246 5747
	433577	ESTs	AW007080	Hs.284192	6.8	2989 7028
	418203	CDC28 protein kinase 2	X54942	Hs.83758	6.8	1202 1203 5719
	427337	Fc fragment of IgG, low affinity IIb,	Z46223	Hs.176653	6.7	2318 2319 6521
	409012	DKFZP434I216 protein	AL117435	Hs.49725	6.6	293 294 5013
55	444784	eclonucleotide pyrophosphatase/phosphod	D12485	Hs.11951	6.6	3724 3725 7673
	431183	KDEL (Lys-Asp-Glu-Leu) endoplasmic ret	NM_006855	Hs.250696	6.5	2756 2757 6845
	448672	ESTs	AJ955511	Hs.89582	6.5	4025 7917
	433075	sortilin 1	NM_002959	Hs.3 51872	6.4	2936 2937 6987
	448390	hypothetical protein	AL035414	Hs.21068	6.4	3999 7897
60	413436	sphingosine kinase 1	AF238083	Hs.68061	6.4	721 722 5339
	434149	hypothetical protein MGC5469	Z43829	Hs.244624	6.4	3030 7063
	452363	Homo sapiens, Similar to complement com	AI582743	Hs.94953	6.3	4322 8159
	424870	ESTs	T15545	Hs.244624	6.3	2014 6308
	439285	hypothetical protein FLJ20093	AL133916	Hs.47860	6.3	3389 7372
65	422667	ESTs	H25642	Hs.132821	6.3	1723 6102
	448520	doublecortin and CaM kinase-like 1	AB002367	Hs.21355	6.3	4010 4011 7907
	452291	CDC7 (cell division cycle 7, S. cerevis	AF015592	Hs.28853	6.3	4310 4311 8150
	417355	endothelin receptor type B	D13168	Hs.82002	6.3	1100 1101 5640
	427418	LAT1-3TM protein	AA402587	Hs.356667	6.3	2327 6527
70	437696	hypothetical protein dJ37E16.5	Z83844	Hs.5790	6.2	3281 7274
	428450	KIAA0175 gene product	NM_014791	Hs.1 84339	6.2	2443 2444 6621
	426457	chimerin (chimaerin) 1	AW894667	Hs.380138	6.1	2229 6459
	448595	KIAA0644 gene product	AB014544	Hs.21572	6.1	4015 4016 7910
	418322	cyclin-dependent kinase inhibitor 3 (CD	AA284166	Hs.84113	6.0	1214 5727
75	429903	cyclin-dependent kinase 5, regulatory s	AL134197	Hs.93597	6.0	2616 6746
	408938	ESTs	AA059013	Hs.22607	6.0	279 5002
	417079	interleukin 1 receptor antagonist	U65590	Hs.81134	6.0	1073 1074 5616
	413795	ESTs	AL040178	Hs.142003	6.0	743 5358
	443907	TYRO protein tyrosine kinase binding pr	AU076484	Hs.9963	5.9	3656 7617
80	456534	phospholipase C, beta 3, neighbor pseud	X91195	Hs.100623	5.9	4522 8326
	420162	cyclin-dependent kinase 4	BE378432	Hs.95577	5.8	1422 5883
	447217	neuropilin 2	BE465754	Hs.17778	5.8	3904 7819
	419138	ryanodine receptor 1 (skeletal)	U48508	Hs.89631	5.8	1309 1310 5796
	427378	melanoma antigen, family D, 1	BE515037	Hs.177556	5.8	2322 6523
	424263	L1 cell adhesion molecule (hydrocephalu	M77640	Hs.1757	5.8	1925 1926 6246
85	439668	frizzled (Drosophila) homolog 8	AI091277	Hs.302634	5.8	3414 7397
	412507	EphA4	L36645	Hs.73964	5.7	596 597 5243

	429921	collagen, type XI, alpha 1	AA526911	Hs.82772	5.7	2620 6749
	414555	phospholipase A2, group IIA (platelets,	N98569	Hs.76422	5.7	830 5431
	426968	amphiphysin (Stiff-Mann syndrome with b	U07616	Hs.173034	5.7	2290 2291 6499
5	411021	tilin	F00055	Hs.172004	5.7	508 5169
	424829	nerve growth factor receptor (TNFR supe	NM_002507	Hs.1 827	5.7	2007 2008 6303
	411089	cell division cycle 2-like 1 (PITSLRE p	AA456454	Hs.214291	5.6	513 5173
	435905	KIAA0456 protein	AW997484	Hs.5003	5.6	3160 7168
	447343	ESTs, Highly similar to S02392 alpha-2-	AA256641	Hs.236894	5.6	3916 7828
	400263	Eos Control		Hs.75309	5.6	4613
10	418299	Integrin, beta 2 (antigen CD18 (p95), I	AA279530	Hs.83968	5.5	1212 5725
	448961	ESTs	AI610643	Hs.187285	5.5	4052 7937
	429170	dual specificity phosphatase 4	NM_001394	Hs.2 359	5.5	2524 2525 6680
	404815	ENSP00000251989*:DJ100N22.1 (NOVEL EGF-			5.5	4761
15	425262	GS3955 protein	D87119	Hs.155418	5.5	2076 2077 6354
	421506	thymidine kinase 1, soluble	BE302796	Hs.105097	5.5	1550 5976
	439039	ESTs	AI656707	Hs.48713	5.5	3373 7356
	432994	ESTs	AA573452	Hs.150941	5.5	2922 6976
	418004	aldehyde dehydrogenase 3 family, member	U37519	Hs.87539	5.5	1174 1175 5695
	410223	caldesmon 1 (fast-twitch, skeletal)	S73775	Hs.60708	5.5	433 434 5115
20	422765	baculoviral IAP repeat-containing 5 (su	AW409701	Hs.1578	5.5	1734 6110
	451598	ESTs	N29102	Hs.79658	5.5	4241 8093
	424078	paternally expressed 3	AB006625	Hs.139033	5.5	1893 1894 6225
	400288	Integrin, alpha 5 (fibronectin receptor	X06256	Hs.149609	5.4	1 2 4614
25	416491	parathyroid hormone receptor 1	U17418	Hs.1019	5.4	1005 1006 5567
	452698	chemokine (C-C motif) receptor 1	NM_001295	Hs.3 01921	5.4	4343 4344 8177
	451292	KIAA1295 protein	AB037716	Hs.26204	5.4	4221 4222 8079
	454071	ESTs	AI041793	Hs.42502	5.4	4487 8295
	410011	PFTAIR protein kinase 1	AB020641	Hs.57856	5.4	406 407 5096
30	412939	eukaryotic translation elongation facto	AW411491	Hs.75069	5.3	657 5292
	432691	mitogen-activated protein kinase 7	U29725	Hs.3080	5.3	2897 2898 6956
	448569	signal transducer and activator of tran	BE382657	Hs.21486	5.3	4014 7909
	414477	amplified in osteosarcoma	U41635	Hs.76228	5.3	822 823 5425
	416140	roundabout (axon guidance receptor, Dro	AI918035	Hs.301198	5.3	978 5545
	441389	endocytic receptor (macrophage mannose	AF134838	Hs.7835	5.3	3514 3515 7488
35	447232	interleukin 10 receptor, alpha	AW499834	Hs.327	5.3	3905 7820
	456181	ras inhibitor	L36463	Hs.1030	5.3	4516 4517 8321
	408482	adenosine A2b receptor	NM_000676	Hs.4 5743	5.3	226 227 4959
	425964	progesterone membrane binding protein	AW889928	Hs.9071	5.2	2157 6408
40	421920	gamma-aminobutyric acid (GABA) receptor	BE551245	Hs.1438	5.2	1614 6022
	427700	dual specificity phosphatase 6	AA262294	Hs.180383	5.2	2361 6554
	414024	gb:zm79g08.r1 Stratagene neuroepitheliu	AA134712	Hs.22410	5.2	769 5379
	443960	hypothetical protein FLJ21986	AI093577	Hs.255416	5.2	3663 7623
	421251	enigma (LIM domain protein)	Z28913	Hs.102948	5.2	1521 5957
	419762	ESTs	AI608647	Hs.32374	5.2	1387 5855
45	422175	ESTs, Highly similar to T00391 hypothet	N79885	Hs.6382	5.2	1657 6053
	426485	platelet-derived growth factor receptor	NM_006207	Hs.1 70040	5.1	2238 2239 6465
	429150	smoothed (Drosophila) homolog	AF120103	Hs.197366	5.1	2519 2520 6677
	409430	splicing factor, arginine/serine-rich 5	R21945	Hs.346735	5.1	348 5052
50	418059	gb:zn56d05.s1 Stratagene muscle 937209	AA211586		5.1	1186 5703
	427647	Homo sapiens cDNA FLJ20653 fis, clone K W19744		Hs.180059	5.1	2354 6548
	438937	ESTs	AW952654	Hs.73964	5.1	3367 7350
	449353	ESTs	AA001220	Hs.242947	5.1	4084 7966
	432101	EphA3	AI918950	Hs.123642	5.1	2841 6909
55	418883	acid phosphatase 5, tartrate resistant	BE387036	Hs.1211	5.1	1281 5774
	417115	small nuclear ribonucleoprotein polypep	AW952792	Hs.334612	5.0	1081 5622
	424291	ephrlin-B1	AL120051	Hs.144700	5.0	1931 6249
	435652	uncharacterized hypothalamus protein HB	N32388	Hs.334370	5.0	3142 7154
	410342	Fc fragment of IgE, high affinity I, re	R31350	Hs.743	5.0	453 5129
60	453880	ESTs, Weakly similar to I38022 hypothet	AI803166	Hs.135121	5.0	4458 8272
	419452	PTK7 protein tyrosine kinase 7	U33635	Hs.90572	5.0	1340 1341 5821
	434431	ESTs	AW131454	Hs.168571	5.0	3056 7082
	406621	Immunoglobulin lambda locus	X57809	Hs.181125	5.0	26 27 4810
	419250	U5 snRNP-specific protein, 116 kD	AW770185	Hs.356066	5.0	1322 5806
65	419073	Homo sapiens cDNA FLJ12797 fis, clone N AW372170		Hs.183918	5.0	1296 5786
	440700	guanine nucleotide binding protein (G p	AW952281	Hs.296184	5.0	3481 7458
	417089	Homo sapiens cDNA: FLJ21909 fis, clone H52280		Hs.18612	5.0	1077 5619
	432211	hypothetical protein FLJ10986	BE274530	Hs.273333	5.0	2852 6917
	412972	ESTs	AA771898	Hs.33412	4.9	663 5296
70	414883	CDC28 protein kinase 1	AA926960	Hs.348669	4.9	885 5471
	427557	plasminogen activator, urokinase recept	NM_002659	Hs.1 79657	4.9	2343 2344 6539
	439706	ESTs, Weakly similar to DAP1_HUMAN DEAT	AW872527	Hs.59761	4.9	3421 7404
	452682	progesterone membrane binding protein	AA456193	Hs.374574	4.9	4340 8174
	446291	interferon, gamma-inducible protein 30	BE397753	Hs.14623	4.9	3833 7760
75	418741	ESTs, Weakly similar to S41044 chromoso	H83265	Hs.8881	4.9	1272 5767
	448379	KIAA1130 protein	AI097463	Hs.21035	4.9	3995 7894
	447198	ESTs	D61523	Hs.283435	4.9	3898 7814
	412926	macrophage myristoylated alanine-rich C	AI879076	Hs.75061	4.9	655 5290
80	411263	kinesin-like 6 (mitotic centromere-asso,	BE297802	Hs.69360	4.9	523 5182
	407239	leukocyte immunoglobulin-like receptor,	AA076350	Hs.67846	4.9	129 4879
	439453	thyroid hormone receptor interactor 13	BE264974	Hs.6566	4.9	3399 7382
	413031	phosphofructokinase, muscle	BE515051	Hs.75160	4.8	671 5304
	418526	solute carrier family 16 (monocarboxyli	BE019020	Hs.85838	4.8	1251 5752
	410422	Homo sapiens, clone MGC:15203, mRNA, co	AL042014	Hs.63348	4.8	462 5136
	429470	guanine nucleotide binding protein (G p	AI878901	Hs.203862	4.8	2564 6711
85	445930	Homo sapiens clone 24747 mRNA sequence	AF055009	Hs.13456	4.8	3804 7734
	425525	ESTs	AA358883	Hs.23871	4.8	2111 6377

	443623	complement component 1, q subcomponent, AA345519	Hs.9541	4.8	3631 7594
	4417421	nuclear receptor subfamily 4, group A, AL138201	Hs.82120	4.8	1118 6653
	449579	ESTs, Weakly similar to T46425 hypothet AW207260	Hs.134014	4.8	4097 7978
5	450296	hepatocyte growth factor-regulated tyro AL041949	Hs.24756	4.8	4153 8023
	453905	UIM domain kinase 1 NM_002314	Hs.3 6566	4.8	4462 4483 8276
	418532	neurotrophic tyrosine kinase, receptor, F00797	Hs.374321	4.8	1252 5753
	443402	elastin (supraaortic stenosis, U77846	Hs.9295	4.8	3619 3620 7585
	431385	membrane-spanning 4-domains, subfamily BE178536	Hs.11090	4.8	2779 6863
10	425003	apurinic/apurimidine endonuclease/APEX AF119046	Hs.154149	4.8	2038 2039 6326
	410781	ESTs AI375672	Hs.165028	4.8	495 5159
	420261	fibroblast growth factor receptor 1 (fm AW206093	Hs.748	4.8	1440 5897
	452110	Homo sapiens cDNA FLJ11309 fis, clone P T47667	Hs.28005	4.7	4290 8132
	419066	PRO1073 protein Z98492	Hs.203862	4.7	1295 5785
15	448386	KIAA1329 protein AB037750	Hs.21061	4.7	3997 3998 7896
	449029	solute carrier family 7 (cationic amino N28889	Hs.22891	4.7	4058 7942
	451752	KIAA1171 protein AB032997	Hs.353087	4.7	4252 4253 8102
	416737	UIM domain protein AF154335	Hs.78691	4.7	1028 1029 5582
	430280	interleukin 7 receptor AA361258	Hs.237858	4.7	2673 6787
20	429345	hypothetical protein R11141	Hs.199695	4.7	2548 6700
	425514	Integrin, alpha 10 AF112345	Hs.158237	4.7	2108 2109 6375
	449523	chemokine (C-C motif) receptor 5 NM_000579	Hs.5 4443	4.7	4094 4095 7976
	422599	non-metastatic cells 1, protein (NM23A) BE387202	Hs.118638	4.7	1710 6092
	409098	pleckstrin homology, Sec7 and coiled/co AA132672	Hs.7984	4.7	303 5020
25	412641	heat shock 90kD protein 1, beta M16660	Hs.74335	4.7	620 621 5260
	424982	phosphorylase, glycogen U94777	Hs.351580	0.0	2036 2037 6325
	400991	Target Exon		4.7	4641
	413441	Src-like-adaptor AI929374	Hs.75367	4.7	723 5340
	422609	sialidase 1 (lysosomal sialidase) Z46023	Hs.118721	4.6	1711 6093
30	424442	ESTs, Weakly similar to ZN91_HUMAN ZINC AW051949	Hs.90035	4.6	1954 6268
	433895	mitogen-activated protein kinase kinase AI287912	Hs.3628	4.6	3014 7048
	410711	KIAA0318 protein AB002316	Hs.65746	4.6	489 490 5155
	435232	cyclin-dependent kinase inhibitor 2C (p NM_001262	Hs.4 854	4.6	3114 3115 7132
	424512	integrin, beta 5 X53002	Hs.149846	4.6	1968 1969 6277
35	421707	lectomedin-2 NM_014921	Hs.1 07054	4.6	1581 1582 5995
	451050	ESTs AW937420	Hs.351869	4.6	4588 8067
	447200	Homo sapiens cDNA FLJ14028 fis, clone H BE543146	Hs.281434	4.6	3899 7815
	424503	Integrin, alpha 5 (fibronectin receptor NM_002205	Hs.1 49609	4.6	1965 1966 6275
	447359	adenylate kinase 5 NM_012093	Hs.1 8268	4.6	3918 3919 7830
40	437763	tissue inhibitor of metalloproteinase 1 AA469369	Hs.5831	4.6	3285 7278
	448775	nudix (nucleoside diphosphate linked mo AB025237	Hs.388	4.6	4036 4037 7927
	419088	Integrin, beta 8 AI538323	Hs.380684	4.6	1303 5791
	414809	transferrin receptor (p90, CD71) AI434699	Hs.77356	4.6	873 5463
	448030	membrane-spanning 4-domains, subfamily N30714	Hs.325960	4.6	3971 7873
45	419693	FXD domain-containing ion transport re AA133749	Hs.301350	4.6	1371 5844
	417098	frizzled (Drosophila) homolog 7 AB017365	Hs.173859	4.6	1078 1079 5620
	414907	polo (Drosophila)-like kinase X90725	Hs.77597	4.6	886 887 5472
	414561	Homo sapiens amino acid transport syste AI054813	Hs.195155	4.6	831 5432
	400262	Eos Control	Hs.75309	4.6	4612
50	428484	solute carrier family 7 (cationic amino AF104032	Hs.184601	4.6	2449 2450 6624
	447674	cyclin-dependent kinase 2 BE270640	Hs.19192	4.6	3947 7854
	411027	leukocyte immunoglobulin-like receptor, AF072099	Hs.67846	4.5	509 510 5170
	422034	Ets2 repressor factor AC006486	Hs.333069	4.5	1627 1628 6032
	447321	Homo sapiens cDNA FLJ14028 fis, clone H AW271217	Hs.281434	4.5	3915 7827
55	425741	Homo sapiens clone 24628 mRNA sequence AF052152	Hs.129997	4.5	2133 6391
	451811	hypothetical protein MGC1136 AA663485	Hs.8719	4.5	4259 8106
	435575	triggering receptor expressed on myeloi AF213457	Hs.44234	4.5	3139 3140 7152
	412773	similar to vaccinia virus HindIII K4L O H15785	Hs.74573	4.5	639 5276
	447898	6.2 kd protein AW969638	Hs.380920	4.5	3966 7868
60	409799	phosphoserine phosphatase-like D11928	Hs.76845	4.5	387 5081
	417640	protein C receptor, endothelial (EPCR) D30857	Hs.82353	4.5	1143 5669
	416982	creatine kinase, mitochondrial 2 (sarco J05401	Hs.80691	4.5	1055 1056 5602
	427274	colony stimulating factor 1 receptor, f NM_005211	Hs.1 74142	4.5	2313 2314 6517
	410290	hypothetical protein DKFZp564A176 AA402307	Hs.322844	4.5	449 5126
65	413048	mannose receptor, C type 1 M93221	Hs.75182	4.4	672 673 5305
	444143	ESTs, Moderately similar to A56194 thro AW747996	Hs.160999	4.4	3679 7637
	425082	Inositol 1,4,5-triphosphate receptor, I N44238	Hs.102991	4.4	2048 6333
	429455	CD209 antigen AI472111	Hs.278694	4.4	2563 6710
	421917	KIAA1020 protein AB028943	Hs.109445	4.4	1612 1613 6021
70	445033	cyclin-dependent kinase inhibitor 2B (p AV652402	Hs.72901	4.4	3740 7685
	452203	transporter 1, ATP-binding cassette, su X57522	Hs.352018	4.4	4298 4299 8140
	446566	membrane-spanning 4-domains, subfamily H95741	Hs.17914	4.4	3857 7778
	409512	melanoma differentiation associated pro AW979187	Hs.293591	4.4	354 5057
	456629	histone deacetylase 3 AW891965	Hs.367942	4.4	4526 8329
75	425776	parathyroid hormone receptor 2 U25128	Hs.159499	4.4	2138 2139 6394
	439963	platelet-activating factor acetylhydrol AW247529	Hs.6793	4.4	3441 7423
	414280	zyxin BE410769	Hs.75873	4.4	796 5403
	451820	ESTs AW058357	Hs.199248	4.4	4260 8107
	416084	deoxythymidylate kinase (thymidylate ki L16991	Hs.79006	4.3	972 973 5540
80	424905	NIMA (never in mitosis gene a)-related NM_002497	Hs.1 53704	4.3	2022 2023 6315
	425770	spastic ataxia of Charlevoix-Saguenay (NM_014363	Hs.1 59492	4.3	2136 2137 6393
	434826	pyruvate dehydrogenase phosphatase AF155661	Hs.22265	4.3	3078 3079 7101
	426265	ESTs AA421069	Hs.97896	4.3	2189 6432
	410240	synaptotagmin 2 AL157424	Hs.61289	4.3	437 5117
	433028	AD-017 protein AI199144	Hs.283737	4.3	2928 6980
85	436856	ESTs AI469355	Hs.127310	4.3	3220 7221
	407603	Homo sapiens, clone IMAGE:4299322, mRNA AW955705	Hs.62604	4.3	144 4890

439223	UL16 binding protein 2	AW238299	Hs.250618	4.3	3383 7366
425289	interferon, gamma-inducible protein 16	AW139342	Hs.155530	4.3	2082 6358
431429	reticulin 3	AF072813	Hs.252831	4.3	2783 6867
438209	aryl-hydrocarbon receptor nuclear trans	AL120659	Hs.6111	4.3	3309 7301
410055	gene for serine/threonine protein kinas	AJ250839	Hs.58241	4.3	414 415 5102
416860	actin filament associated protein	D25248	Hs.80306	4.3	1043 5593
448888	gamma-aminobutyric acid (GABA) A recept	Y09763	Hs.22785	4.3	4055 4056 7940
420173	ESTs	AA256151	Hs.22999	4.3	1426 5886
408331	dual specificity phosphatase 12	NM_007240	Hs.4 4229	4.3	211 212 4948
417920	adenosine monophosphate deaminase 2 (is	S47833	Hs.82927	4.3	1167 1168 5690
402233	NM_030760*:Homo sapiens endothelial dif			4.3	4674
447357	ESTs	AJ375922	Hs.132821	4.3	3917 7829
408056	ephrin-A4	AA312329	Hs.42331	4.3	188 4930
425322	protein kinase, DNA-activated, catalyti	U63630	Hs.155637	4.3	2089 2090 6363
427509	complement component 5 receptor 1 (C5a	M62505	Hs.2161	4.3	2338 2339 6535
451154	ESTs	AA015879	Hs.33536	4.3	4215 8074
414368	uridine monophosphate kinase	W70171	Hs.75939	4.2	809 5414
417426	laminin, beta 1	NM_002291	Hs.8 2124	4.2	1119 1120 5654
431674	G-protein coupled receptor	AA098901	Hs.301642	4.2	2809 6885
453922	budding uninhibited by benzimidazoles 1	AF053306	Hs.36708	4.2	4467 4468 8279
410552	fibroblast growth factor receptor 1 (fm	X66945	Hs.748	4.2	474 475 5144
411213	neuropilin 1	AA676939	Hs.69285	4.2	519 5179
414178	ESTs, Weakly similar to I38022 hypothet	AW957372	Hs.46791	4.2	788 5396
452873	hypothetical protein FLJ10385	AK001247	Hs.30922	4.2	4362 4363 8192
429687	nucleoporin 153kD	AI675749	Hs.211608	4.2	2605 6737
452960	protein tyrosine phosphatase, receptor	AK001335	Hs.31137	4.2	4373 8201
448888	caspase recruitment domain protein 6	AW196663	Hs.200242	4.2	4049 7935
416914	brain and reproductive organ-expressed	AA344481	Hs.80426	4.2	1045 5595
411704	hypothetical protein FLJ10074	AI499220	Hs.71573	4.2	547 5202
415817	protein tyrosine phosphatase, receptor-	U88967	Hs.78867	4.2	950 951 5522
452908	neuronal Shc adaptor homolog	AB001451	Hs.30965	4.2	4369 4370 8198
412723	hypothetical protein AF301222	AA648459	Hs.335951	4.2	634 5271
428259	ESTs	AA424793	Hs.255416	4.2	2415 6597
414774	plasminogen activator, urokinase	X02419	Hs.77274	4.2	869 870 5461
425966	cyclin F	NM_001761	Hs.1 973	4.2	2158 2159 6409
424893	Homo sapiens cDNA FLJ13303 fis, clone	O AW295112	Hs.153648	4.1	2020 6313
437162	thyroid hormone receptor coactivating p	AW005505	Hs.5464	4.1	3239 7237
425354	complement component 3a receptor 1	U62027	Hs.155935	4.1	2093 2094 6365
441965	ESTs	AA972712	Hs.269737	4.1	3544 7516
405516	ENSP00000200457*:Thyroid receptor inter			4.1	4785
413053	ESTs, Moderately similar to KIAA1399 pr	AW963263	Hs.65377	4.1	674 5306
424415	enolase 2, (gamma, neuronal)	NM_001975	Hs.1 46580	4.1	1947 1948 6263
450747	ESTs, Highly similar to 1818357A EWS ge	AI064821	Hs.129953	4.1	4188 8052
419911	BN51 (BHK21) temperature sensitivity co	L15301	Hs.1276	4.1	1393 1394 5861
441834	KIAA0736 gene product	AL138034	Hs.7979	4.1	3539 7511
400252	NM_004651*:Homo sapiens ubiquitin speci		Hs.171501	4.1	4609
446006	deafness, autosomal dominant 5	NM_004403	Hs.1 3530	4.1	3808 3809 7738
416389	integrin, beta 5	AA180072	Hs.149846	4.1	998 5561
415149	calthepsin L	X12451	Hs.78056	4.1	911 912 5490
448633	tubulin, gamma 1	AA311426	Hs.21635	4.1	4021 7913
416224	reticulocalbin 2, EF-hand calcium bindi	NM_002902	Hs.7 9088	4.1	983 984 5550
413658	A kinase (PRKA) anchor protein 10	AA055369	Hs.372446	4.1	734 5351
409132	protein kinase, AMP-activated, beta 2 n	AJ224538	Hs.50732	4.1	309 310 5025
445133	ESTs	AW157646	Hs.198689	4.1	3745 7690
412749	signal sequence receptor, beta (translo	AA378417	Hs.74564	4.1	635 5272
408716	Homo sapiens mRNA for KIAA1769 protein,	AI567839	Hs.151714	4.1	251 4981
443669	ESTs	AI140462	Hs.134587	4.1	3633 7596
424494	phosphatidylinositol-4-phosphate 5-kina	U78575	Hs.149255	4.1	1961 1962 6273
440524	ESTs	R71264	Hs.16798	4.1	3474 7452
449030	Homo sapiens mRNA for FLJ00016 protein,	AI365582	Hs.57100	4.1	4059 7943
425367	protein tyrosine phosphatase, receptor	BE271188	Hs.155975	4.1	2095 6366
424954	tumor protein p53 (Li-Fraumeni syndrome	NM_000546	Hs.1 846	4.1	2031 2032 6322
448610	nei (chicken)-like 1	NM_008157	Hs.2 1602	4.1	4019 4020 7912
440129	ESTs, Weakly similar to S71886 Ste20-li	AA865818	Hs.369523	4.1	3456 7436
414998	oxidised low density lipoprotein (lecti	NM_002543	Hs.7 7729	4.0	898 899 5480
406137	NM_000179*:Homo sapiens mutS (E. coli)			4.0	4802
439246	membrane-associated tyrosine- and threo	AI498072	Hs.351474	4.0	3386 7369
430713	eukaryotic translation elongation facto	AA351647	Hs.2642	4.0	2726 6824
434158	ESTs	T86534	Hs.14372	4.0	3031 7064
436703	RNA binding motif protein, X chromosome	AW880614	Hs.374352	4.0	3211 7212
436576	ESTs	AI458213	Hs.77542	4.0	3203 7205
416062	Homo sapiens cDNA FLJ14609 fis, clone	N AA724811	Hs.334791	4.0	967 5535
456115	titin	F01082	Hs.172004	4.0	4515 8320
427315	Homo sapiens mRNA	AA179949	Hs.175563	0.0	2316 6519
412942	mitogen-activated protein kinase-activa	AL120344	Hs.75074	4.0	658 5293
430233	Homo sapiens mRNA	AW367902	Hs.236443	0.0	2664 6781
446272	hematopoietic cell-specific Lyn substra	BE268912	Hs.14601	4.0	3832 7759
429922	H1 histone family, member 0	Z97630	Hs.226117	4.0	2621 2622 6750
450746	general transcription factor II, I	D82673	Hs.276589	4.0	4187 8051
408805	vaccinia related kinase 1	H59912	Hs.48269	4.0	262 4989
448950	CGI-152 protein	AF288687	Hs.9275	4.0	4050 4051 7936
409208	Integrin, alpha X (antigen CD11C (p150)	Y00093	Hs.172631	4.0	326 327 5038
418918	CD2 antigen (p50), sheep red blood cell	X07871	Hs.89476	4.0	1282 1283 5775
422801	nuclear receptor co-repressor 2	AF125672	Hs.287994	4.0	1739 1740 6114
421846	protein kinase C substrate 80K-H	AA017707	Hs.1432	4.0	1601 6012
427157	thymine-DNA glycosylase	U51168	Hs.173824	4.0	2305 2306 6511

449444	solute carrier family 16 (monocarboxylate)	AW818436	Hs.351306	4.0	4088 7970
415910	chamokine (C-X3-C) receptor 1	U20350	Hs.78913	4.0	957 958 5527
445826	Homo sapiens mRNA	BE313754	Hs.13350	0.0	3800 7730
424441	H2A histone family, member X	X14850	Hs.147097	4.0	1952 1953 6267
428134	ESTs	AA421773	Hs.161008	4.0	2401 6586
452355	G protein-coupled receptor 34	N54926	Hs.29202	4.0	4320 8157
416847	enhancer of filamentation 1 (cas-like d	L43821	Hs.80261	4.0	1039 1040 5590
443163	ESTs	AI082610	Hs.132079	4.0	3605 7572
405203	NM_002086*:Homo sapiens growth factor r			4.0	4772
407844	ESTs	AW073716	Hs.8037	4.0	168 4912
410545	interleukin 11 receptor, alpha	U32324	Hs.64310	4.0	472 473 5143
408847	ESTs	AW290997	Hs.190153	3.9	268 4993
443068	ESTs	AI188710	Hs.374480	3.9	3597 7565
412182	Splicing factor, arginine/serine-rich,	AA205588	Hs.73737	3.9	577 5226
452256	Homo sapiens cDNA FLJ10071 fis, clone	HAK000933	Hs.28661	3.9	4306 8146
449335	STAT induced STAT inhibitor 3	AW150717	Hs.345728	3.9	4081 7963
453018	ESTs, Weakly similar to Trad [H.sapiens	AA054522	Hs.61581	3.9	4379 8207
452888	ephrin-B2	AW955454	Hs.30942	3.9	4366 8195
403668	Target Exon			3.9	4727
431629	interferon, alpha-inducible protein (cl	AU077025	Hs.265827	3.9	2803 6881
407102	glycerol-3-phosphate dehydrogenase 1 (s	AA007629	Hs.348601	3.9	109 4861
418005	collagen, type XV, alpha 1	AI186220	Hs.83164	3.9	1176 5696
415801	Fc fragment of IgG, low affinity IIb, r	R24219	Hs.278443	3.9	948 5520
451253	claudin 10	H48299	Hs.26126	3.9	4220 8078
428245	anaphase promoting complex subunit 11	AF151048	Hs.183180	3.9	2412 2413 6595
424439	ligase I, DNA, ATP-dependent	AA579635	Hs.1770	3.9	1950 6265
423201	growth hormone receptor	NM_000163	Hs.1 25180	3.9	1782 1783 6146
430053	SEC13 (S. cerevisiae)-like 1	AF052155	Hs.227949	3.9	2643 6766
405372	NM_005841:Homo sapiens transporter prot			3.9	4778
452239	protein tyrosine phosphatase, receptor	AW379378	Hs.356289	3.9	4303 8143
450377	KIAA1265 protein	AB033091	Hs.355925	3.9	4160 4161 8029
406519	C10001858.gi 6679124 ref NP_032759.1 n			3.9	4808
413186	solute carrier family 16 (monocarboxylate)	AU077141	Hs.75231	3.9	685 5315
432860	ESTs	AW974077	Hs.283349	3.9	2912 6967
409649	hypothetical protein FLJ20442	AA159216	Hs.55505	3.9	373 5070
458997	ESTs	AW937420	Hs.351869	3.9	4588 8384
451063	HLA-B associated transcript-2	AW163702	Hs.25911	3.9	4209 8069
412810	platelet-derived growth factor receptor	M21574	Hs.74615	3.9	649 650 5285
426156	natriuretic peptide receptor A/guanylat	BE244537	Hs.167382	3.9	2183 6427
416110	hypothetical protein DKFZp564A176	Z42262	Hs.322844	3.9	974 5541
437056	gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_	AI147061		3.9	3234 7233
414260	KIAA0218 gene product	NM_014760	Hs.7 5863	3.9	793 794 5401
429002	junction plakoglobin	AW248439	Hs.2340	3.8	2498 6661
435553	KIAA0176 protein	D79998	Hs.4935	3.8	3134 3135 7149
428479	cell division cycle 2, G1 to S and G2 I	Y00272	Hs.334562	3.8	2447 2448 6623
407202	ESTs	N58172	Hs.109370	3.8	120 4872
439863	paired immunoglobulin-like receptor bet	BE547830	Hs.375208	3.8	3434 7417
409264	KIAA0966 protein	NM_014937	Hs.5 2463	3.8	335 336 5043
423798	solute carrier family 4, sodium bicarbo	AF047033	Hs.132904	3.8	1850 1851 6196
449843	solute carrier family 31 (copper transp	R85337	Hs.24030	3.8	4117 7995
446055	mucoilin 1	AI815981	Hs.12809	3.8	3817 7745
438330	ESTs	AW450572	Hs.257316	3.8	3316 7307
418827	HT021	BE327311	Hs.47166	3.8	1275 5770
419913	ESTs	AW270040	Hs.34455	3.8	1395 5862
422241	protein tyrosine phosphatase, receptor	Y00062	Hs.170121	3.8	1663 1664 6058
423354	calcium channel, voltage-dependent, alp	AB011130	Hs.127436	3.8	1798 1799 6157
433556	calcium/calmodulin-dependent protein ki	W56321	Hs.111460	3.8	2987 7026
402260	NM_001436*:Homo sapiens fibrillar in (FB			3.8	4576
436648	ESTs	R18656	Hs.349845	3.8	3209 7210
400292	NAME OMITTED ... receptor kinase	AA250737	Hs.72472	3.8	5 4616
411756	discoilin domain receptor family, membe	BE294350	Hs.71891	3.8	550 5205
426691	PCTAIRE protein kinase 1	NM_006201	Hs.1 71834	3.8	2262 2263 6480
408486	sodium channel, voltage-gated, type IV,	L04236	Hs.46038	3.8	228 229 4960
424240	calcium/calmodulin-dependent protein ki	AB023185	Hs.143535	3.8	1919 1920 6242
436434	putative 47 kDa protein	N50465	Hs.372732	3.8	3188 7193
412432	ESTs	AA126311	Hs.9879	3.8	585 5234
421487	serine/threonine kinase 23	AF027406	Hs.104865	3.8	1548 1549 5975
400205	NM_006265*:Homo sapiens RAD21 (S. pombe		Hs.81848	3.8	4598
429482	transformation/transcription domain-ass	AF076974	Hs.203952	3.8	2567 2568 6713
415906	Homo sapiens cDNA: FLJ22256 fis, clone	AI751357	Hs.288741	3.8	956 5526
424232	protein kinase C, nu	AB015982	Hs.143460	3.8	1917 1918 6241
417412	interleukin 1 receptor, type I	X16896	Hs.82112	3.8	1116 1117 5652
422105	endosulfine alpha	AI929700	Hs.111680	3.8	1645 6043
424837	N-acetyltransferase, homolog of S. cere	BE276113	Hs.333034	3.8	2010 6305
412970	dual specificity phosphatase 10	AB026436	Hs.177534	3.8	661 662 5295
427217	ESTs	AA399272	Hs.144341	3.8	2310 6514
437275	ESTs, Weakly similar to A47582 B-cell g	AW976035	Hs.292396	3.8	3251 7248
435466	G protein beta subunit-like	BE619165	Hs.29203	3.7	3128 7144
408972	DKFZP586D0919 protein	AL050100	Hs.49378	3.7	287 288 5008
400229	NM_021724*:Homo sapiens nuclear recepto		Hs.276916	3.7	4602
450254	neuropeptide G protein-coupled receptor	NM_004885	Hs.9 9231	3.7	4147 4148 8018
413472	solute carrier family 1 (glial high aff	BE242870	Hs.75379	3.7	725 5342
408105	ESTs, Weakly similar to I38022 hypothet	AW152207	Hs.270977	3.7	190 4932
453613	ESTs	F06838	Hs.374476	3.7	4430 8250
435732	leucine rich repeat and death domain co	AF229178	Hs.123136	3.7	3147 3148 7159
450998	splicing factor 3b, subunit 4, 49kD	BE387614	Hs.25797	3.7	4205 8065

409882	heat shock 27kD protein family, member	AJ243191	Hs.56874	3.7	395 395 5087
424779	CD37 antigen	AL046851	Hs.153053	3.7	1999 6298
426108	programmed cell death 5	AA622037	Hs.166468	3.7	2173 6420
428727	general transcription factor IIH, poly	AF078847	Hs.78452	3.7	2466 2467 6637
439237	ESTs, Weakly similar to A47582 B-cell g	AW408158	Hs.318893	3.7	3384 7367
413407	inositol polyphosphate phosphatase-like	AI356293	Hs.75339	3.7	713 5333
430066	signal recognition particle 72kD	AI929659	Hs.237825	3.7	2647 6769
428293	solute carrier family 1 (neutral amino	BE250944	Hs.183556	3.7	2424 6605
438707	amino acid system N transporter 2	L08239	Hs.5326	0.0	3350 3351 7335
418043	AXL receptor tyrosine kinase	AW377752	Hs.83341	3.7	1182 5700
424909	cell division cycle 25B	S78187	Hs.153762	3.7	2024 2025 6316
418836	ESTs	AI655499	Hs.161712	3.7	1276 5771
425717	retinoic acid receptor, beta	X07282	Hs.171495	3.7	2131 2132 6390
428283	Homo sapiens mRNA	AI439096	Hs.323079	0.0	2420 6602
410017	Homo sapiens clone 24775 mRNA sequence	AW952426	Hs.109438	3.7	408 5097
407330	gb:nn51b05.s1 NCI_CGAP_Kid6 Homo sapien	AA582607	Hs.156289	3.7	136 4884
412760	ESTs	AW379030	Hs.41324	3.7	638 5276
446254	Homo sapiens cDNA FLJ12832 fis, clone	N BE179829	Hs.179852	3.7	3830 7757
437429	Homo sapiens mRNA	H79981	Hs.5613	0.0	3260 7255
416041	hypothetical protein FLJ13287	AA345547	Hs.53263	3.7	964 5532
429379	KIAA0537 gene product	NM_014840	Hs.2 00598	3.7	2552 2553 6703
442831	ESTs	AI798959	Hs.131686	3.7	3586 7554
453327	tryptophanyl-tRNA synthetase	AW500180	Hs.356109	3.7	4412 8235
445701	lymphocyte adaptor protein	AF055581	Hs.13131	3.7	3792 3793 7724
411887	ESTs	AW182924	Hs.128790	3.7	557 5210
420311	Human DNA sequence from clone RP4-53011	AW445044	Hs.38207	3.7	1444 5901
449222	ESTs	AW293984	Hs.197621	3.7	4071 7954
422851	hypothetical protein FLJ22415	AA318060	Hs.135121	3.7	1750 6121
417767	acyloxyacyl hydrolase (neutrophil)	BE242241	Hs.82542	3.7	1155 5678
407235	SAC2 (suppressor of actin mutations 2,	D20569	Hs.169407	3.6	128 4878
452093	Homo sapiens mRNA	AA447453	Hs.27860	0.0	4286 8129
430440	nerve growth factor, beta polypeptide	X52599	Hs.2561	3.6	2637 2698 6804
421524	GDNF family receptor alpha 1	AA312082	Hs.105445	3.6	1556 5980
452882	folate transporter/carrier	AW972990	Hs.196270	3.6	4365 8194
429558	nucleolar autoantigen (55kD) similar to	AI391454	Hs.207251	3.6	2579 6721
409190	sarcoma amplified sequence	AU076536	Hs.50984	3.6	321 5034
411411	ESTs, Weakly similar to KIAA1330 protei	AA345241	Hs.55950	3.6	537 5194
414176	EDG-2 (endothelial differentiation, ly	BE140638	Hs.75794	3.6	787 5395
442875	Homo sapiens clone TCCCTA00142 mRNA seq	BE623003	Hs.23625	3.6	3587 7555
428820	integrin, alpha M (complement component	AA436187	Hs.172631	3.6	2476 6644
429732	lymphocyte cytosolic protein 2 (SH2 dom	U20158	Hs.2488	3.6	2610 2611 6742
422573	integrin, alpha V (vitronectin recepto	AW297985	Hs.295726	3.6	1704 6088
432268	8'-phosphoadenosine 5'-phosphosulfate s	BE311856	Hs.274230	3.6	2861 6925
408243	interleukin 8	Y00787	Hs.624	3.6	207 208 4946
428648	potassium voltage-gated channel, subfam	AF052728	Hs.188021	3.6	2459 2460 6632
423072	solute carrier family 12 (sodium/potass	AI792946	Hs.123116	3.6	1776 6141
412791	ESTs, Weakly similar to S72481 probable	AI131192	Hs.143199	3.6	641 5278
441054	ESTs	AA913591	Hs.126480	3.6	3496 7472
439490	ESTs, Weakly similar to A46302 PTB-asso	AW249197	Hs.100043	3.6	3401 7384
432179	EphB3	X75208	Hs.2913	3.6	2849 2850 6915
447560	phospholipase A2, group IVC (cytosolic,	AF065214	Hs.18858	3.6	3937 3938 7845
454146	calcineurin-binding protein calsarcin-1	BE086548	Hs.381047	3.6	4495 8302
429320	ESTs, Weakly similar to I78885 serine/t	AA449838	Hs.119334	3.6	2545 6697
413900	stress-induced-phosphoprotein 1 (Hsp70/	AW409747	Hs.75612	3.6	751 5365
438014	Homo sapiens cDNA FLJ11971 fis, clone	H N71183	Hs.121806	3.6	3296 7289
435021	ESTs	AA922192	Hs.73962	3.6	3097 7116
434398	serum-inducible kinase (SNK)	AA121098	Hs.3838	3.6	3052 7079
448499	p53-regulated DDA3	BE613280	Hs.77550	3.6	4008 7905
424156	myotubularin related protein 4	AF264717	Hs.141727	3.6	1905 1906 6234
419700	galactokinase 1	AF084935	Hs.92357	3.6	1373 1374 5846
457918	hypothetical protein DKFZp762M186	AL359590	Hs.162604	3.6	4562 4563 8360
413132	protein kinase (cAMP-dependent, catalyt	NM_006823	Hs.7 5209	3.6	683 684 5314

TABLE 10B:

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Pkey	CAT Number	Accession
418059	1164438_1	AA211586 F35799 F29720 AW937408 AW937387 AA211641
437056	428504_3	AW976398 AI147061 AA765223 AA743380 AI803927

TABLE 10C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NI_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
405001	6015406	Minus	104646-104819
403088	8954241	Plus	169894-170193,170504-170806
400499	9796071	Minus	148495-148806

	404815	5911819	Minus	64494-64691
	400991	8096825	Plus	159197-159320
	402233	7690102	Plus	90281-91477
5	405516	9454624	Plus	112707-112876, 113876-113854
	406137	9166422	Minus	30487-31058
	405203	7230116	Plus	125295-125463
	403668	7259739	Plus	39942-40150
	405372	2078459	Minus	10148-10272, 11205-11349, 11436-11560, 1178
10	406519	3962489	Plus	34617-34928
	402260	3399665	Minus	113765-113910, 115653-115765, 116808-11694

TABLE 11A:

15	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
	Seq ID No:	Sequence Identification Number linking the information in Table 11A to the sequences in Table 12

20	Pkey	ExAccn	UnigenelD	Unigene Title	Seq ID No
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain	Seq ID No.1 & 32
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	Seq ID No.2 & 33
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-type 1)	Seq ID No.3 & 34
25	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	Seq ID No.4 & 35
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me)	Seq ID No.5 & 36
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me)	Seq ID No.6 & 37
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me)	Seq ID No.7 & 38
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me)	Seq ID No.8 & 39
30	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	Seq ID No.9 & 40
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	Seq ID No.10 & 41
	404977			Insulin-like growth factor 2 (somatomedin B)	Seq ID No.11 & 42
	450701	H39960	Hs.409224	hypothetical protein XP_098151 (leucine-rich repeat protein)	Seq ID No.12 & 43
	406687	M31126	Hs.396790	matrix metalloproteinase 11 (stromelysin)	Seq ID No.13 & 44
35	415989	AI267700	Hs.4288	ESTs	Seq ID No.14
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose inducible	Seq ID No.15 & 45
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnoid)	Seq ID No.16 & 46
	411789	AF245505	Hs.72157	Adicran	Seq ID No.17 & 47
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	Seq ID No.18 & 48
40	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary osteoblast)	Seq ID No.19 & 49
	426300	U15979	Hs.194693	delta-like homolog (Drosophila)	Seq ID No.20 & 50
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease with thrombospondin type 1 motifs	Seq ID No.21 & 51
	429329	AA456140	Hs.99235	Homo sapiens pannexin 3 (PANX3)	Seq ID No.22 & 52
	428305	AA446628	Hs.2799	cartilage linking protein 1	Seq ID No.23 & 53
45	422871	AL031228	Hs.121509	collagen, type XI, alpha 2	Seq ID No.24 & 54
	441636	AA081846	Hs.407951	Homo sapiens mRNA; cDNA DKFZp566E183 (fr)	Seq ID No.25 & 55
	416399	AF131781	Hs.301989	hypothetical protein FLJ12442	Seq ID No.26 & 56
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	Seq ID No.27 & 57
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	Seq ID No.28 & 58
50	420376	AL137471	Hs.97266	protocadherin 18	Seq ID No.29 & 59
	414477	U41635	Hs.76228	amplified in osteosarcoma	Seq ID No.30 & 60
	457869	AU077186	Hs.108885	Homo sapiens, alpha-1 (VI) collagen	Seq ID No.31 & 61

TABLE 11C:

55	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
		sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
60	NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404977	3738341	Minus	43081-43229

It is understood that the examples described above in no way serve to limit the true scope of this invention to specific embodiments, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each
5 individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of detecting soft tissue sarcoma comprising:
 - a. obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same individual or from a different individual;
 - b. determining the expression of a gene of Tables 1A-11C in the first soft tissue sample and the normal soft tissue sample; and
 - c. comparing the expression of said gene in the first soft tissue sample to expression of said gene in the normal soft tissue sample;
- 10 wherein a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma.
2. The method of Claim 1, wherein said expression is measured using a labeled nucleic acid probe.
- 15 3. The method of Claim 1, wherein said first soft tissue sample and said normal soft tissue sample comprises isolated nucleic acids.
4. The method of Claim 3, wherein the isolated nucleic acids are amplified.
- 20 5. The method of Claim 3, wherein said isolated nucleic acids are mRNA.
6. The method of Claim 1, wherein said first soft tissue sample and said normal soft tissue sample comprises isolated polypeptides or proteins.
- 25 7. The method of Claim 6, wherein said protein expression is evaluated using antibodies.
8. The method of Claim 1, wherein said expression is measured utilizing a biochip.
- 30 9. The method of Claim 8, wherein said biochip comprises nucleic acids complementary to the gene of Tables 1A-11C.

10. The method of Claim 8, wherein said biochip comprises antibodies capable of binding a polypeptide or protein encoded by the gene of Tables 1A-11C.

5 11. An antibody that specifically binds a polypeptide or protein encoded by a gene of Tables 1A-11C.

12. The antibody of Claim 11, wherein the antibody is a humanized antibody.

10 13. The antibody of Claim 11, wherein the antibody is conjugated to an effector moiety.

14. The antibody of Claim 13, wherein the effector moiety is a labeling moiety or a therapeutic moiety.

15 15. A method for treating an individual with soft tissue sarcoma comprising administering an antibody of Claim 13.

20 16. A method for determining the prognosis of a human individual with soft tissue sarcoma cancer comprising determining the expression of a gene of Tables 1A-11C in a soft tissue sample of said human individual at different disease stages, wherein the expression of the gene at different disease stages is used to determine the prognosis of the human individual.

25 17. A method for generating an immune response in an individual to inhibit soft tissue sarcoma cancer comprising:

- a. purifying a polypeptide encoded by a gene of Tables 1A-11C; and
- b. administering said polypeptide of (a) to an individual.

30 18. A method for generating an immune response in an individual to inhibit soft tissue sarcoma cancer comprising:

- a. purifying a nucleic acid of Tables 1A-11C; and
- b. administering said nucleic acid of (a) to an individual.

19. A method for generating a marker for detecting soft tissue sarcoma in a pathological assay, comprising:

- a. purifying a polypeptide encoded by a gene of Tables 1A-11C;
- 5 b. generating a binding partner to the polypeptide of (a); and
- c. labeling the binding partner.

20. The method of Claim 19, wherein the binding partner is an antibody.

10 21. A method for screening for an agent capable of binding to a polypeptide encoded by a gene of Tables 1A-11C comprising:

- a. purifying a polypeptide encoded by a gene of Tables 1A-11C;
- b. combining said polypeptide with a plurality of labeled agents;
- c. capturing said labeled agent(s) bound to the polypeptide of (a)
- 15 d. identifying the captured agent(s) of (d).

22. The method of Claim 21, wherein said capturing utilizes an antibody to the polypeptide of (a).

20 23. A method for screening for an agent capable of binding to a nucleic acid of Tables 1A-11C comprising:

- a. purifying a nucleic acid of Tables 1A-11C;
- b. combining said nucleic acid with a plurality of labeled agents;
- c. capturing said labeled agent(s) bound to the labeled nucleic acid of (a);
- 25 d. identifying the captured agent(s) of (c).

24. A method of screening for a compound that modulates the expression of a gene associated with soft tissue sarcoma comprising:

- a. monitoring the expression level of a gene of Tables 1A-11C in a
- 30 biological system expressing the gene of Tables 1A-11C;
- b. administering a compound to said biological system;
- c. comparing the expression of the gene of (a) prior to and after administering the compound;

wherein a change in expression level prior to and after administering the compound indicates that the compound is capable of modulating the expression of the gene.

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25. A method for detecting the presence of antibodies specific to soft tissue sarcoma, the method comprising:

- a. obtaining a first soft tissue sample from an individual;
- b. contacting said soft tissue sample with a polypeptide encoded by a nucleotide sequence of Tables 1A-11C:

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detecting the binding of antibodies from the soft tissue sample to the polypeptide of (b).